

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:40:39 ; Search time 57.74 Seconds
(without alignments)
8.038 Million cell updates/sec

Title: US-09-821-726-1

Perfect score: 90

Sequence: 1 VKEXKXGKGGPGXPPK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_A8:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	50.0	133	1	US-07-917-722-3
2	45	50.0	878	4	US-09-141-212-8
3	45	50.0	878	4	US-09-561-138-8
4	45	50.0	879	4	US-09-141-212-6
5	45	50.0	879	4	US-09-561-138-6
6	45	50.0	880	2	US-08-916-917-12
7	45	50.0	880	3	US-09-225-170-12
8	45	50.0	880	4	US-09-378-255-6
9	45	50.0	880	4	US-09-141-212-2
10	45	50.0	880	4	US-09-141-212-4
11	45	50.0	880	4	US-09-552-351-4
12	45	50.0	880	4	US-09-251-372-6
13	45	50.0	880	4	US-09-561-138-2
14	45	50.0	880	4	US-09-561-138-4
15	45	50.0	880	4	US-09-715-336-6
16	45	50.0	880	4	US-09-811-241-6
17	45	50.0	880	4	US-09-802-839-4
18	44	48.9	298	3	US-08-767-942A-25
19	43.5	48.3	821	1	US-07-935-311A-4
20	43.5	48.3	821	1	US-08-368-079-4
21	43.5	48.3	821	5	PCT-US93-07996-4
22	42.5	47.2	402	2	US-08-709-979A-3
23	42.5	47.2	402	3	US-08-709-979A-1
24	42.5	47.2	402	3	US-08-709-974A-5
25	42.5	47.2	415	2	US-08-833-642A-5
26	42.5	47.2	415	3	US-08-709-974A-4
27	42.5	47.2	415	4	US-09-069-632-1

28	42.5	47.2	435	1	US-08-361-920-27	Sequence 27, Appl
29	42.5	47.2	435	1	US-08-479-939-27	Sequence 27, Appl
30	42.5	47.2	435	1	US-08-483-432-27	Sequence 27, Appl
31	42.5	47.2	435	4	US-09-069-632-3	Sequence 3, Appl
32	42	46.7	18	3	US-08-630-916A-9	Sequence 9, Appl
33	42	46.7	99	4	US-09-314-268-133	Sequence 133, App
34	41	45.6	311	2	US-08-318-837-9	Sequence 9, Appl
35	41	45.6	738	4	US-08-989-385-1	Sequence 1, Appl
36	40	44.4	147	4	US-09-347-833-10	Sequence 10, Appl
37	40	44.4	377	4	US-09-342-681C-4	Sequence 4, Appl
38	40	44.4	391	4	US-09-342-681C-2	Sequence 2, Appl
39	40	44.4	1912	4	US-08-913-832A-2	Sequence 2, Appl
40	39	43.3	59	2	US-08-469-412A-5	Sequence 5, Appl
41	39	43.3	59	4	US-09-021-715-5	Sequence 5, Appl
42	39	43.3	269	2	US-07-857-224B-14	Sequence 14, Appl
43	39	43.3	269	2	US-07-857-224B-16	Sequence 16, Appl
44	39	43.3	356	2	US-08-700-607-6	Sequence 6, Appl
45	39	43.3	369	2	US-08-424-224-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-917-722-3
; Sequence 3, Application US/07917722
; Patent No. 5534525
; GENERAL INFORMATION:
; APPLICANT: Sondermeyer, Paulus Jacobus Antonius
; APPLICANT: Claessens, Johannes Antonius Joseph
; TITLE OF INVENTION: Chicken Anemia Virus vaccine and
; TITLE OF INVENTION: diagnostic
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; ADDRESSEE: Biotechnology Research Institute
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION NUMBER: US/07917,722
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/605,881
FILING DATE: October 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Donna Bobrowicz
REGISTRATION NUMBER: 32,196
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301)258-5200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-917-722-3

Query Match 50.0%; Score 45; DB 1; Length 133;
Best Local Similarity 41.2%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 2 KEXKXGKGGPGXPPK 18
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Db      9 RDSKAGRRPGGPP 25

RESULT 2
US-09-141-212-8
; Sequence 8, Application US/09141212
; Patent No. 6200777
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,212
; FILING DATE: 27-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97306807.5
; FILING DATE: 01-SEP-1997
; APPLICATION NUMBER: EP 98300687.5
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: GB 9807720.9
; FILING DATE: 08-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 878 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-141-212-8

Query Match      50.0%; Score 45; DB 4; Length 878;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      5 KXXGKGGXPPK 19
       | : | | | |
Db      562 KRSHGTSPGACPPR 576

RESULT 4
US-09-141-212-6
; Sequence 6, Application US/09141212
; Patent No. 6200777
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/141,212
; FILING DATE: 27-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97306807.5
; FILING DATE: 01-SEP-1997
; APPLICATION NUMBER: EP 98300687.5
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: GB 9807720.9
; FILING DATE: 08-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-30012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 879 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-141-212-6

Query Match      50.0%; Score 45; DB 4; Length 878;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      5 KXXGKGGXPPK 19
       | : | | | |
Db      562 KRSHGTSPGACPPR 576

RESULT 3
US-09-561-138-8
; Sequence 8, Application US/09561138
; Patent No. 6258580
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30012-D1
; CURRENT APPLICATION NUMBER: US/09/561,138
; CURRENT FILING DATE: 2000-04-28

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US-09-141-212-6

Query Match 50.0%; Score 45; DB 4; Length 879;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPK 19

I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 5

US-09-561-138-6

; Sequence 6, Application US/09561138

; Patent No. 6258580

; GENERAL INFORMATION:

; APPLICANT: MACPHEE, COLIN

; APPLICANT: PATEL, LISA

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30012-D1

; CURRENT APPLICATION NUMBER: US/09/561,138

; CURRENT FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 09/141,212

; PRIOR FILING DATE: 1998-08-27

; PRIOR APPLICATION NUMBER: EP 97306807.5

; PRIOR FILING DATE: 1997-09-01

; PRIOR APPLICATION NUMBER: EP 98300687.5

; PRIOR FILING DATE: 1998-01-30

; PRIOR APPLICATION NUMBER: GB 9807720.9

; PRIOR FILING DATE: 1998-04-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 879

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-561-138-6

Query Match 50.0%; Score 45; DB 4; Length 879;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPK 19

I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 6

US-09-916-917-12

; Sequence 12, Application US/08916917

; Patent No. 5856132

; GENERAL INFORMATION:

; APPLICANT: Stephens, Len

; APPLICANT: Hawkins, Phillip Thomas

; APPLICANT: Braselmann, Sylvia

; TITLE OF INVENTION: G-BETA-GAMMA REGULATED

; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds, LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 880 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5856132e
US-08-916-917-12

Query Match

Best Local Similarity 50.0%; Score 45; DB 2; Length 880;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKGGGXPXPK 19

I: | | | | |

Db 562 KRSHGTSPGACPPPR 576

RESULT 7

US-09-225-170-12

; Sequence 12, Application US/09225170

; Patent No. 6017763

; GENERAL INFORMATION:

; APPLICANT: Stephens, Len

; APPLICANT: Hawkins, Phillip Thomas

; APPLICANT: Braselmann, Sylvia

; TITLE OF INVENTION: G-BETA-GAMMA REGULATED

; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds, LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/225,170

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/916,917

; FILING DATE: 15-AUG-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Abrams, Samuel B

; REGISTRATION NUMBER: 30,605

; REFERENCE/DOCKET NUMBER: 8549-0006-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 880 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-141-212-4

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 11
 US-09-552-351-4
 ; Sequence 4, Application US/09552351
 ; Patent No. 6225090
 ; GENERAL INFORMATION:
 ; APPLICANT: Lisa Patel
 ; TITLE OF INVENTION: No. 6225090e1 Compounds
 ; FILE REFERENCE: GP-30203
 ; CURRENT APPLICATION NUMBER: US/09/552,351
 ; CURRENT FILING DATE: 2000-04-19
 ; PRIOR APPLICATION NUMBER: US/99-04-19
 ; PRIOR FILING DATE: 1999-04-19
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 880
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-552-351-4

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 12
 US-09-251-372-6
 ; Sequence 6, Application US/09251372
 ; Patent No. 6238886
 ; GENERAL INFORMATION:
 ; APPLICANT: PATEL, LISA
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ratner & Prestia
 ; STREET: P.O. Box 980
 ; CITY: Valley Forge
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19482
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/251,372
 FILING DATE: 16-FEB-1999
 CLASSIFICATION:
 PRIOR APPLICATION NUMBER: 9900823.7
 FILING DATE: 14-JAN-1999
 APPLICATION NUMBER: 9803290.7
 FILING DATE: 16-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GP-30012A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 880 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-251-372-6

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 13
 US-09-561-138-2
 ; Sequence 2, Application US/09561138
 ; Patent No. 6258580
 ; GENERAL INFORMATION:
 ; APPLICANT: MACPHEE, COLIN
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30012-D1
 ; CURRENT APPLICATION NUMBER: US/09/561,138
 ; CURRENT FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 09/141,212
 ; PRIOR FILING DATE: 1998-08-27
 ; PRIOR APPLICATION NUMBER: EP 97306807.5
 ; PRIOR FILING DATE: 1997-09-01
 ; PRIOR APPLICATION NUMBER: EP 98300687.5
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: GB 9807720.9
 ; PRIOR FILING DATE: 1998-04-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 880
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-561-138-2

Query Match 50.0%; Score 45; DB 4; Length 880;
 Best Local Similarity 46.7%; Pred. No. 70;
 Matches 7; Conservative 2; Mismatches 6; Indels 6; Gaps 0;

QY 5 KXXGKGGGXPXPPK 19
 I: | | | | |
 Db 562 KRSRGTSPGACPPPR 576

RESULT 14

Thu Sep 5 11:23:23 2002

Job time: 326 sec

US-09-561-138-4
; Sequence 4, Application US/09561138
; Patent No. 6258580
; GENERAL INFORMATION:
; APPLICANT: MACPHEE, COLIN
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30012-D1
; CURRENT APPLICATION NUMBER: US/09/561,138
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/141,212
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: EP 97306807.5
; PRIOR FILING DATE: 1997-09-01
; PRIOR APPLICATION NUMBER: EP 98300687.5
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: GB 9807720.9
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 880
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-561-138-4

Query Match 50.0%; Score 45; DB 4; Length 880;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKPGGXPPK 19
| : | || |||
DB 562 KRSRGTSPGACPPR 576

RESULT 15
US-09-715-336-6
; Sequence 6, Application US/09715336
; Patent No. 6261819
; GENERAL INFORMATION:
; APPLICANT: Colin Houston MacPhee
; APPLICANT: Lisa Patel
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30173-D1
; CURRENT APPLICATION NUMBER: US/09/715,336
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: UK 9818435.1
; PRIOR FILING DATE: 1998-08-24
; PRIOR APPLICATION NUMBER: UK 9903414.2
; PRIOR FILING DATE: 1999-02-15
; PRIOR APPLICATION NUMBER: 09/378,255
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 880
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-715-336-6

Query Match 50.0%; Score 45; DB 4; Length 880;
Best Local Similarity 46.7%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 KXXGKPGGXPPK 19
| : | || |||
DB 562 KRSRGTSPGACPPR 576

Search completed: September 4, 2002, 16:46:05

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:42:19 ; Search time 124.34 Seconds
(without alignments)
26.435 Million cell updates/sec

Title: US-09-821-726-1

Perfect score: 90

Sequence: 1 VREXKXKXGKPGXPXPPK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: - 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp Unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriaph.*
- 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	58.9	706	16 Q97E35	Q97E35 clostridium
2	49	54.4	1677	11 Q70373	Q70373 mus musculus
3	48	53.3	501	10 Q9FHM0	Q9FHM0 arabidopsis
4	48	53.3	1194	5 Q9W485	Q9W485 drosophila
5	48	53.3	1284	5 Q960F1	Q960F1 drosophila
6	47	52.2	338	10 Q9C9S8	Q9C9S8 arabidopsis
7	47	52.2	355	4 Q9UKR6	Q9UKR6 homo sapien
8	47	52.2	355	4 Q9UJS5	Q9UJS5 homo sapien
9	47	52.2	653	10 Q9XEW2	Q9XEW2 oryza sativ
10	47	52.2	668	10 Q9FRE1	Q9FRE1 oryza sativ
11	47	52.2	774	5 Q9V620	Q9V620 drosophila
12	47	52.2	813	5 Q95TY2	Q95TY2 drosophila
13	47	52.2	941	10 Q9AYJ3	Q9AYJ3 oryza sativ
14	47	52.2	1016	10 Q9AUX7	Q9AUX7 oryza sativ
15	47	52.2	1073	10 Q9XE01	Q9XE01 sorghum bic
16	46	51.1	998	5 Q21301	Q21301 caenorhabdi

17	46	51.1	1283	4	O95451	O95451 homo sapien
18	46	51.1	1289	10	Q9FLQ7	Q9FLQ7 arabidopsis
19	46	51.1	1300	12	O36421	O36421 alcelaphine
20	46	51.1	1321	4	O95291	O95291 homo sapien
21	46	51.1	1594	4	Q9HC84	Q9HC84 homo sapien
22	46	51.1	1994	10	Q9LPI9	Q9LPI9 arabidopsis
23	45	50.0	118	2	O934B5	O934B5 aeromonas s
24	45	50.0	133	12	O90704	O90704 chicken ane
25	45	50.0	494	5	O76941	O76941 drosophila
26	45	50.0	705	4	Q9H624	Q9H624 homo sapien
27	45	50.0	880	4	Q9Y2Y2	Q9Y2Y2 homo sapien
28	45	50.0	889	11	Q9CUD6	Q9CUD6 mus musculu
29	45	50.0	914	5	Q22715	Q22715 caenorhabdi
30	45	50.0	983	4	Q9C0A4	Q9C0A4 homo sapien
31	45	50.0	986	4	Q9H0N3	Q9H0N3 homo sapien
32	45	50.0	1209	4	Q9V4D3	Q9V4D3 homo sapien
33	45	50.0	1518	5	Q9VN58	Q9VN58 drosophila
34	45	50.0	1932	5	O01483	O01483 caenorhabdi
35	45	50.0	2061	5	Q9V0H9	Q9V0H9 drosophila
36	45	50.0	2301	10	Q9ATK5	Q9ATK5 chlamydomon
37	44.5	49.4	543	5	Q9V852	Q9V852 drosophila
38	44.5	49.4	1134	4	Q96JH1	Q96JH1 homo sapien
39	44	48.9	101	2	Q9FBP0	Q9FBP0 streptomyce
40	44	48.9	377	16	O69559	O69559 mycobacteri
41	44	48.9	389	3	Q96039	Q96039 neurospora
42	44	48.9	495	5	Q95YB0	Q95YB0 caenorhabdi
43	44	48.9	551	4	O16630	O16630 homo sapien
44	44	48.9	588	4	Q9BW18	Q9BW18 homo sapien
45	44	48.9	639	4	Q9NV29	Q9NV29 homo sapien

ALIGNMENTS

RESULT	1
Q97E35	PRELIMINARY; PRT; 706 AA.
ID	Q97E35
AC	O1-OCT-2001 (TREMBLrel. 18, Created)
DT	O1-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT	O1-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	ABC-TYPE MULTIDRUG/PROTEIN/LIPID TRANSPORT SYSTEM, ATPASE COMPONENT.
DE	COMPONENT.
GN	CAC3281
OS	Clostridium acetobutylicum.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC	Clostridium.
OX	NCBI_TaxID=1488;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX	MEDLINE=21359325; PubMed=11466286;
RA	Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA	Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA	Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA	Bennett G.N., Koonin E.V., Smith D.R.;
RT	"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
RT	J. Bacteriol. 183:4823-4838(2001).
RL	EMBL: AE007824; AAK81215.1; -.
DR	InterPro: IPR003593; AAA.
DR	InterPro: IPR001140; ABC transporter_tmem.
DR	InterPro: IPR003439; ABC_transportr.
DR	InterPro: IPR001687; ATP_GTP_A.
DR	Pfam: PF00664; ABC_membrane; 1.
DR	Pfam: PF00005; ABC_tran; 1.
DR	SMART: SM00382; AAA; 1.
DR	PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW	Complete proteome.
SQ	SEQUENCE 706 AA; 78003 MW; 14A1B3F2285332DD CRC64;
Query Match	58.9%; Score 53; DB 16; Length 706;

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Best Local Similarity 57.9%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 VKEXKXG--KGPGGXPP 17
   : ||| | ||||| ||
Db 1 MSERKKTGMSKGGGPP 19

RESULT 2
ID 070373 PRELIMINARY; PRT; 1677 AA.
AC 070373;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed-9159189;
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;
RT "Differential display of mRNAs from the atrioventricular region of
RT developing chicken hearts at stages 15 and 21."
RL Front. Biosci. 1:a1-al5(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=99146891; PubMed=10021346;
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,
RA Krob S.L., Schultheiss T.M., Evans S., Lin J.J.-C.;
RT "Requirement of a novel gene, Xin, in cardiac morphogenesis."
RL Development 126:1281-1294(1999).
DR EMBL; AF051945; AAC06023.1; -
DR MGD; MGI:1333878; Xin.
SQ SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;

Query Match 54.4%; Score 49; DB 11; Length 1677;
Best Local Similarity 76.9%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 9 GRGPGGXPP--PK 19
   ||||| |||
Db 575 GRGPGGPPPELPK 587

RESULT 3
ID 09FHM0 PRELIMINARY; PRT; 501 AA.
AC 09FHM0;
DT 01-NAR-2001 (TrEMBLrel. 16, Created)
DT 01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE LEAF-SENESCENCE-RELATED PROTEIN.
GN YLS7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLOMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asanizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC

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clones."
RL DNA Res. 7:31-63(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida S., Masaki I., Nishida I., Watanabe A.;
RT "Isolation and expression analysis of molecular markers for leaf
RT senescence in Arabidopsis thaliana."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB018109; BAB08680.1; -
DR EMBL; AB047810; BAB32887.1; -
SQ SEQUENCE 501 AA; 56525 MW; 7AB4739CBF50FD98 CRC64;

Query Match 53.3%; Score 48; DB 10; Length 501;
Best Local Similarity 53.3%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXKXGPGGXPPPK 19
   || :||| |||
Db 452 KKITRKGPDGQPPQ 466

RESULT 4
ID 09W485 PRELIMINARY; PRT; 1194 AA.
AC 09W485;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CG3125 PROTEIN.
GN CG3125.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Prannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M., M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000)
DR EMBL: AE003435; AAF46073.1;
DR FlyBase: FBgn0029797; CG3125.
SQ SEQUENCE 1194 AA; 127551 MW; F0F2D3A55C7F6C59 CRC64;

Query Match 53.3%; Score 48; DB 5; Length 1194;
Best Local Similarity 52.9%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXKGPGGXPP 17
Db | | | | | | |
610 VAPMKSPNGPGGAPP 626

RESULT 5
ID Q960F1 PRELIMINARY; PRT; 1284 AA.
AC Q960F1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE SD04165P.
GN CG3125.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY052093; AAK93517.1;
SQ SEQUENCE 1284 AA; 137152 MW; E322BE35961525A1 CRC64;

Query Match 53.3%; Score 48; DB 5; Length 1284;
Best Local Similarity 52.9%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXKGPGGXPP 17
Db | | | | | | |
654 VAPMKSPNGPGGAPP 670

RESULT 6
ID Q9C9S8 PRELIMINARY; PRT; 338 AA.
AC Q9C9S8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE PROLINE-RICH PROTEIN PRECURSOR.
GN F25P22.26.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. COLOMBIA;
RC MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Feidblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL: AC012679; AAG52077.1;
DR InterPro: IPR002965; P-rich.extensn.
DR PRINTS: PR01217; PRICHEXTENS.
SQ SEQUENCE 338 AA; 36412 MW; 64362CC1146F09AB CRC64;

Query Match 52.2%; Score 47; DB 10; Length 338;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPPK 19
Db | | | | | |
286 GPGGGPPPR 294

RESULT 7
ID Q9UKR6 PRELIMINARY; PRT; 355 AA.
AC Q9UKR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KRUPPEL-LIKE FACTOR LKLF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=99389728; PubMed=10458913;
RA Wani M.A., Konkright M.D., Jeffries S., Hughes M.J., Lingrel J.B.;
RT "cDNA isolation, genomic structure, regulation, and chromosomal
RT localization of human lung kruppel-like factor.";
RL Genomics 60:78-86(1999).
DR EMBL: AF134053; AAD55891.1;
DR HSSP: P08047; 1SP2.
DR InterPro: IPR002965; P-rich.extensn.
DR InterPro: IPR000822; Znf-C2H2.
DR Pfam: PF00096; ZF-C2H2; 3.
DR PRINTS: PR01217; PRICHEXTENS.
DR SMART: SM00355; Znf-C2H2; 3.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 3.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 355 AA; 37454 MW; CDD1735CC516DE24 CRC64;

Query Match 52.2%; Score 47; DB 4; Length 355;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KGPGGXPPP 18
Db | | | | | |
161 RGPGGRPPP 169

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RESULT 8
Q9UJSS ID Q9UJSS PRELIMINARY; PRT; 355 AA.
AC Q9UJSS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KRÜPPEL-LIKE FACTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.J., Kim M.K., Kim Y.H., Seo J.M., Lee H.M., Chung H.J.,
RA Sohn M.Y., Hwang S.Y., Im S.U., Jung E.J., Kim J.C.;
RT "A catalogue of genes in the human dermal papilla cells as identified
RT by expressed sequence tags.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF205849; AAF13295.1; -.
DR HSSP; P08047; ISP2.
DR InterPro; IPR002965; P-rich_extensn.
DR InterPro; IPR000822; Znf-C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00355; ZnfC2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
KW DNA-binding; Metal-binding; Zinc-finger.
SQ SEQUENCE 355 AA; 37419 MW; D5849C831D676AE1 CRC64;

Query Match 52.2%; Score 47; DB 4; Length 355;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 KPGGXPPP 18
Db 161 RGPGRPPP 169

RESULT 9
Q9XEW2 ID Q9XEW2 PRELIMINARY; PRT; 653 AA.
AC Q9XEW2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RIM2 PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Dong H., Dong J., He Z., Li D.;
RT "A Rice Transposon Protein-like cDNA Is Induced by Magnaporthe grisea
RT (Accession No. AF121139). (PGR99-042).";
RL Plant Physiol. 119:1149-1149(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA He Z., Dong H., Dong J., Li D.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121139; AAD24042.2; -.
DR InterPro; IPR002203; Intein.
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
DR PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.
SQ SEQUENCE 653 AA; 75811 MW; 8639D15235005C20 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 653;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXKXGKPGGXP 16
Db 303 VKDLKVVFGKPGSQP 318

RESULT 11
Q9V620 ID Q9V620 PRELIMINARY; PRT; 774 AA.
AC Q9V620;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG8991 PROTEIN.
GN CG8991.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Harwell T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster".
RL Science 287:2185-2195(2000).
DR EMBL: AE003824; AAF58619.1; -
DR FlyBase; FBgn0033654; CG8991.
DR InterPro; IPR002965; P-rich_extensions.
DR PRINTS; PR01217; PRICHEXTENS.
SQ SEQUENCE 774 AA; 83718 MW; 04A64D97952CF90D CRC64;

Query Match 52.2%; Score 47; DB 5; Length 774;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXGKGGGPGPPP 18
:| | | | | | |
Db 366 QKSPGPGGAPPPP 379

RESULT 12
ID Q95TY2 PRELIMINARY; PRT; 813 AA.
AC Q95TY2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GH22790P.
GN CG8991.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phoumenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY058444; AAL13673.1; -
SQ SEQUENCE 813 AA; 88199 MW; 9B9F9571EA08308C CRC64;

Query Match 52.2%; Score 47; DB 5; Length 813;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KXXGKGGGPGPPP 18
:| | | | | | |
Db 405 QKSPGPGGAPPPP 418

RESULT 13
ID Q9AYJ3 PRELIMINARY; PRT; 941 AA.
AC Q9AYJ3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE TAM1 TRANSPONOSON PROTEIN TNP2.
GN OSJNBA0071K19.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soderlund C.,
RA Kim H., Rambo T., Henry D., Simmons J., Willson R., Johnson D.,
RA Bradshaw H., Du H.;
RT "Rice Genomic Sequence".
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC069324; AAK00419.1; -
SQ SEQUENCE 941 AA; 107815 MW; 6CD3DD2EF0EAB31D CRC64;

Query Match 52.2%; Score 47; DB 10; Length 941;
Best Local Similarity 56.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXKXGKGGGXP 16
||:| | | | | | |
Db 442 VKDLKVVFGKPGSQP 457

RESULT 14
ID Q9AUX7 PRELIMINARY; PRT; 1016 AA.
AC Q9AUX7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSPONOSON PROTEIN.
GN OSJNBB0028C01.11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA Utterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBB0028C01 genomic sequence".
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC079029; AAK38319.1; -
SQ SEQUENCE 1016 AA; 116605 MW; A3CE9E26A82C5C71 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 1016;

Thu Sep 5 11:23:25 2002

Best Local Similarity 56.2%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGXP 16
||: | |||| |
Db 421 VKDLKVVFGKGGSQP 436

RESULT 15

O9XEQ1 PRELIMINARY; PRT: 1073 AA.
AC O9XEQ1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TNP2-LIKE PROTEIN.
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RA Llaca V., Lou A., Young S., Messing J.;
RT "Retrotransposable elements of Sorghum bicolor.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF114171; AAD27566.1; -
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
SQ SEQUENCE 1073 AA; 123055 MW; B46A38EC3882B197 CRC64;

Query Match 52.2%; Score 47; DB 10; Length 1073;

Best Local Similarity 52.6%; Pred. No. 28;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 VKEXKXXGKGGXP 19
||: | || | | | |
Db 617 VKDIKVVFGKGGSEPIPK 635

Search completed: September 4, 2002, 17:01:31
Job time: 1152 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: September 4, 2002, 16:41:24 ; Search time 75.48 Seconds
(without alignments)
24.188 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VREXKXKXGKGGXPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	53	58.9	706	D97303	ABC-type multidrug
2	49	54.4	1677	T14267	Xin protein, stage
3	47	52.2	338	H96765	hypothetical prote
4	47	52.2	687	T34082	hypothetical prote
5	46	51.1	998	T23427	hypothetical prote
6	46	51.1	1300	T03166	probable immediate
7	46	51.1	1321	JE0352	mucin MUC5B, trach
8	46	51.1	1994	D86452	protein F6N18.13 [
9	45	50.0	914	T25220	hypothetical prote
10	45	50.0	1209	T00373	hypothetical prote
11	45	50.0	1922	T25525	hypothetical prote
12	44	48.9	298	A49630	ubiquitin conjugat
13	44	48.9	377	E87022	probable conserved
14	44	48.9	551	E57447	HPBRII-7 protein -
15	44	48.9	669	A97443	hypothetical prote
16	44	48.9	669	AC2661	hypothetical prote
17	44	48.9	719	T52510	hypothetical prote
18	44	48.9	1323	PN0568	connectin 3B - chi
19	43.5	48.3	821	C39983	eps8 protein - mou
20	43	47.8	118	C43256	hypothetical prote
21	43	47.8	533	T10216	hypothetical prote
22	43	47.8	810	I38361	TRPCL protein - hu
23	43	47.8	3124	A40020	collagen alpha 1(X
24	42	46.7	76	T09262	glycine-rich cell
25	42	46.7	152	S46272	another-specific pr
26	42	46.7	161	S12246	another-specific pr
27	42	46.7	188	JH0481	basic proline-rich
28	42	46.7	326	T29810	hypothetical prote
29	42	46.7	326	JS0169	collagen col-14 -

ALIGNMENTS

RESULT 1

D97303

ABC-type multidrug/protein/lipid transport system, ATPase component CAC3281 [imported
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97303
R: Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L
J. Bacteriol. 183, 4823-4838, 2001
A: Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A: Reference number: A96900; MUID:21359325; PMID:21359325
A: Accession: D97303
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-706 <KUR>
A: Cross-references: GB:AE001437; PIDN:AAK81215.1; PID:gl5026358; GSPDB:GN00168
A: Experimental source: Clostridium acetobutylicum ATCC824
C: Genetics:
A: Gene: CAC3281

30	42	46.7	384	2	S51796	vasodilator-stimul
31	42	46.7	440	2	S71795	transcription fact
32	42	46.7	443	2	T33150	hypothetical prote
33	42	46.7	502	2	T35356	probable regulator
34	42	46.7	544	2	I55454	neuroglycan C prec
35	42	46.7	618	2	T42664	hypothetical prote
36	42	46.7	627	2	A70888	hypothetical prote
37	42	46.7	647	2	JE0337	Frizzled-1 protein
38	42	46.7	775	2	E83400	pyrroloquinoline q
39	42	46.7	891	2	T47507	hypothetical prote
40	42	46.7	1168	1	MWAXIC	myosin heavy chain
41	42	46.7	1504	2	T49896	glycine/proline-r1
42	42	46.7	3436	2	S58659	tegument protein 6
43	41.5	46.1	315	2	T29525	hypothetical prote
44	41.5	46.1	822	2	I38728	epidermal growth f
45	41	45.6	22	2	C42856	hypothetical prote

Query Match 58.9%; Score 53; DB 2; Length 706;

Best Local Similarity 57.9%; Pred. No. 5.4;

Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 VREXKXKXG--KGPGGXPP 17

Db 1 MSERKKSTGMSKGGGGPP 19

RESULT 2

T14267

Xin protein, stage early embryo - mouse
C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R: Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1677 <WAB>

A:Cross-references: EMBL:AF051945; NID:g2970645; PID:g2970646; PIDN:AAO6023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match

Best Local Similarity 54.4%; Score 49; DB 2; Length 1677;

Matches 10; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

QY 9 GKGGGXPP--PK 19
||||| || ||
Db 575 GKGGGPPPELPK 587

RESULT 3
H96765
hypothetical protein F25p22.26 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96765
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H96765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <STO>
A:Cross-references: GB:AF005173; NID:g6692747; PIDN:AAF24853.1; GSPDB:GN00141
C:Genetics:
A:Gene: F25p22.26
A:Map position: 1

Query Match 52.2%; Score 47; DB 2; Length 338;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPK 19
||||| |||
Db 286 GPGGGPPR 294

RESULT 4
T34082
hypothetical protein C02F12.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C:Accession: T34082
R:Miller, N.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C02F12.
A:Reference number: Z21473
A:Accession: T34082
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-687 <MIL>
A:Cross-references: EMBL:U41545; PIDN:AAA83191.1; CESP:C02F12.8
C:Genetics:
A:Gene: CESP:C02F12.8
A:Introns: 34/3; 118/3; 288/3; 445/2; 548/1; 634/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C02F12.8

Query Match 52.2%; Score 47; DB 2; Length 687;
Best Local Similarity 52.9%; Pred. No. 37;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 KEXKXXKGKGGXPPP 18
|: || || | |||
Db 545 KDOKKRGKRPVSNPPP 561

RESULT 5
T23427
hypothetical protein K07G5.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23427
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19739
A:Accession: T23427
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-998 <WIL>
A:Cross-references: EMBL:Z71264; PIDN:CAA95828.1; GSPDB:GN00019; CESP:K07G5.1
A:Experimental source: clone K07G5
C:Genetics:
A:Gene: CESP:K07G5.1
A:Map position: 1
A:Introns: 17/1; 56/2; 131/1; 264/2; 297/1; 335/2; 360/3; 551/3; 775/3; 943/2

Query Match 51.1%; Score 46; DB 2; Length 998;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18
||||| |||
Db 945 GPGGAPPP 952

RESULT 6
T03166
probable immediate early protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C:Accession: T03166
R:Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: Z14840; MUID:97404659
A:Accession: T03166
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1300 <ENS>
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 51.1%; Score 46; DB 2; Length 1300;
Best Local Similarity 47.1%; Pred. No. 92;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 KEXKXXKGKGGXPPP 18
|: || ||| |||
Db 65 KKKRKVTGEGPGGEGP 81

RESULT 7
JE0352
mucin MUC5B, tracheobronchial - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0352
R:Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afshar, N.H.; Troxler, R.F.
Biochem. Biophys. Res. Commun. 251, 350-355, 1998
A:Title: The amino-terminal sequence of MUC5B contains conserved multifunctional D do
A:Reference number: JE0352; MUID:99009274
A:Molecule type: mRNA
A:Residues: 1-1321 <OFF>
A:Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927
C:Comment: This protein is large multimeric glycoproteins which is secreted by epithe
C:Genetics:
A:Gene: MUC5B

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Qy 11 GPGXPPP 18
| | | | |
| | | | |

Proc. Natl. Acad. Sci. U.S.A.

A:Reference number: A49630; MUID:94068425

A:Accession: A49630

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298 <RES>

A:Cross-references: GB:I22005; NID:g388308; PIDN:AAC37534.1; PID:g388309

C:Superfamily: human ubiquitin-protein ligase E2

Query Match 48.9%; Score 44; DB 2; Length 298;

Best Local Similarity 53.8%; Pred. No. 45;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 KXXGKGGGXP 17

DB 21 EEEAGGGGGSP 33

RESULT 13

probable conserved membrane protein ML0907 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: E87022

R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holt

R: Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: E87022

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 <STO>

A:Cross-references: GB:AL450380; NID:gl3092977; PIDN:CAC31288.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML0907

Query Match 48.9%; Score 44; DB 2; Length 377;

Best Local Similarity 87.5%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18

DB 254 GPGGPPPP 261

RESULT 14

S57447

HPBRII-7 protein - human

N:Alternate names: HPBRII-4 protein

C:Species: Homo sapiens (man)

C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C:Accession: S57447; S57489

R: Fleischhauer, K.L.

submitted to the EMBL Data Library, June 1992

A:Reference number: S57447

A:Accession: S57447

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-551 <FLE>

A:Cross-references: EMBL:X67336; NID:g871300; PIDN:CAA47751.1; PID:g871301

A:Accession: S57489

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-551 <FL2>

A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299

C:Genetics:

A:Introns: 231/3

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

F:82151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 48.9%; Score 44; DB 2; Length 551;

Best Local Similarity 87.5%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPGGXPPP 18

DB 222 GPGGPPPP 229

RESULT 15

A97443

hypothetical protein AGR_C1238 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: A97443

R: Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: A97443

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-669 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK86498.1; PID:gl51555650; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C1238

A:Map position: circular chromosome

Query Match 48.9%; Score 44; DB 2; Length 669;

Best Local Similarity 72.7%; Pred. No. 95;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 KXXGKGGGXP 16

DB 645 KPGKGPGGKP 655

Search completed: September 4, 2002, 16:47:29

Job time: 365 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:38:44 : Search time 158.52 Seconds
(without alignments)
13.313 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VKEXKXXGKPGGXPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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15: /SIDSL/gcgdata/hold-genseq/genseq-emb1/AA1994.DAT.*
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21: /SIDSL/gcgdata/hold-genseq/genseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-genseq/genseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	70.0	185	AAW99667	Human secreted pro
2	63	70.0	185	AA24067	Human PRO1005 prot
3	63	70.0	185	AA187272	Human signal pepti
4	63	70.0	185	AA166686	Membrane-bound pro
5	63	70.0	185	AA165209	Human PRO1005 (UNQ
6	63	70.0	185	AA150957	Human PRO1005 prot
7	63	70.0	186	AA138329	Human secreted pro
8	63	70.0	194	AA169974	Cancer associated
9	63	70.0	194	AA165591	Human ovarian tumo
10	55	61.1	140	AA008289	Human polypeptide
11	55	61.1	147	AA006887	Human polypeptide

12	54	60.0	52	21	AA59108	Breast and ovarian
13	51	56.7	106	22	AA002086	Human polypeptide
14	51	56.7	107	22	AA004646	Human polypeptide
15	48	53.3	108	22	AA004166	Human polypeptide
16	48	53.3	354	21	AA48744	Arabidopsis thalia
17	48	53.3	503	21	AA48743	Arabidopsis thalia
18	48	53.3	536	21	AA48742	Arabidopsis thalia
19	48	53.3	1194	22	AA59646	Drosophila melanog
20	47	52.2	120	22	AA000290	Human polypeptide
21	47	52.2	774	22	AA000290	Human polypeptide
22	46	51.1	59	21	AA53249	Drosophila melanog
23	46	51.1	106	22	ABG1453	Human colon cancer
24	46	51.1	122	22	AA000825	Novel human diagno
25	46	51.1	150	22	AA010242	Human polypeptide
26	46	51.1	223	21	AA43835	Human polypeptide
27	45	50.0	62	21	AA59111	Human cancer assoc
28	45	50.0	96	22	AA004073	Breast and ovarian
29	45	50.0	109	22	AA009868	Human polypeptide
30	45	50.0	133	13	AA23830	Human polypeptide
31	45	50.0	245	21	AA43357	Chicken anaemia vi
32	45	50.0	281	22	ABG13340	Human ORFX ORF3121
33	45	50.0	600	22	AA94233	Novel human diagno
34	45	50.0	878	20	AAW97850	Human protein sequ
35	45	50.0	879	20	AAW97849	Human p101/P13 kin
36	45	50.0	880	20	AAW97847	Human p101/P13 kin
37	45	50.0	880	20	AAW97847	Human full-length
38	45	50.0	880	20	AAW97848	Human p101/P13 kin
39	45	50.0	880	20	AAW90088	Human p101/P13 kin
40	45	50.0	880	21	AA28644	Human G-protein re
41	45	50.0	880	21	AA08523	Human p101 protein
42	45	50.0	880	21	AAW70430	Amino acid sequenc
43	45	50.0	880	21	AAW76800	Human phosphatidy
44	45	50.0	1518	22	AB64829	Human p101 regulat
45	45	50.0	2061	22	AB671759	Drosophila melanog

ALIGNMENTS

RESULT 1
ID AAW99667 standard; Protein; 185 AA.
AC AAW99667;
DT 07-JUN-1999 (first entry)
XX Human secreted protein clone ej90_5 protein.
DE Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.
OS Homo sapiens.
XX
XX WO9907840-A1.
XX
XX 18-FEB-1999.
XX
XX 06-AUG-1998; 98WO-US16318.
XX
XX 04-AUG-1998; 98US-0130189.
PR 06-AUG-1997; 97US-0906708.
XX
XX (GENY) GENETICS INST INC.
XX
XX Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;
PI Merberg D, Racie LA, Steininger RJ, Treacy M;
XX WPI; 1999-167419/14.
DR N-PSDB; AAX19493.

XX PT New polynucleotides encoding secreted human proteins - derived from
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
 PT or adult retina cDNA libraries
 XX PS Claim 34; Page 98-99; 107pp; English.
 XX
 CC The present sequence represents a human secreted protein. The secreted
 CC protein can have activities such as: nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. The
 CC polynucleotides are also stated to be useful for gene therapy.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 70.0%; Score 63; DB 20; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 DB 101 vke-kklgkpgg-pppk 117
 III I I I I I I I I I I
 RESULT 2
 AAB24067
 ID AAB24067 standard; Protein: 185 AA.
 AC AAB24067;
 XX
 DT 29-JAN-2001 (first entry)
 DE Human PRO1005 protein sequence SEQ ID NO:34.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoealic disorder;
 KW inflammatory disorder; immunologic disorder.
 KW
 XX Homo sapiens.
 OS
 XX WO200053755-A2.
 PN
 XX 14-SEP-2000.
 PD
 XX 06-JAN-2000; 2000WO-US00376.
 PF
 XX 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 30-NOV-1999; 99WO-US28313.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX

DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58377.
 XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 XX
 XX Claim 61; Fig 22; 286pp; English.
 PS
 XX The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO335,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO334, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoealic disorders, and inflammatory, PCR
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX
 XX Sequence 185 AA;
 SQ
 Query Match 70.0%; Score 63; DB 21; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGXPPPK 19
 DB 101 vke-kklgkpgg-pppk 117
 III I I I I I I I I I I
 RESULT 3
 AAY87272
 ID AAY87272 standard; Protein: 185 AA.
 XX
 AC AAY87272;
 XX
 DT 11-MAY-2000 (first entry)
 DE Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
 XX
 KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neutropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX Homo sapiens.
 OS
 XX WO200000610-A2.
 PN
 XX 06-JAN-2000.
 PD
 XX 25-JUN-1999; 99WO-US14484.
 PF
 XX 26-JUN-1998; 98US-0090762.
 PR


```

PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akersblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI: 2000-160673/14.
DR N-PSDB; AAZ98157.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 193-194; 327pp; English.
XX
CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPp-1 to HSPp-134. HSPps have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. HSPps can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPp. Antagonists of
CC HSPp are used to treat or prevent disorders associated with increased
CC activity or function of HSPp. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPp
CC nucleic acids can be used for the recombinant production of HSPp, for
CC detecting HSPp in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSPp are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSPp-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSPp
CC from natural sources.
XX
SQ Sequence 185 AA;

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.18;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXGKGGGKPPPK 19
   ||| || ||||| ||||
Db 101 vke-kk1qgkpgg-pppk 117

RESULT 4
AAY66686
ID AAY66686 standard; protein; 185 AA.
XX
AC AAY66686;
XX
XX 05-APR-2000 (first entry)
DT
DE Membrane-bound protein PRO1005.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
XX WO9963088-A2.
XX

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PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088555.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090689.
PR 25-JUN-1998; 98US-0090690.

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PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091828.
PR 02-JUL-1998; 98US-0091833.
PR 02-JUL-1998; 98US-0091846.
PR 02-JUL-1998; 98US-0091873.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX

DR WPI; 2000-072883/06.
DR N-PSDB; AAZ65023.
XX Membrane-bound proteins and related nucleotide sequences -
PT claim 12; Fig 139; 822pp; English.
PS The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents to block
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
SQ Sequence 185 AA;

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.18;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VREXKXKXGKPGGPPPK 19
||| || ||||| ||||
Db 101 vke-kk1gkpgg-pppk 117

RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
AC AAB65209;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
XX
KW Human; secreted and transmembrane protein; PRO: cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 13-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 02-MAR-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA;
 XX
 Query Match 70.0%; Score 63; DB 22; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 Oy 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| |||||
 Db 101 vke-kklqgkpgg-pppk 117
 XX
 RESULT 6
 AAB50957
 ID AAB50957 standard; Protein; 185 AA.
 XX
 AC AAB50957;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human PRO1005 protein.
 XX
 KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200073348-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAY-2000; 2000WO-US14941.

XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28634.
 PR 16-DEC-1999; 99WO-US28551.
 PR 20-DEC-1999; 99WO-US30095.
 PR 06-JAN-2000; 99WO-US30999.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 02-MAR-2000; 2000WO-US04342.
 PR 03-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000US-0187202.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 30-MAR-2000; 2000WO-US06884.
 PR 17-MAY-2000; 2000WO-US08439.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-016509/02.
 DR N-PSDB; AAC91559.
 XX
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA;
 XX
 Query Match 70.0%; Score 63; DB 22; Length 185;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 Oy 1 VKEXKXKXGKGGXPPPK 19
 ||| || ||||| |||||
 Db 101 vke-kklqgkpgg-pppk 117
 XX
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 9 clone HNSAD53.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cyostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW neotropic; antibacterial; virucide; fungicide; opthalmological; human;
 KW vulnary; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 OS
 XX
 PN W0200061623-A1.
 XX
 XX 19-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US08979.
 XX
 XX 09-APR-1999; 99US-0128693.
 PR 26-APR-1999; 99US-0130991.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX
 XX WPI; 2000-647418/62.
 DR
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 XX diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 PT
 XX
 XX Claim 11; Page 598; 716pp; English.
 PS
 XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC angiotensin; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX
 XX Sequence 186 AA;
 SQ
 Query Match 70.0%; Score 63; DB 21; Length 186;
 Best Local Similarity 78.9%; Pred. No. 0.18;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGGPPPK 19
 ||| || ||||| |||||
 Db 101 vke-kklgkpgg-pppk 117
 RESULT 8
 AAW69974
 ID AAW69974 standard; Protein; 194 AA.
 XX
 AC AAW69974;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Cancer associated protein.
 XX
 KW Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX
 OS Synthetic.
 XX

PN W09837187-A1.
 XX
 PD 27-AUG-1998.
 XX
 XX 18-FEB-1998; 98WO-JP00667.
 PF
 XX 21-FEB-1997; 97JP-0052508.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 PI
 XX WPI; 1998-467552/40.
 DR
 XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX
 XX Claim 14; Page 64-65; 92pp; Japanese.
 PS
 XX The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 70.0%; Score 63; DB 19; Length 194;
 Best Local Similarity 78.9%; Pred. No. 0.19;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXKXGKGGGPPPK 19
 ||| || ||||| |||||
 Db 110 vke-kklgkpgg-pppk 126
 RESULT 9
 AAY76591
 ID AAY76591 standard; Protein; 194 AA.
 XX
 AC AAY76591;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human ovarian tumor EST fragment encoded protein 87.
 XX
 XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 KW
 XX Homo sapiens.
 OS
 XX DEL9817557-A1.
 PN
 XX 21-OCT-1999.
 PD
 XX 09-APR-1998; 98DE-1017557.
 XX
 XX 09-APR-1998; 98DE-1017557.
 PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX
 XX

DR WPI; 1999-591920/51.
 XX N-PSDB; AAZ77487.
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents -
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-Z77572.
 XX
 SQ Sequence 194 AA;

Query Match 70.08; Score 63; DB 20; Length 194;
 Best Local Similarity 78.9%; Pred. No. 0.19;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
 QY 1 VKEXKXXKGGGPGGXPPEK 19
 ||| || ||||| |||||
 Db 110 vke-kkigkgpgg-pppk 126

RESULT 10
 AAO08289
 ID AAO08289 standard; Protein; 140 AA.
 XX
 AC AAO08289;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 22181.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI88220.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing

PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS PS
 XX
 CC Claim 20; SEQ ID NO 22181; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 140 AA;

Query Match 61.1%; Score 55; DB 22; Length 140;
 Best Local Similarity 81.8%; Pred. No. 1.8;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 9 GKGPGGXPPEK 19
 ||||| |||||
 Db 27 gkgpggakpppk 37

RESULT 11
 AAO06887
 ID AAO06887 standard; Protein; 147 AA.
 XX
 AC AAO06887;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 20779.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US04927.
 XX
 PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI86818.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX
 PS Claim 20; SEQ ID NO 20779; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to

CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 147 AA;

Query Match 61.1%; Score 55; DB 22; Length 147;
 Best Local Similarity 58.8%; Pred. No. 1.9;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 KEXKXXGKGGGXPPP 18
 I: || || | |||
 Db 20 kkkkkkgknppggppp 36

RESULT 12

AA059108
 ID AAB59108 standard; Protein: 52 AA.

XX AAB59108;

XX 27-MAR-2001 (first entry)

XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 816.

XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.

XX Homo sapiens.

XX WO200055173-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05881.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI: 2000-611515/58.

XX N-PSDB; AAF22011.

XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -

XX Claim 11; Page 1276; 1299pp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the

CC

CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC polynucleotide; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
 CC antidiabetic; antifungal; antiparasitic and cardiac activity. The
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemias; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.

XX Sequence 52 AA;

Query Match 60.0%; Score 54; DB 21; Length 52;
 Best Local Similarity 64.7%; Pred. No. 1;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KEXKXXGKGGGXPPP 18
 I: || | |||||
 Db 32 kkkkkkkkxpggxppp 48

RESULT 13

AA02086
 ID AAO02086 standard; Protein: 106 AA.

XX AAO02086;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 15978.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

XX 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-514838/56.

XX N-PSDB; AAI82017.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX Claim 20; SEQ ID NO 15978; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA03910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating

Qy 9 GKPGGXPPP 18
1 1111 111
Db 57 gggpggpppp 66

Search completed: September 4, 2002, 16:45:01
Job time: 377 sec

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:09 ; Search time 166.13 Seconds
(without alignments)
28.128 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VKEXKXXGKGGXPPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	63	70.0	185	5	US-09-991-150-211
2	63	70.0	185	5	US-09-720-533-49
3	63	70.0	185	6	US-10-119-480-148
4	63	70.0	185	6	US-10-119-480-148
5	63	70.0	185	6	US-10-119-480-148
6	63	70.0	185	6	US-10-216-159A-148
7	63	70.0	185	6	US-10-216-162-148
8	63	70.0	185	6	US-10-216-163-148
9	63	70.0	185	6	US-10-216-164-148
10	63	70.0	185	6	US-10-216-165-148
11	63	70.0	185	6	US-10-216-166-148
12	63	70.0	185	6	US-10-216-167-148
13	63	70.0	185	6	US-10-216-168-148
14	63	70.0	185	6	US-10-216-169-148
15	63	70.0	185	6	US-10-218-849-148
16	63	70.0	185	6	US-10-218-930-148
17	63	70.0	185	6	US-10-219-003-148
18	63	70.0	185	6	US-10-218-612-148
19	63	70.0	185	6	US-10-218-956-148
20	63	70.0	185	6	US-10-219-010-148
21	63	70.0	185	6	US-10-218-765-148
22	63	70.0	185	6	US-10-218-784-148
23	63	70.0	185	6	US-10-219-061-148
24	63	70.0	185	6	US-10-219-062-148
25	63	70.0	185	6	US-10-219-063-148
26	63	70.0	185	6	US-10-219-064-148
27	63	70.0	185	6	US-10-219-065-148
28	63	70.0	185	6	US-10-219-066-148

27	63	70.0	185	6	US-10-219-070-148	Sequence 148, App
28	63	70.0	185	6	US-10-219-071-148	Sequence 148, App
29	63	70.0	185	6	US-10-219-072-148	Sequence 148, App
30	63	70.0	185	6	US-10-219-073-148	Sequence 148, App
31	63	70.0	185	6	US-10-219-074-148	Sequence 148, App
32	63	70.0	185	6	US-10-219-075-148	Sequence 148, App
33	63	70.0	185	6	US-10-219-076-148	Sequence 148, App
34	63	70.0	185	6	US-10-219-077-148	Sequence 148, App
35	63	70.0	185	6	US-10-219-464-148	Sequence 148, App
36	63	70.0	185	6	US-10-219-465-148	Sequence 148, App
37	63	70.0	185	6	US-10-219-466-148	Sequence 148, App
38	63	70.0	185	6	US-10-219-467-148	Sequence 148, App
39	63	70.0	185	6	US-10-219-470-148	Sequence 148, App
40	63	70.0	185	6	US-10-219-471-148	Sequence 148, App
41	63	70.0	185	6	US-10-219-474-148	Sequence 148, App
42	63	70.0	185	6	US-10-219-475-148	Sequence 148, App
43	63	70.0	185	6	US-10-219-476-148	Sequence 148, App
44	63	70.0	185	6	US-10-219-478-148	Sequence 148, App
45	63	70.0	185	6	US-10-219-480-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-991-150-211
; Sequence 211, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 211
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-211

Query Match 70.0%; Score 63; DB 5; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGXPPPK 19
||| || ||||| |||||

Db 101 VKE-KKLGKGGG-PPPK 117

us-09-821-726-1.rapn

Thu Sep 5 11:23:24 2002

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
DB 101 VKE-KKLOGKGGG-PPPK 117

RESULT 4

US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
DB 101 VKE-KKLOGKGGG-PPPK 117

RESULT 5

US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 70.0%; Score 63; DB 5; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXKXGKGGXPPPK 19
DB 101 VKE-KKLOGKGGG-PPPK 117

RESULT 3

US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application data removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C2
; CURRENT APPLICATION NUMBER: US/10/216,162
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

```

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Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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QY 1 VKEXKXXGKGGGXPXPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163

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```

; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

```

```

Query Match          70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```

```

QY 1 VKEXKXXGKGGGXPXPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117

```

```

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

```

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 VKEXKXXGKGGGPPPK 19
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148
Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 VKEXKXXGKGGGPPPK 19
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148
Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 VKEXKXXGKGGGPPPK 19
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC7
; CURRENT APPLICATION NUMBER: US/10/216,165
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148

```
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148
```

```
Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
```

```
OY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117
```

```
RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
```

```
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148
```

```
Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
```

```
OY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117
```

```
RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148
```

```
Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
```

```
OY 1 VKEXKXKXGKGGXPPPK 19
    ||| || ||||| ||||
Db 101 VKE-KKLGKGGG-PPPK 117
```

RESULT 13
US-10-218-849-148
; Sequence 148, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; Prior Filing Date: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXXGKGGGPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 14
US-10-218-930-148
; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C13
; CURRENT APPLICATION NUMBER: US/10/218,930
; CURRENT Filing Date: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148

Query Match 70.0%; Score 63; DB 6; Length 185;
Best Local Similarity 78.9%; Pred. No. 0.3;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXXGKGGGPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLGKGGG-PPPK 117
RESULT 15
US-10-219-003-148
; Sequence 148, Application US/10219003
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT Filing Date: 2002-08-12
; Prior Application Number: 10/119,480
; Prior Filing Date: 2002-04-09
; Prior Application Number: 60/059113
; Prior Filing Date: 1997-09-17
; Prior Application Number: 60/062287
; Prior Filing Date: 1997-10-17
; Prior Application Number: 60/063549
; Prior Filing Date: 1997-10-28
; Prior Application Number: 60/064103
; Prior Filing Date: 1997-10-31
; Prior Application Number: 60/069873
; Prior Filing Date: 1997-12-17
; Prior Application Number: 60/078910
; Prior Filing Date: 1998-03-20
; Prior Application Number: 60/079294
; Prior Filing Date: 1998-03-25
; Prior Application Number: 60/079656
; Prior Filing Date: 1998-03-26
; Prior Application Number: 60/079728
; Prior Filing Date: 1998-03-27
; Prior Application Number: 60/081819
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/081955
; Prior Filing Date: 1998-04-15
; Prior Application Number: 60/082804
; Prior Filing Date: 1998-04-22
; Prior Application Number: 60/084441
; Prior Filing Date: 1998-05-06
; Prior Application Number: 60/085323
; Prior Filing Date: 1998-05-13
; Prior Application Number: 60/085579
; Prior Filing Date: 1998-05-15
; Prior Application Number: 60/086392
; Prior Filing Date: 1998-05-22
; Prior Application Number: 60/089532
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089538
; Prior Filing Date: 1998-06-17
; Prior Application Number: 60/089905
; Prior Filing Date: 1998-06-18
; Prior Application Number: 60/090472
; Prior Filing Date: 1998-06-24
; Prior Application Number: 60/090557
; Prior Filing Date: 1998-06-24
; Prior Application Number: 60/090691
; Prior Filing Date: 1998-06-25
; Prior Application Number: 60/090695
; Prior Filing Date: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/095302
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095318
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: 60/095916
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: 60/095146
 ; PRIOR FILING DATE: 1998-08-11
 ; PRIOR APPLICATION NUMBER: 60/096791
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/097986
 ; PRIOR FILING DATE: 1998-08-26
 ; PRIOR APPLICATION NUMBER: 60/098544
 ; PRIOR FILING DATE: 1998-08-31
 ; PRIOR APPLICATION NUMBER: 60/099596
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099598
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099803
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099811
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099812
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099816
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/100038
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: 60/100385
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100390
 ; PRIOR FILING DATE: 1998-09-15
 ; PRIOR APPLICATION NUMBER: 60/100627
 ; PRIOR FILING DATE: 1998-09-16
 ; PRIOR APPLICATION NUMBER: 60/100848
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: 60/100919
 ; PRIOR FILING DATE: 1998-09-17
 ; PRIOR APPLICATION NUMBER: 60/101477
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: 60/101738
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101741
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101786
 ; PRIOR FILING DATE: 1998-09-25
 ; PRIOR APPLICATION NUMBER: 60/101916
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/101922
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 60/106178
 ; PRIOR FILING DATE: 1998-10-28
 ; PRIOR APPLICATION NUMBER: 60/106248
 ; PRIOR FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: 60/106464
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 60/106905
 ; PRIOR FILING DATE: 1998-11-03
 ; PRIOR APPLICATION NUMBER: 60/108787
 ; PRIOR FILING DATE: 1998-11-17
 ; PRIOR APPLICATION NUMBER: 60/108801
 ; PRIOR FILING DATE: 1998-11-17
 ; PRIOR APPLICATION NUMBER: 60/108849
 ; PRIOR FILING DATE: 1998-11-18
 ; PRIOR APPLICATION NUMBER: 60/112422
 ; PRIOR FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: 60/113296
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/113605
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/115558
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/115565
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/115733
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/119549
 ; PRIOR FILING DATE: 1999-02-10
 ; PRIOR APPLICATION NUMBER: 60/123618
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/125259
 ; PRIOR FILING DATE: 1999-03-19
 ; PRIOR APPLICATION NUMBER: 60/125775
 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: 60/126773
 ; PRIOR FILING DATE: 1999-03-29
 ; PRIOR APPLICATION NUMBER: 60/127887
 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 60/130232
 ; PRIOR FILING DATE: 1999-04-21
 ; PRIOR APPLICATION NUMBER: 60/131022
 ; PRIOR FILING DATE: 1999-04-26
 ; PRIOR APPLICATION NUMBER: 60/131270
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/131291
 ; PRIOR FILING DATE: 1999-04-27
 ; PRIOR APPLICATION NUMBER: 60/131445
 ; PRIOR FILING DATE: 1999-04-28
 ; PRIOR APPLICATION NUMBER: 60/134287
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 60/140650
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/140723
 ; PRIOR FILING DATE: 1999-06-22
 ; PRIOR APPLICATION NUMBER: 60/141037
 ; PRIOR FILING DATE: 1999-06-23
 ; PRIOR APPLICATION NUMBER: 60/144758
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 60/145698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: 60/146222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: 60/146963
 ; PRIOR FILING DATE: 1999-08-03
 ; PRIOR APPLICATION NUMBER: 60/149320
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/149638
 ; PRIOR FILING DATE: 1999-08-17
 ; PRIOR APPLICATION NUMBER: 60/151733
 ; PRIOR FILING DATE: 1999-08-31
 ; PRIOR APPLICATION NUMBER: 60/164418
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 60/166361
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835
 ; PRIOR FILING DATE: 1999-12-07

Query Match 70.0%; Score 63; DB 6; Length 185;
 Best Local Similarity 78.9%; Pred.No. 0.3;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 VKEXKXKXGKPGXPPPK 19
 |||||
 Db 101 VWE-KKLOGKPGG-PPPK 117

Job time: 1154 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:14 ; Search time 34.18 Seconds
(without alignments)
21.523 Million cell updates/sec

Title: US-09-821-726-1
Perfect score: 90
Sequence: 1 VKEXKXKXGKGGPPPK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	63	70.0	199	1	CL1P_HUMAN
2	56.5	62.8	184	1	CL1P_MOUSE
3	47	52.2	355	1	KL2_HUMAN
4	47	52.2	687	1	YL18_CAEEL
5	43.5	48.3	721	1	E2BE_HUMAN
6	43.5	48.3	821	1	EP8_MOUSE
7	43	47.8	118	1	MOBC_THIFE
8	43	47.8	379	1	CYRG_BOVIN
9	43	47.8	2339	1	CCAB_RABIT
10	43	47.8	3124	1	CALC_CHICK
11	42.5	47.2	402	1	GUN1_HUMAN
12	42	46.7	161	1	ASF1_HELAN
13	42	46.7	326	1	CC14_CAEEL
14	42	46.7	384	1	VASP_CANFA
15	42	46.7	440	1	FXGA_CHICK
16	42	46.7	648	1	FZD1_HUMAN
17	42	46.7	775	1	POOF_PSEAE
18	42	46.7	1168	1	MYSC_ACACA
19	41.5	46.1	822	1	EP8_MOUSE
20	41	45.6	109	1	HM26_APTME
21	41	45.6	142	1	YPUB_KLEPN
22	41	45.6	351	1	KL2_RAT
23	41	45.6	354	1	KL2_MOUSE
24	41	45.6	356	1	E2F3_MOUSE
25	41	45.6	523	1	SK1L_HUMAN
26	41	45.6	684	1	E2BD_HUMAN
27	41	45.6	722	1	Z219_HUMAN
28	41	45.6	738	1	PL03_HUMAN
29	41	45.6	929	1	CALC_NOTVI
30	41	45.6	994	1	CLC1_MOUSE
31	41	45.6	994	1	CLC1_MOUSE
32	41	45.6	1464	1	CAL1_HUMAN
33	41	45.6	1638	1	BRM_DROME

34 40 44.4 198 1 RB16_RAT P35291 rattus norv
35 40 44.4 211 1 CAB4_HUMAN P37796 homo sapien
36 40 44.4 219 1 RB3D_MOUSE Q63942 rattus norv
37 40 44.4 219 1 RB3D_MOUSE Q63942 rattus norv
38 40 44.4 259 1 RNPH_MYCLE Q37939 mycobacteri
39 40 44.4 375 1 HXA2_CHICK Q08727 gallus gall
40 40 44.4 375 1 SOX3_MOUSE P53784 mus musculu
41 40 44.4 391 1 EDA_HUMAN Q52838 homo sapien
42 40 44.4 391 1 EDA_MOUSE O54693 mus musculu
43 40 44.4 464 1 S3A2_HUMAN Q15428 homo sapien
44 40 44.4 510 1 FKHL_DROME P14734 drosophila
45 40 44.4 656 1 HS7C_DROME P29844 drosophila

ALIGNMENTS

RESULT 1
CL1P_HUMAN
ID CL1P_HUMAN STANDARD; PRT; 199 AA.
AC Q9NSYL;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein.
GN Call.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer.";
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -!- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB039886; BAA92433.1; -
CC MIM; 606402; -
CC SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;
Query Match 70.0%; Score 63; DB 1; Length 199;
Best Local Similarity 78.9%; Pred. No. 0.026;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
Qy 1 VKEXKXKXGKGGPPPK 19
Db 115 VKE-KKLOGKGGG-PPPK 131
RESULT 2
CL1P_MOUSE
ID CL1P_MOUSE STANDARD; PRT; 184 AA.
AC Q9CR36; Q9D7K7; Q9CTZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Call protein homolog.
GN Call.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

YL18_CAEEL
ID YL18_CAEEL STANDARD; PRT; 687 AA.
AC Q11103;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 76.7 kDa protein C02F12.8 in chromosome X.
GN C02F12.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC STRAIN=BRISTOL N2;
RA Miller N.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U41545; AAK39136.1; -.
DR WormPep; C02F12.8; C03902.
KW Hypothetical protein.
SQ SEQUENCE 687 AA; 76730 MW; C96D04DB4AF1DA18 CRC64;

Query Match 52.2%; Score 47; DB 1; Length 687;
Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 2 KEKKKKXGKGGCGXPPP 18
|: || | | | | | | | | |
Db 545 KDQKKKRGKRPVSNPPP 561

RESULT 5
E2BE_HUMAN
ID E2BE_HUMAN STANDARD; PRT; 721 AA.
AC Q13144; Q96D04;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP
DE exchange factor).
GN EIF2B5 OR EIF2BE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Lung carcinoma;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 81-721 FROM N.A.
RX MEDLINE=96305354; PubMed=8688466;
RA Asuru A.I., Mellor H., Thomas N.S.B., Yu L., Chen J.-J., Crosby J.S.,
RA Hartson S.D., Kimball S.R., Jefferson L.S., Matts R.L.;
RT "Cloning and characterization of cDNAs encoding the epsilon subunit
RT of eukaryotic initiation factor-2B from rabbit and human.";
RL Biochim. Biophys. Acta 1307:309-317(1996).
RN [3]
RP VARIANTS VWM G-73; A-91; F-106; H-113; G-315; H-299; G-315; H-315;
RP P-339; Q-339; W-386; A-430; R-628 AND K-650, AND VARIANT I-567.
RX MEDLINE=21583742; PubMed=11704758;
RA Leegwater P.A.J., Vermeulen G., Konst A.A.M., Naidu S., Mulders J.,

Visser A., Kersbergen P., Mobach D., Fonds D., van Berkel C.G.M.,
Lemmers R.J.L.F., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,
Prank J.C., van der Knaap M.S.;
"Subunits of the translation initiation factor eIF2B are mutant in
leukoencephalopathy with vanishing white matter.";
Nat. Genet. 29:383-388(2001).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR
CC 2-BOUND GDP FOR GTP.
CC -!- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
CC DELTA AND EPSILON.
CC -!- DISEASE: Defects in EIF2B5 are a cause of leukoencephalopathy with
CC vanishing white matter (VWM), a brain disease that occurs mainly
CC in children. The neurological signs of VWM include progressive
CC cerebellar ataxia, spasticity, inconstant optic atrophy and
CC relatively preserved mental abilities. The disease is chronic-
CC progressive with, in most individuals, additional episodes of
CC rapid deterioration following febrile infections or minor head
CC trauma. Head trauma leads only to motor deterioration, whereas
CC infections with fever may end in coma. Death occurs after a
CC variable period of a few years to a few decades, usually following
CC an episode of fever and coma.
CC -!- SIMILARITY: BELONGS TO THE EIF-2B GAMMA/EPSILON SUBUNITS FAMILY.
CC -----
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CC -----
DR EMBL; BC013590; AAH13590.1; -.
DR EMBL; U23028; AAC50646.1; -.
DR MIM; 603945; -.
DR MIM; 603986; -.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR003307; eIF5C.
DR Pfam; PF00132; hexapep; 3.
DR Pfam; PF02020; W2; 1.
DR SMART; SM00515; eIF5C; 1.
KW Amino-acid biosynthesis; Translation regulation; Disease mutation;
KW Polymorphism.
FT DOMAIN 505 509 POLY-GLU
FT VARIANT 73 73 V -> G (IN VWM).
FT VARIANT 91 91 /FTID=VAR_012323.
FT VARIANT 106 106 T -> A (IN VWM).
FT VARIANT 113 106 /FTID=VAR_012291.
FT VARIANT 113 113 L -> F (IN VWM).
FT VARIANT 113 113 /FTID=VAR_012324.
FT VARIANT 299 299 R -> H (IN VWM).
FT VARIANT 299 299 /FTID=VAR_012292.
FT VARIANT 315 315 R -> H (IN VWM).
FT VARIANT 315 315 /FTID=VAR_012325.
FT VARIANT 315 315 R -> G (IN VWM).
FT VARIANT 339 315 /FTID=VAR_012326.
FT VARIANT 339 339 R -> H (IN VWM).
FT VARIANT 339 339 /FTID=VAR_012327.
FT VARIANT 339 339 R -> P (IN VWM).
FT VARIANT 339 339 /FTID=VAR_012328.
FT VARIANT 339 339 R -> Q (IN VWM).
FT VARIANT 339 339 /FTID=VAR_012329.
FT VARIANT 386 386 R -> W (IN VWM).
FT VARIANT 430 386 /FTID=VAR_012330.
FT VARIANT 430 430 G -> V (IN VWM).
FT VARIANT 587 430 /FTID=VAR_012293.
FT VARIANT 587 587 V -> A (IN VWM).
FT VARIANT 587 587 /FTID=VAR_012331.
FT VARIANT 628 587 V -> I.
FT VARIANT 628 628 /FTID=VAR_012332.
FT VARIANT 650 628 W -> R (IN VWM).
FT VARIANT 650 650 /FTID=VAR_012294.
FT VARIANT 650 650 E -> K (IN VWM).
FT VARIANT 650 650 /FTID=VAR_012333.

SQ SEQUENCE 721 AA; 80365 MW; 10109D3A464D336 CRC64;

Query Match 48.3%; Score 43.5; DB 1; Length 721;
Best Local Similarity 34.5%; Pred. No. 48;
Matches 10; Conservative 0; Mismatches 8; Indels 11; Gaps 1;

Qy 1 VKEXKXXKGGPGGX-----PPP 18
| | | | |
Db 13 VSRANKSGAGPGGGGGGARGAEPPPP 41

RESULT 6
EFS8_MOUSE
ID EFS8_MOUSE STANDARD; PRT; 821 AA.
AC Q08509;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epidermal growth factor receptor kinase substrate EFS8.
GN EFS8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94008987; PubMed=8404850;
RA Fazloli F., Minichello L., Matoska V., Castagnino P., Miki T.,
Wong W.T., di Fiore P.P.;
RT Eps8, a substrate for the epidermal growth factor receptor kinase,
enhances EGF-dependent mitogenic signals.;
RL EMBO J. 12:3799-3808(1993).
RN [2]
X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 532-591.
MEDLINE=97448677; PubMed=9303002;
RA Kishan K.V.R., Scita G., Wong W.T., di Fiore P.P., Newcomer M.E.;
RT "The SH3 domain of Eps8 exists as a novel intertwined dimer.";
RL Nat. Struct. Biol. 4:739-743(1997).
CC -!- FUNCTION: UPON BINDING TO EGF RECEPTOR ENHANCES EGF-DEPENDENT
MITOGENIC SIGNALS. CAN BIND MULTIPLE CELLULAR TARGETS.
CC -!- PTM: PHOSPHORYLATED BY SEVERAL RECEPTOR TYROSINE KINASES.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN. IT IS SPLIT IN TWO PARTS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L21671; AAA16358.1; -
DR PDB; LAOJ; 08-JUL-98.
DR MGD; MGI:104684; Eps8.
DR InterPro; IPR000050; PID_domain.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00462; PTB; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PSS0002; SH3; 1.
KW SH3 domain; Phosphorylation; 3D-structure.
FT DOMAIN 69 129 PH (FIRST PART).
FT DOMAIN 210 213 POLY-PRO.
FT DOMAIN 322 325 POLY-PRO.
FT DOMAIN 381 414 PH (SECOND PART).
FT DOMAIN 421 440 PRO-RICH.
FT DOMAIN 532 591 SH3.
FT DOMAIN 620 650 PRO-RICH.
FT DOMAIN 658 663 POLY-SER.
SQ SEQUENCE 821 AA; 91738 MW; 6B9EB95DD22D910C CRC64;

Query Match 48.3%; Score 43.5; DB 1; Length 821;
Best Local Similarity 41.7%; Pred. No. 54;
Matches 10; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy 2 KEXKXXKGGPG-----GXPPP 18
| | | | |
Db 301 KKSKKSRKRGEGVLTLRAPPP 324

RESULT 7
MOBC_THIFE
ID MOBC_THIFE STANDARD; PRT; 118 AA.
AC P22899;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE MOBC protein.
GN MOBC.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
OG Plasmid pTF-FC2.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015664; PubMed=1400173;
RA Rohrer J., Rawlings D.E.;
RT "Sequence analysis and characterization of the mobilization region of
a broad-host-range plasmid, pTF-FC2, isolated from Thiobacillus
ferrooxidans.";
RL J. Bacteriol. 174:6230-6237(1992).
CC -----
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CC -----
DR EMBL; M57717; AAA27390.1; -
DR PIR; C43256; C43256.
DR PIR; S27623; S27623.
KW Plasmid
SQ SEQUENCE 118 AA; 12956 MW; 13EAA3B1F1E707DE CRC64;

Query Match 47.8%; Score 43; DB 1; Length 118;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 KEXKXXKGGPGGXPPP 18
| | | | |
Db 78 KPTRKAPVQAPGDTPPP 94

RESULT 8
CYRG_BOVIN
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC Q95118;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

CC -!- PTM: GLYCOSYLATED, CHONDROITIN-SULFATED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH
 CC INTERRUPTED HELICES (FACIT) FAMILY.
 CC -!- SIMILARITY: CONTAINS 4 VWFA DOMAINS.
 CC -!- SIMILARITY: CONTAINS 18 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -----
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 CC -----
 DR EMBL; D00824; BAA00701.1; -
 DR EMBL; X61024; CAA43358.1; -
 DR EMBL; M17375; AAA48718.1; -
 DR EMBL; J05137; AAA48635.1; -
 DR EMBL; X67327; CAA47744.1; -
 DR PIR; A28037; A28037.
 DR PIR; A34485; A34485.
 DR HSSP; P17301; IAOX.
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003962; FNIII_repeat.
 DR InterPro; IPR003129; TSPN.
 DR Pfam; PF01391; Collagen; 4.
 DR Pfam; PF00041; fn3; 17.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00092; vwa; 4.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00060; FN3; 17.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00327; VWA; 4.
 DR PROSITE; PS50234; VWFA; 4.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 3124 COLLAGEN ALPHA 1(XII) CHAIN.
 FT DOMAIN 25 114 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 139 311 VWFA 1.
 FT DOMAIN 332 425 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 439 615 VWFA 2.
 FT DOMAIN 629 720 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 721 811 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 812 904 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 905 998 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 999 1085 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1086 1178 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1199 1371 VWFA 3.
 FT DOMAIN 1384 1473 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1474 1565 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1566 1654 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1655 1755 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1756 1846 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1847 1936 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1937 2027 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2028 2118 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 2119 2206 FIBRONECTIN TYPE-III 17.
 FT DOMAIN 2207 2295 FIBRONECTIN TYPE-III 18.
 FT DOMAIN 2327 2500 VWFA 4.
 FT DOMAIN 2455 2750 NONHELICAL REGION (NC3).
 FT DOMAIN 2751 2902 TRIPLE-HELICAL REGION (COL2)
 FT WITH 1 IMPERFECTION.
 FT DOMAIN 2903 2945 NONHELICAL REGION (NC2).
 FT DOMAIN 2946 3048 TRIPLE-HELICAL REGION (COL1)
 FT WITH 2 IMPERFECTIONS.
 FT DOMAIN 3049 3124 NONHELICAL REGION (NC1).
 FT DOMAIN 3086 3096 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 3111 3123 ARG/LYS-RICH (BASIC).
 FT BINDING 797 TO CHONDROITIN SULFATE (POTENTIAL).
 CC

FT BINDING 890 TO CHONDROITIN SULFATE (POTENTIAL).
 FT BINDING 981 TO CHONDROITIN SULFATE (POTENTIAL).
 FT SITE 2438 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 2899 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 32 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1006 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1032 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1044 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1512 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1767 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2210 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2273 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2532 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 2683 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 25 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 1258 T -> S (IN REF. 4).
 FT CONFLICT 1264 D -> E (IN REF. 4).
 FT CONFLICT 2759 P -> A (IN REF. 2).
 FT CONFLICT 2803 L -> F (IN REF. 2).
 FT CONFLICT 2977 V -> F (IN REF. 2).
 FT CONFLICT 3075 QP -> AG (IN REF. 3).
 SQ SEQUENCE 3124 AA: 340578 MW: 094285AFE7F346CF CRC64;
 Query Match 47.8%; Score 43; DB 1; Length 3124;
 Best Local Similarity 77.8%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 10 KGPGXPPP 18
 Db 1380 KGPGLPPP 1388
 IIII III
 RESULT 11
 GUNI_HUMIN
 ID GUNI_HUMIN STANDARD; PRT: 402 AA.
 AC P56680;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 GN CEL7B.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
 RX MEDLINE=97475713; PubMed=935168;
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schulein M.;
 RT "Oligosaccharide specificity of a family 7 endoglucanase: Insertion
 RT of potential sugar-binding subsites.";
 RL J. Biotechnol. 57:91-100(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE=98437137; PubMed=9761741;
 RA MacKenzie L.F., Sulzenbacher G., Dwyne C., Jones T.A., Woelldike H.F.,
 RA Schulein M., Withers S.G., Davies G.J.;
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from
 RT Humicola insolens at 2.2 A resolution and identification of the
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
 RT intermediate.";
 RL Biochem. J. 335:409-416(1998).
 CC -!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) EXOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
CC HYDROLASES).
CC
CC PDB; 1A39; 02-MAR-99.
CC PDB; 2A39; 16-FEB-99.
CC InterPro: IPR001722; Glyco_hydro_7.
CC DR Pfam: PF00840; Glyco_hydro_7; 1.
CC DR PRINTS: PR00734; GLHYDLASE7.
CC DR ProDom: PD186135; Glyco_hydro_7; 1.
CC DR Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
CC 3D-structure.
CC KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 197 197 NUCLEOPHILE.
CC FT ACT_SITE 202 202 PROTON DONOR.
CC FT DISULFID 18 24
CC FT DISULFID 51 73
CC FT DISULFID 63 69
CC FT DISULFID 140 365
CC FT DISULFID 172 195
CC FT DISULFID 176 194
CC FT DISULFID 215 234
CC FT DISULFID 223 228
CC FT DISULFID 239 315
CC FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
CC FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
CC SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 47.2%; Score 42.5; DB 1; Length 402;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 6 KXGKGPG-----GXPPK 19
DB 42 RAELGPGCGDGNPPK 50

RESULT 12
ASFL_HELAN
ID ASFL_HELAN STANDARD; PRT; 161 AA.
AC P22357;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Anther-specific protein SF18 precursor (Fragment).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_HA401B / CARGILL; TISSUE=Anther;
RX MEDLINE=91338702; PubMed=2102380;
RA Domon C., Evrard J.-L., Herdenberger F., Pillay D.T.N., Steinmetz A.;
RT "Nucleotide sequence of two anther-specific cDNAs from sunflower
RT (Helianthus annuus L.).";
RL Plant Mol. Biol. 15:643-646(1990).
CC -1- FUNCTION: ANOTHER-SPECIFIC CELL WALL PROTEIN WHICH COULD CONTRIBUTE
CC TO THE CELL WALL ARCHITECTURE OF EPIDERMAL ANOTHER CELLS VIA
CC INTERMOLECULAR DISULFIDE BRIDGES.
CC -1- TISSUE SPECIFICITY: EPIDERMAL ANOTHER CELLS.
CC -1- DEVELOPMENTAL STAGE: LATE DEVELOPMENTAL STAGES.
CC -1- SIMILARITY: BELONGS TO THE GAMMA-PURTHONIN FAMILY.
CC
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DR EMBL; X53375; CAA37455.1; -.
DR PIR; S12246; S12246.
DR HSSP; P30231; IAYJ.
DR InterPro: IPR002118; Gamma-thionin.
DR InterPro: IPR003614; Knot1.
DR Pfam; PF00304; Gamma-thionin; 1.
DR ProDom; PD002594; Gamma-thionin; 1.
DR SMART; SM00505; Knot1; 1.
DR PROSITE; PS00940; GAMMA_THIONIN; 1.
KW Signal; Cell wall.
FT NON_TER 1 1
FT SIGNAL <1 8
FT CHAIN 9 161 ANOTHER-SPECIFIC PROTEIN SF18.
FT DOMAIN 9 65 GAMMA-THIONIN LIKE DOMAIN.
FT DOMAIN 70 161 PROLINE DOMAIN.
FT DISULFID 18 65 BY SIMILARITY.
FT DISULFID 29 50 BY SIMILARITY.
FT DISULFID 35 59 BY SIMILARITY.
FT DISULFID 39 61 BY SIMILARITY.
SQ SEQUENCE 161 AA; 15363 MW; 27A9CF4633ADA02B CRC64;

Query Match 46.7%; Score 42; DB 1; Length 161;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GRGPGGXPPP 18
DB 127 GDGGGGAPP 136

RESULT 13
CC14_CAEEL
ID CC14_CAEEL STANDARD; PRT; 326 AA.
AC P18834;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Cuticle collagen 14.
OS COL-14.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=89326131; PubMed=2753356;
RA Cox G.N., Fields C., Kramer J.M., Rosenzweig B., Hirsh D.;
RT "Sequence comparisons of developmentally regulated collagen genes of
RT Caenorhabditis elegans.";
RL Gene 76:331-344(1989).
CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A
CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
CC LINKS.
CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
CC COLLAGENS.
CC
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CC
CC EMBL; M25480; AAA27986.1; -.
CC PIR; JS0169; JS0169.
CC InterPro: IPR002486; Col_cuticle_N.
CC InterPro: IPR000087; Collagen.

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FT DOMAIN 321 330 POLY-PRO.
SQ SEQUENCE 440 AA; 44669 MW; 82266C2E1E103A48 CRC64;

Query Match 46.7%; Score 42; DB 1; Length 440;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 GKPGGXPPP 18
| | | | |
Db 92 GDGPGSRPP 101

Search completed: September 4, 2002, 17:05:03
Job time: 1129 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:41:59 ; Search time 704.77 Seconds
(without alignments)
9.489 Million cell updates/sec

Title: US-09-821-726-1

Perfect score: 90

Sequence: 1 VKEXKXKXGKGGXPPK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PTCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
- 11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
- 13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
- 14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
- 15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
- 16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
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- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	91.1	19	22	US-09-821-726-1
2	63	70.0	21	22	US-09-821-726-8
3	63	70.0	25	22	US-09-821-726-10
4	63	70.0	42	22	US-09-821-726-6
5	63	70.0	150	13	US-08-906-708-24
6	63	70.0	182	20	US-09-684-524-212
7	63	70.0	182	24	US-10-050-704-212

8	63	70.0	185	1	PCT-US98-16318-18	Sequence 18, Appl
9	63	70.0	185	15	US-09-130-189-18	Sequence 18, Appl
10	63	70.0	185	20	US-09-584-524-105	Sequence 105, App
11	63	70.0	185	21	US-09-709-238-211	Sequence 211, App
12	63	70.0	185	21	US-09-746-783-146	Sequence 146, App
13	63	70.0	185	22	US-09-821-726-13	Sequence 13, Appl
14	63	70.0	185	22	US-09-821-726-18	Sequence 18, Appl
15	63	70.0	185	23	US-09-941-992-211	Sequence 211, App
16	63	70.0	185	23	US-09-989-279-211	Sequence 211, App
17	63	70.0	185	23	US-09-989-293A-211	Sequence 211, App
18	63	70.0	185	23	US-09-989-721-211	Sequence 211, App
19	63	70.0	185	23	US-09-989-722-211	Sequence 211, App
20	63	70.0	185	23	US-09-989-723-211	Sequence 211, App
21	63	70.0	185	23	US-09-989-724-211	Sequence 211, App
22	63	70.0	185	23	US-09-989-725-211	Sequence 211, App
23	63	70.0	185	23	US-09-989-726-211	Sequence 211, App
24	63	70.0	185	23	US-09-989-727-211	Sequence 211, App
25	63	70.0	185	23	US-09-989-728-211	Sequence 211, App
26	63	70.0	185	23	US-09-989-729A-211	Sequence 211, App
27	63	70.0	185	23	US-09-989-730-211	Sequence 211, App
28	63	70.0	185	23	US-09-989-731-211	Sequence 211, App
29	63	70.0	185	23	US-09-989-732-211	Sequence 211, App
30	63	70.0	185	23	US-09-989-734-211	Sequence 211, App
31	63	70.0	185	23	US-09-989-735-211	Sequence 211, App
32	63	70.0	185	23	US-09-989-862-211	Sequence 211, App
33	63	70.0	185	23	US-09-990-427-211	Sequence 211, App
34	63	70.0	185	23	US-09-990-436-211	Sequence 211, App
35	63	70.0	185	23	US-09-990-437-211	Sequence 211, App
36	63	70.0	185	23	US-09-990-438-211	Sequence 211, App
37	63	70.0	185	23	US-09-990-439-211	Sequence 211, App
38	63	70.0	185	23	US-09-990-440-211	Sequence 211, App
39	63	70.0	185	23	US-09-990-441-211	Sequence 211, App
40	63	70.0	185	23	US-09-990-442-211	Sequence 211, App
41	63	70.0	185	23	US-09-990-443-211	Sequence 211, App
42	63	70.0	185	23	US-09-990-444-211	Sequence 211, App
43	63	70.0	185	23	US-09-990-456-211	Sequence 211, App
44	63	70.0	185	23	US-09-990-562-211	Sequence 211, App
45	63	70.0	185	23	US-09-990-711-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: Lys or Gln
; NAME/KEY: MOD_RES
; LOCATION: (7)..(8)
; OTHER INFORMATION: Variable amino acid
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: Variable amino acid
; OTHER INFORMATION: Description of Unknown Organism: Illustrative
; OTHER INFORMATION: peptide

US-09-821-726-6
; Sequence 6, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-6

Query Match 70.0%; Score 63; DB 22; Length 42;
Best Local Similarity 78.9%; Pred. No. 0.6;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
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Db 24 VKE-KKLGKGG-PPPK 40

RESULT 5
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-906-708-24

US-09-821-726-1
; Sequence 8, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-8

Query Match 70.0%; Score 63; DB 22; Length 21;
Best Local Similarity 78.9%; Pred. No. 0.29;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
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Db 5 VKE-KKLGKGG-PPPK 21

RESULT 3
US-09-821-726-10
; Sequence 10, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-10

Query Match 70.0%; Score 63; DB 22; Length 25;
Best Local Similarity 78.9%; Pred. No. 0.35;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGKGGXPPPK 19
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Db 5 VKE-KKLGKGG-PPPK 21

RESULT 4

Query Match 70.0%; Score 63; DB 13; Length 150;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19
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Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 6
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match 70.0%; Score 63; DB 20; Length 182;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19
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Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 7
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 70.0%; Score 63; DB 24; Length 182;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19
||| || ||||| |||||
Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 8
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 70.0%; Score 63; DB 1; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19
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Db 101 VKE-KKLOGKGGG-PPPK 117

RESULT 9
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 70.0%; Score 63; DB 15; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Thu Sep 5 11:23:23 2002

us-09-821-726-1.rapm

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QY 1 VKEXKXXKGGPGGXPPPK 19
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Db 101 VKE-KKLGKGGPGG-PPPK 117

RESULT 10
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 70.0%; Score 63; DB 20; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXKGGPGGXPPPK 19
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Db 101 VKE-KKLGKGGPGG-PPPK 117

RESULT 11
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 60/087,607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/087,759
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: US 60/087,827
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,030

; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: US 60/088,326
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: US 60/088,217
; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: US 60/088,722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,730
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,740
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; PRIOR APPLICATION NUMBER: US 60/088,741
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; PRIOR APPLICATION NUMBER: US 60/088,811
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; PRIOR APPLICATION NUMBER: US 60/088,824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/088,858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/088,876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: US 60/089,090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/089,440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,907
; PRIOR FILING DATE: 1998-06-18
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;; PRIOR APPLICATION NUMBER: US 60/089,908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: US 60/089,947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 60/089,948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 60/089,952
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/090,863
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: US 60/091,358
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,486
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: US 60/091,626

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,628
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,646
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,673
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: US 60/091,978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/091,982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: US 60/092,182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: US 60/092,472
;; PRIOR FILING DATE: 1998-07-10
;; PRIOR APPLICATION NUMBER: US 60/093,339
;; PRIOR FILING DATE: 1998-07-20
;; PRIOR APPLICATION NUMBER: US 60/094,651
;; PRIOR FILING DATE: 1998-07-30

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred No. 2.8;

Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VXEXKXKXGPGGPPPK 19
||| || ||||| ||||
Db 101 VKE-KKLGKPGG-PPPK 117

RESULT 12

US-09-746-783-146

; Sequence 146, Application US/09746783

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

; McCoy, John M.

; LaVallie, Edward R.

; Racie, Lisa A.

; Treacy, Maurice

; Spaulding, Vikki

; Agostino, Michael J.

; Howes, Steven H.

; Rehtel, Kim

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

; NUMBER OF SEQUENCES: 231

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09746.783

; FILING DATE: 21-Dec-2000

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Milasincic, Debra J.

; REGISTRATION NUMBER: 46,931

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 146:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 185 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 70.0%; Score 63; DB 21; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19

Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 13

US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match 70.0%; Score 63; DB 22; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19

Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 14

US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match 70.0%; Score 63; DB 22; Length 185;
Best Local Similarity 78.9%; Pred. No. 2.8;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VKEXKXXGKGGGPPPK 19

||| || ||||| |||||

Db 101 VKE-KKLGKGGG-PPPK 117

RESULT 15

US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730Plc1
; CURRENT APPLICATION NUMBER: US/09/941,992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
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; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029

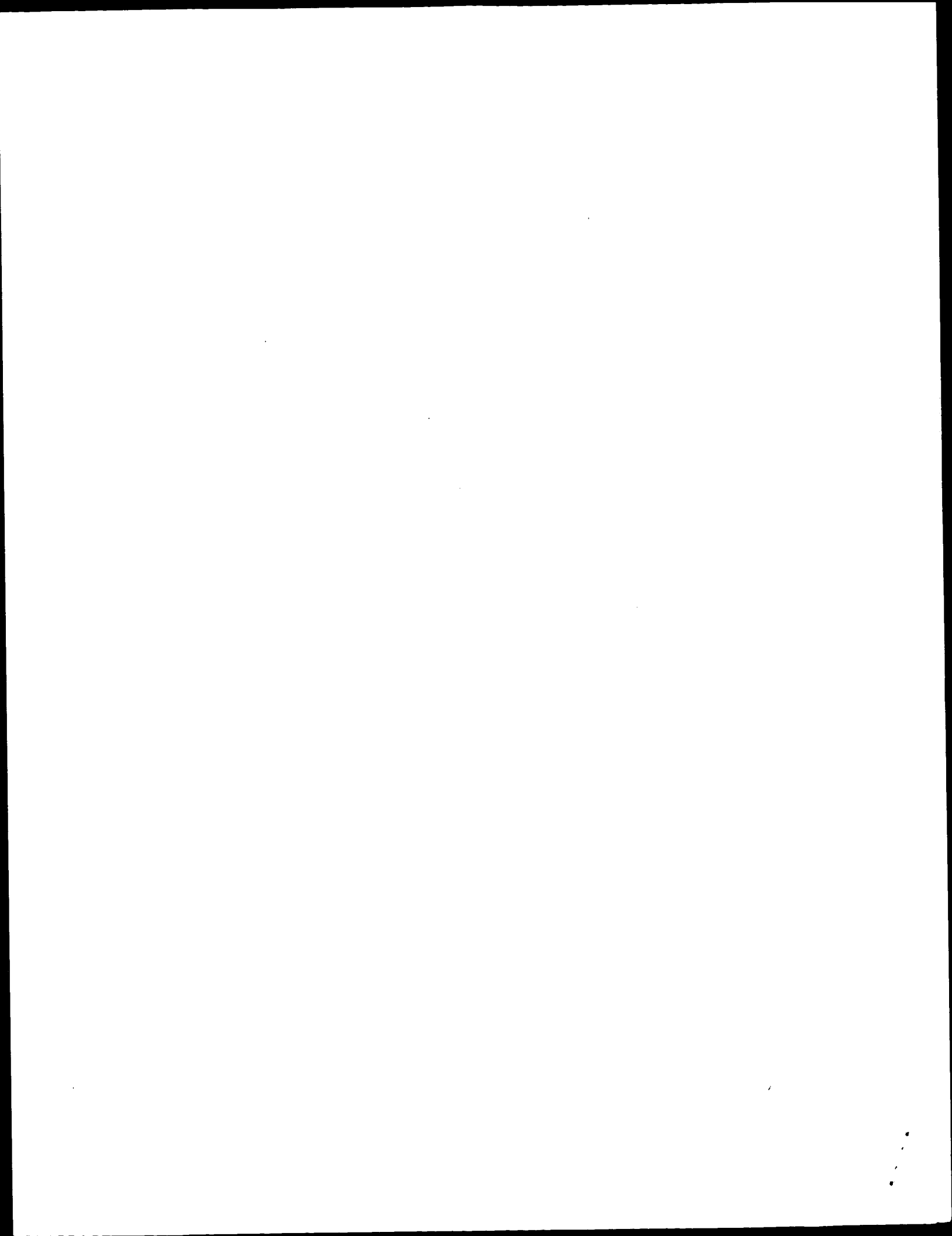
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 ; PRIOR FILING DATE: 1998-06-19
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 ; PRIOR FILING DATE: 1998-06-22
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 ; PRIOR FILING DATE: 1998-06-22
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; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
 ; PRIOR APPLICATION NUMBER: 60/092472

Query Match 70.0%; Score 63; DB 23; Length 185;
 Best Local Similarity 78.9%; Pred No. 2.8;
 Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 VREXXKXGKGGPGGPPPK 19
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 Db 101 VKE-KKLOGKGGG-PPPK 117

Search completed: September 4, 2002, 16:59:19
 Job time: 1040 sec



1 SerValHisCysPheArgGluAspIysMetLysPheThrIleValAlaPheAla 17

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63  TGGACTTCTGTTGCTTCTGACTCCTGCTTGTGCTATAGTATCA 112
17  AGTLeuLeuGlyValPheLeuAlaProAlaLeuAlaAsnTyrAsnIleA 34
113 GTGTCAACGACGACGCGCAAGTGTGGAGTGGGCGAGCGTGTGAGT 162
34  snValAsnAspAspAsnAsnAsnAlaGlySerGlyGlnGlnSerValSer 50
163 GTCAACATGTAACCAACGTCGACCACTGTCACATATACATGATGGA 212
51  ValAsnAsnGlnHisAsnValAlaAsnValAspAsnAsnAsnGlyTyrPAs 67
213 CTCCTGGAATGCCCTCTGGACCTATAGACTGCTTGTCTGTACCAAC 262
67  pSerTyrPAsnSerIleTyrPAsPtyrGlyAsnGlyPheAlaIleThrArgL 84
263 TCTTGCAGAGAAGATCATGTCATGTCGACAAATGACAGAGAAGCCATG 312
84  euPheGlnLysLysThrCysIleValHisLysMetAsnLysGluValMet 100
313 CCTCCCTTCAGCCCTTGATGCGCTGGTCAAGAAAGAAAGCTTCAAGG 362
101 ProSerIleGlnSerLeuAspAlaLeuValLysGlyLysLysLeuGlnG 117
363 TAAGGCGCCAGGGGAGACACCTTCCCAAGAGCTGAGACTGACGCAAC 412
117  yLysGlyProGlyGlyProProLysGlyLeuMetCysTyrSerValAsn 134
413 CCAACGAGCTGCACAACTGACAACTTGGAAATTCATCGTTCGCAAT 462
134  roAsnLysValAspAspLeuSerLysPheGlyLysAsnIleAlaAsnMet 150
463 TGCAGAGGATTCACACATACATGCTGTAAGAGATTCAGAGAGCAACT 512
151  CysArgGlyIleProThrTyrMetAlaGlnGluMetGlnGluAlaSerLe 167
513 GATTGGTGTCTCGAAGAGTCAGTCAGTCCATATACTCTGGATTCTTA 562
167  uPhePheTyrSerGlyThrCysTyrThrThrSerValLeuIleTyrPheVal 184
563 ACATTTCTCTCTGTGAGGAAATGCGGAGAGAC 594
184  splLeSerPheCysGlyAspThrValGluAsn 194

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AC  AA176591;
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XX  10-APR-2000 (first entry)
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XX  Human ovarian tumor EST fragment encoded protein 87.
DE
XX  Expressed sequence tag; EST; human; ovarian tumor; anticancer;
KW  gene therapy; treatment.
XX
XX  Homo sapiens.
OS
XX  DE19817557-A1.
XX
XX  21-OCT-1999.
XX
XX  09-APR-1998; 98DE-1017557.
XX
XX  09-APR-1998; 98DE-1017557.
XX
XX  (META-) METAGEN GBS GENOMFORSCHUNG MBH.
XX
XX  Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX  WPI; 1999-591920/51.
XX
DR

```

DR N-PSDB; AA277487.

XX New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents -

XX Claim 25; Page 279; 310pp; German.

CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of the
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AA176505-176638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AA277450-277572.

XX Sequence 194 AA:

alignment_scores: length: 194
 Quality: 803.00
 Ratio: 4.412 Gaps: 0
 Percent Similarity: 93.814 Percent Identity: 74.227

alignment_block:
 US-09-821-726-17 x AA176591 ..

Align seg 1/1 to: AA176591 from: 1 to: 194

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13  TCACTTTCATGTCATGTCGTAAGCCAAAGTGAATTCACATTCGCTTGC 62
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1  SerValHisCysPheArgGluAspLysMetLysPheThrIleValAlaPheAl 17
63  TGGACTTCTGTTGCTTCTGACTCCTGCTTGTGCTATAGTATCA 112
17  AGTLeuLeuGlyValPheLeuAlaProAlaLeuAlaAsnTyrAsnIleA 34
113 GTGTCAACGACGACGCGCAAGTGTGGAGTGGGCGAGCGTGTGAGT 162
34  snValAsnAspAspAsnAsnAsnAlaGlySerGlyGlnGlnSerValSer 50
163 GTCAACATGTAACCAACGTCGACCACTGTCACATATACATGATGGA 212
51  ValAsnAsnGlnHisAsnValAlaAsnValAspAsnAsnAsnGlyTyrPAs 67
213 CTCCTGGAATGCCCTCTGGACCTATAGACTGCTTGTCTGTACCAAC 262
67  pSerTyrPAsnSerIleTyrPAsPtyrGlyAsnGlyPheAlaIleThrArgL 84
263 TCTTGCAGAGAAGATCATGTCATGTCGACAAATGACAGAGAAGCCATG 312
84  euPheGlnLysLysThrCysIleValHisLysMetAsnLysGluValMet 100
313 CCTCCCTTCAGCCCTTGATGCGCTGGTCAAGAAAGAAAGCTTCAAGG 362
101 ProSerIleGlnSerLeuAspAlaLeuValLysGlyLysLysLeuGlnG 117
363 TAAGGCGCCAGGGGAGACACCTTCCCAAGAGCTGAGACTGACGCAAC 412
117  yLysGlyProGlyGlyProProLysGlyLeuMetCysTyrSerValAsn 134
413 CCAACGAGCTGCACAACTGACAACTTGGAAATTCATCGTTCGCAAT 462

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PF 25-JUN-1999; 99WO-US14484.
 XX
 XX 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akersblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 XX WPI: 2000-160673/14.
 DR N-PSDB; AA298157.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 193-194; 327pp; English.

XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC antitumor, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy), HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSP
 CC from natural sources.
 XX

SQ Sequence 185 AA:

alignment_scores:
 Quality: 775.00 Length: 185
 Ratio: 4.429 Gaps: 0
 Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
 US-09-821-726-17 x AAY87272 ..

Align seg 1/1 to: AAY87272 from: 1 to: 185

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 90 TGCCCTTGGTACTATAGTATAGTGTCAACAGCAGCGCAACAGTGTG 139
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 17 AlaLeuAlaIAsnTrpAsnIleAsnValAsnAspAsnAsnAlaG 34
 140 GAATGGGAGCAGTCACTAGTGTCAACATGAACACACAACTGGCCAC 189
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 34 LysSerGlyGlnInsValSerValAsnAsnGlnHisnValAlaAsn 50
 190 GTTGACAATAACATGATGATGAACTCTGGAAATGCCCTCTGGACTATAG 239

51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrG1 67
 240 AACTGGCTTGGTGTACCACTCTTGCAGAGAGAGAGATCATGATGTC 289
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 67 yAsnGlyPheAlaIleThrArgLeuPheGlnLysThrCysIleValH 84
 290 ACAAAATGAAGAAGAGCAAGCCATGCCCTCCCTCAAGCCCTGATGGCT 339
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 84 LysMetAsnLysGlyValMetProSerIleGlnSerLeuAspAlaLeu 100
 340 GTCAAGCAAAAGACCTTCAAGGTAAGGCGCCAGGAGGACCACTCCCA 389
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 101 ValLysGlnLysLysLeuGlnLysGlyProGlyGlyProPropolY 117
 390 GAGCTGAGTACTGATGTCACCAAGCAAGCTGACAGCACTGACCAACT 439
 |||||
 117 SGIyleuMetLysSerValAsnProAsnLysValAspAspLeuSerLysP 134
 440 TTGGAATTCATCGTTCGATGTGCAAGGCGATTCACATACATGCT 489
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 134 heGlyLysAsnIleAlaAsnMetCysArgLyleProThrTyrMetAla 150
 490 GAAGGATTCAGAGCAAGCAACTGATTTCTGACTCAGAAAAGTCATCAG 539
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 151 GluGluMetGlnGlnAlaSerLeuPhePheThrCysGlyThrCysTyrH 167
 540 TGCCAAATATCTGATGATTCATTCATTCCTCTGAGGAGAAATACCGG 589
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 167 ThrSerValLeuTrpIleValAlaAspIleSerPheCysGlyAspThrValG 184
 590 AGAAC 594
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 184 LAsn 185
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAV66686
 seq_documentation_block:
 ID AAV66686 standard: protein; 185 AA.
 AC AAV66686;
 XX
 XX 05-APR-2000 (first entry)
 DT
 XX
 DE Membrane-bound protein PRO1005.
 DE
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmacological; receptor immunoadhesin; gene mapping.
 OS Homo sapiens.
 XX
 PN MO9963088-A2.
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US12252.
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 PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 02-JUN-1998; 98US-0087759.
 PR 03-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
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 PR 04-JUN-1998; 98US-0088028.
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PR 10-JUN-1998; 98US-0088722.
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 PR 09-JUL-1998; 98US-0092182.

PR 10-JUL-1998; 98US-0092472.
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 PR 30-JUL-1998; 98US-0094651.
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 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
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 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 (GETH) GENENTECH INC.
 XX PA
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 DR N-PSDB; AAZ65023.
 XX WPI: 2000-072883/06.
 PT Membrane-bound proteins and related nucleotide sequences
 XX
 PS claim 12; Fig 139; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially

alignment_scores: length: 185
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 Ratio: 4.429
 Percent Similarity: 94.595 Percent Identity: 75.135

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 US-09-821-726-17 x AAB65209 ..

Align seg 1/1 to: AAB65209 from: 1 to: 185

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90 TGCCCTTGTCTACTTACTTACTGAGTTCACAGCAGCAGCAAGTGGTG 139
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17 calaleuhalasnlyrasnilleasnvalasnspaspsnsmnsmnlaag 34
140 GAAGTGGCAGCAGTCACTGAGTCAATCAATGAACACAGCGCCCAAC 189
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34 lyserylglnglnlservalservalasnnglnhlnlshnvalalasn 50
190 GTTGACATTAACATGATGAGAACCTCCGAAATGCCCTGGGACTATAG 239
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51 Valaspsnsmnsmnnglytrpaspsertrpanserllettrpasptrygl 67
240 AACTGCTTGTCTGTAAACAGACTCTTCGAGAAGAGAGTCAATGTCGTC 289
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67 yasnnglyphehalalathrarglenpheglnlyslrthrcysilevalh 84
290 ACAAAATGAGAAAGAACCCATGCCCTCCCTTCAGCCCTTGATGGCGTG 339
|||||
84 lsylsmelasnlysgluvalmelproserllelserleuspalaleu 100
340 GTCAAGAAAGAGCTCAGGGTAAGGCCCGCAGGGGAGCCACCTCCCAA 389
|||||
101 Vallysglnlyslsleuglnnglylvsnglylproglylproproproly 117
390 GAGCCTGAGTACTCAGTCAACCCCAAGAGTGCACAACTTGACAAAGT 439
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117 sglyleumetyservalasnproksnlyvalaspsaspleuserlysp 134
440 TTGGAAATTCATCGTGGCATGTGCAAGGGAGTTCACATCATCATGCT 489
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134 heglylshasnillealasnmetcysarglyleprothrtrymetala 150
490 GAAGAGATTCAGAGGAGCAAACTGATTTCTACTCAGAAAAGTGCATCAG 539
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151 Gluljmetglnnglnlaserleuphepserglylthrcyslytrth 167
540 TGGCAATATATCTCTGATTTCTTACATTTCTCTGAGAGAAATAGCG 589
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167 rthservalleutrpilevalasplelleserphcysglyaspthrvalg 184
590 AGAAC 594
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184 luasn 185

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seq_name: /SIDS1/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT:AAB50957

seq_documentation_block:
 ID AAB50957 standard; Protein; 185 AA.

XX AAB50957;

XX AC 21-MAR-2001 (first entry)

XX DE Human PRO1005 protein.

XX XX Human: PRO: cytostatic; nootropic; neuroprotective; respiratory general;

KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;

KW PRO agonist; cancer; inflammatory disorder; immunological disorder.

OS Homo sapiens.

XX PN WO200073348-A2.

XX PD 07-DEC-2000.

XX PF 30-MAY-2000; 2000WO-US14941.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 22-JUN-1999; 99US-0140650.

XX PR 23-JUN-1999; 99US-0141037.

XX PR 20-JUL-1999; 99US-0144758.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 08-SEP-1999; 99WO-US20594.

XX PR 29-OCT-1999; 99US-0162506.

XX PR 30-NOV-1999; 99WO-US28313.

XX PR 01-DEC-1999; 99WO-US28634.

XX PR 02-DEC-1999; 99WO-US28531.

XX PR 16-DEC-1999; 99WO-US30095.

XX PR 20-DEC-1999; 99WO-US30999.

XX PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US04341.

XX PR 18-FEB-2000; 2000WO-US04342.

XX PR 02-MAR-2000; 2000WO-US05841.

XX PR 03-MAR-2000; 2000US-0187202.

XX PR 10-MAR-2000; 2000WO-US06319.

XX PR 15-MAR-2000; 2000WO-US06884.

XX PR 30-MAR-2000; 2000WO-US08439.

XX PR 17-MAY-2000; 2000WO-US13705.

(GETH) GENENTECH INC.

PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;

PI Shelton DL, Smith V, Watanabe CK, Wood WI;

DR WPI: 2001-016509/02.

DR N-PSDB: AAC91559.

XX Claim 31; Fig 14; 188pp; English.

XX The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumors, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocellic disorders, and inflammatory, angiogenic and immunological
 CC disorders.

XX Sequence 185 AA;

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Quality: 775.00 Length: 185
 Ratio: 4.429 Gaps: 0
 Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
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 490 GAGAGATTTCAGAGCAACCGTATTCGTACAGCAAAAGTCATCAG 539
 151 GlndImetGlnGluAlaSerLeuPhePheTYrSerGlyThrCysTYrTh 167
 540 TGCCATATACTGTGATTTCTTAACATTTCTTGTGAGAGAAATACCG 589
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 590 AGAAC 594
 184 LuAsn 185

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seq_documentation_block:

ID AAY76592 standard; Protein: 82 AA.

AC AAY76592;

DT 10-APR-2000 (first entry)

XX Human ovarian tumor EST fragment encoded protein 88.

DE Expressed sequence tag; EST; human; ovarian tumor; anticancer;

KW gene therapy; treatment.

XX Homo sapiens.

XX DE19817557-A1.

XX 21-OCT-1999.

XX 09-APR-1998; 98DE-1017557.

XX 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI: 1999-591920/51.

XX N-PSDB: AAY77487.

XX New nucleic acid sequences expressed in ovarian, and some other, cancer
 tissues, and derived polypeptides, for treatment of ovarian cancer and
 identification of therapeutic agents

XX Claim 25; Page 279; 310pp; German.

XX This invention describes novel nucleic acid (cDNA) sequences (A) which
 have anticancer activity and are highly expressed in ovarian tumor
 tissue (and some also in testis and breast cancer tissue). The products
 of the invention can be used for gene therapy. (A) are used (1) for
 recombinant expression of polypeptides (B) and (11) to isolate complete
 genes. (B) are used (1) to identify agents suitable for treatment of
 ovarian cancer: (11) directly for treating this form of cancer
 (including expression from gene therapy vectors) and (111) for generation
 of specific antibodies. (A) are identified by assembling ESTs (expressed
 sequence tags) from a particular tissue type before comparison of the
 expression patterns. This allows a significantly longer fragment of the
 gene to be revealed, so should reduce the number of failures associated
 with the fact that ESTs from different libraries may represent different
 parts of the same unknown gene, distorting the estimated frequency of
 occurrence in a particular tissue. AAY76505-Y76638 represent protein
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 Percent Similarity: 91.463 Percent Identity: 80.488

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 17 ulauphelaAuAspGlnCyslLeLysGlyLeuAsnGlyGlyHisAspPheL 34
 302 TTCTTCATTTTGTGCAACATGCATGACTTCTCTCGAAGAGTCTGTTAC 253
 34 euValHisPheValHisAsnAlaCysLeuLeuLeuLysGlnSerGlyCys 50
 252 AGCAAGCCAGTCTATATATCCAGAGGGCATTCAGAGAGTTCATTCAT 203
 51 SerYsAlaIleSerIleIleProAspGlyIleProGlyValProSerVa 67
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seq_documentation_block:

ID ABB11905 standard; peptide: 47 AA.

AC ABB11905;

DT 11-JAN-2002 (first entry)

XX Human gastric cancer downregulated protein homologue, SEQ ID NO:2275.

XX Human: cytokine; cell proliferation; cell differentiation; growth factor;

KW hematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; cancer; tumour; hematopoietic disorder;

KW proliferation; metastasis; cancer; lymphoid cell disorder; asthma; arthritis;

KW myeloid inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;

KW antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;

KW cytosolic; osteopathic; vasotropic; cardiatic; vitruide; antibacterial;

KW antifungal; vulnerary; antilulcer.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US03800.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;


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PR 23-JUN-1998: 98US-0090349.
PR 23-JUN-1998: 98US-0090355.
PR 24-JUN-1998: 98US-0090421.
PR 24-JUN-1998: 98US-0090439.
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PR 19-AUG-1998: 98US-0097218.
PR 20-AUG-1998: 98US-0097661.
PR 24-AUG-1998: 98US-0097951.
PR 26-AUG-1998: 98US-0097952.

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PR 26-AUG-1998: 98US-0097986.
PR 26-AUG-1998: 98US-0098014.
PR 31-AUG-1998: 98US-0098525.
PR 16-SEP-1998: 98US-0100634.
PR 12-JAN-1999: 98US-0115565.

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(GETH) GENENTECH INC.

```

XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WT, Yuan J;
XX WPI: 2000-072883/06.
XX N-PSDB: AA65029.

```

Membrane-bound proteins and related nucleotide sequences

claim 12; Fig 149; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIR ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential interaction. The PRO encoding sequences of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

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    Ratio: 1.703        Gaps: 4
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Align seg 1/1 to: AAY66690 from: 1 to: 184

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17 nserHISglYTYrGUValAlaPheASnIleIleSerProSerASnAngly 34
140 GAAGTGGCAGCAGTCACTGAGTGTCAACATGAACACAGTGGCCAC 189
34 IyASnValIngluIurValThrIleASpASnIulYASnThrAlaIle 50
190 GTTGACATTAACAAATGATGATGATGATGATGATGATGATGATGATG 239
51 ValASnIleHISAlaGlySerCysSerSerThrThrIlePheASpTYly 67
240 AACTGGCTTGCTGATACCACTCTTCGAGAAGACATGATGATGATG 289
67 SHISglYTYrIleAlaSerArGValIleSerArGValIleAlaCysPheIle 84
290 ACAAAATGAAGAAGAACGACCTCCCTT ..... 321

```

```

|||||
84 eulysmetaspHisGlnAsnIleProLeuAnsnLeuGlnTrpTyr 100
322 .....CAAGCCCTGATGGCGTCAGAGAGAAAGAACCTTCA 359
101 IleTyrGlnGlnAlaLeuAspAsnMetPheSerAsnLysTyrThrTr 117
360 GGCTAAGGCCCGAGGGGACACCTCCCAAGAGAGCTGAGTACTGTCACA 409
117 P.....ValLysTyrAsnProL 123
410 ACCCCACAGATCGACACCTGGACAGTTT.....GGAATTCATC 453
123 euglserleuIleLysAspValAspTrpPheLeuLeuGlySerProIle 139
454 GTTGCATGTCAGAGGCGATTCACATGATGGCTGAGAGATTCACAG 503
140 GlnLysLeuCyLysHisIleProLeuTyrLysGlnValValGlnAs 156
504 ACACAAACCTGATTTGCTACTCAGAAAGTGCATGATCCCATATCT 553
156 nThrHisAsnValGly...AlaGlyGlyCyAlaLysAlaGlyLeuLeuG 172
554 GGATCTTAACATTCCTCTGTGGAGGAATA 585
172 LylleuGlyLysIleSerIleCyAlaAspIle 182

seq_name: /SIDS1/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT: AAB65213
seq_documentation_block:
ID AAB65213 standard; Protein: 184 AA.
XX
AC AAB65213:
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO813 (UNQ465) protein sequence SEQ ID NO:221.
XX
KM Human; secreted and transmembrane protein; PRO; cytosolic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX Homo sapiens.
XX
PN WO20073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.

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PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Garber H, Gertlsen ME, Goddard A, Godowski PJ;
PI Germain CJ, Gurney AL, Kijavini ID, Napier MA, Pan J, Paoletti NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
PI Zhang Z;
XX
XX WPI: 2001-032160/04.
DR N-PSDB; AAF44175.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX
XX Claim 12: Fig 149; 935bp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX can be used for targeted delivery of bioactive molecules, such as
XX toxins, radiolabels or antibodies, that cause cell death, PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX and DNA. They may also be used to produce transgenic animals which are
XX used to develop and screen therapeutically useful reagents. The PRO
XX nucleotide and protein sequence can be used for tissue typing and in
XX treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX sequences given in the exemplification of the present invention.
XX
XX Sequence 184 AA:

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alignment_scores:
Quality: 201.00 Length: 194
Ratio: 1.703 Gaps: 4
Percent Similarity: 60.825 Percent Identity: 26.804

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alignment_block:
US-09-821-726-17 x AAB65213

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Align seq 1/1 to: AAB65213 from: 1 to: 184

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40 ATGAAGTTCAACATTCCTTGGCTTGTGGTCTTCTGACTCC 89
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1 MetLysIleLeuValAlaPheLeuValValIleThrIlePheGlyIleG1 17
90 TGCCCTTCTGACTATGATATGATGATGATGATGATGATGATGATG 139
: : : : : : : : : : : : : : : : : : : : : : : : : : :
17 nserHisGlyTyrGlnValPheAsnIleIleSerProSerAsnAnglyG 34
140 GAAGTGGGAGCAGTACGATGATGATGATGATGATGATGATGATGAT 189
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 LysnValGlnGlnThrValThrIleAspAsnGlnLysAsnThrAlaIle 50
190 GTTGACAAATGACATGATGATGATGATGATGATGATGATGATGATG 239
| : : : : : : : : : : : : : : : : : : : : : : : : : : :
51 ValAsnIleHisAlaGlySerCysSerSerThrThrIlePheAspTyr 67
240 AACTGCTTGTGCTAACCAAGCTTGTGATGATGATGATGATGATGATG 289
: : : : : : : : : : : : : : : : : : : : : : : : : : :
67 SHSGLYTYRILEALASERARGVALLEUSERFARGVALACYSHEIIE 84
290 ACACAAATGACAGAGACCATGCCCTCTT..... 321
||||| : : : : : : : : : : : : : : : : : : : : : : : : :
84 eulysmetaspHisGlnAsnIleProLeuAnsnLeuGlnTrpTyr 100
322 .....CAAGCCCTGATGGCGTCAGAGAGAAAGAACCTTCA 359
||||| : : : : : : : : : : : : : : : : : : : : : : : : :

```

101 ILETYGLULYSGLINALALEUASPASMETPHESEANLSTYTRTHR 117
 360 GGGTAAAGGCCCAAGGGGACACCTCCAGACCTGAGTACTGATCA 409
 117 P.....VallystyranProl 123
 410 ACCCCACAGAGTCGACACCTGACAGATT.....GGAATTCATC 453
 123 euglusterleuilelysaspvalasptripheleuileuglyserProile 139
 454 GTTGCCATGTGCAAGGGGATTCACATACATGCTGAGAGATTCAAG 503
 140 GLULYSLEUCYSLSYSHISILEPROLEUTYLYSGLYGLUVALGLUAS 156
 504 AGCAACCTGATTTCTGCTACACGAAAGATGCAACAGCCCATATACTCT 553
 156 nThrlHsAsnValGly...AlaGlyGlyCysAlaLysAlaGlyLeuLeug 172
 554 GGATTTTAACATTTCCTCTGTGAGAGATA 585
 172 lytleuglyllesterilecysalaaspile 182
 seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AA23556

seq_documentation_block:
 ID AAM23556 standard; Protein; 184 AA.

AC AAM23556;

DT 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1081.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder;
 KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.

XX MO200154477-A2.

PD 02-AUG-2001.

PF 25-JAN-2001; 2001WO-US02687.

PR 25-JAN-2000; 2000US-0491404.

PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

PR 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Dmanac RA, Zhang J, Werhman T;

DR WPI: 2001-476164/51.

DR N-PSDB: AAH98215.

PT Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -

PS Claim 20; Page 814-815; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention.

SO Sequence 184 AA:

alignment_scores:
 Quality: 200.00 Length: 194
 Ratio: 1.695 Gaps: 4
 Percent Similarity: 60.825 Percent Identity: 26.289

alignment_block:
 US-09-821-726-17 x AAM23556 ..

Align seg 1/1 to: AAM23556 from: 1 to: 184

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 1 MetLysIleLeuValAlaIlePheLeuValIleLeuThrIlePheGlyIleG1 17
 90 TGCCCTTGCTGACTATAGTATGATGATGATGATGATGATGATGATG 139
 17 nserHISGLYTYRGLUVALPheAsnIleIleIleProSerPheAsnGlyG 34
 140 GAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
 34 LysAsnValGlnGlnThrValThrIleAspAsnGlnLysAsnThrAlaIle 50
 190 GTTGCAATTAACAATGATGATGATGATGATGATGATGATGATGATG 239
 51 IleAsnIleHisIleGlySerSerSerThrThrIlePheAspTyrlly 67
 240 AACTGGCTTGTGCTGATACCAAGGAGGAGGAGGAGGAGGAGGAGG 289
 67 SHISGLYTYRILEAlaSerTrpValLeuSerArgAlaGlyPheIleL 84
 290 ACAAAATGAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 321
 84 eulysMetAspHisGlnAsnIleProProLeuAsnAsnLeuGlnTrpTy 100
 322CAAGCCTTGATGCGCTGTCAGAGAAAGAGCTTCA 359
 101 ILETYGLULYSGLINALALEUASPASMETPHESEANLSTYTRTHR 117
 360 GGTAAGGGCCCAAGGGGACACCTCCCAAGAGCTGAGTACTGATCA 409
 117 P.....VallystyranProl 123
 410 ACCCCACAGAGTCGACACCTGACAGATT.....GGAATTCATC 453
 123 euglusterleuilelysaspvalasptripheleuileuglyserProile 139
 454 GTTGCCATGTGCAAGGGGATTCACATACATGCTGAGAGATTCAAG 503
 140 GLULYSLEUCYSLSYSHISILEPROLEUTYLYSGLYGLUVALGLUAS 156
 504 AGCAACCTGATTTCTGCTACACGAAAGATGCAACAGCCCATATACTCT 553
 156 nThrlHsAsnValGly...AlaGlyGlyCysAlaLysAlaGlyLeuLeug 172
 554 GGATTTTAACATTTCCTCTGTGAGAGATA 585
 172 lytleuglyllesterilecysalaaspile 182
 seq_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:AAE04211

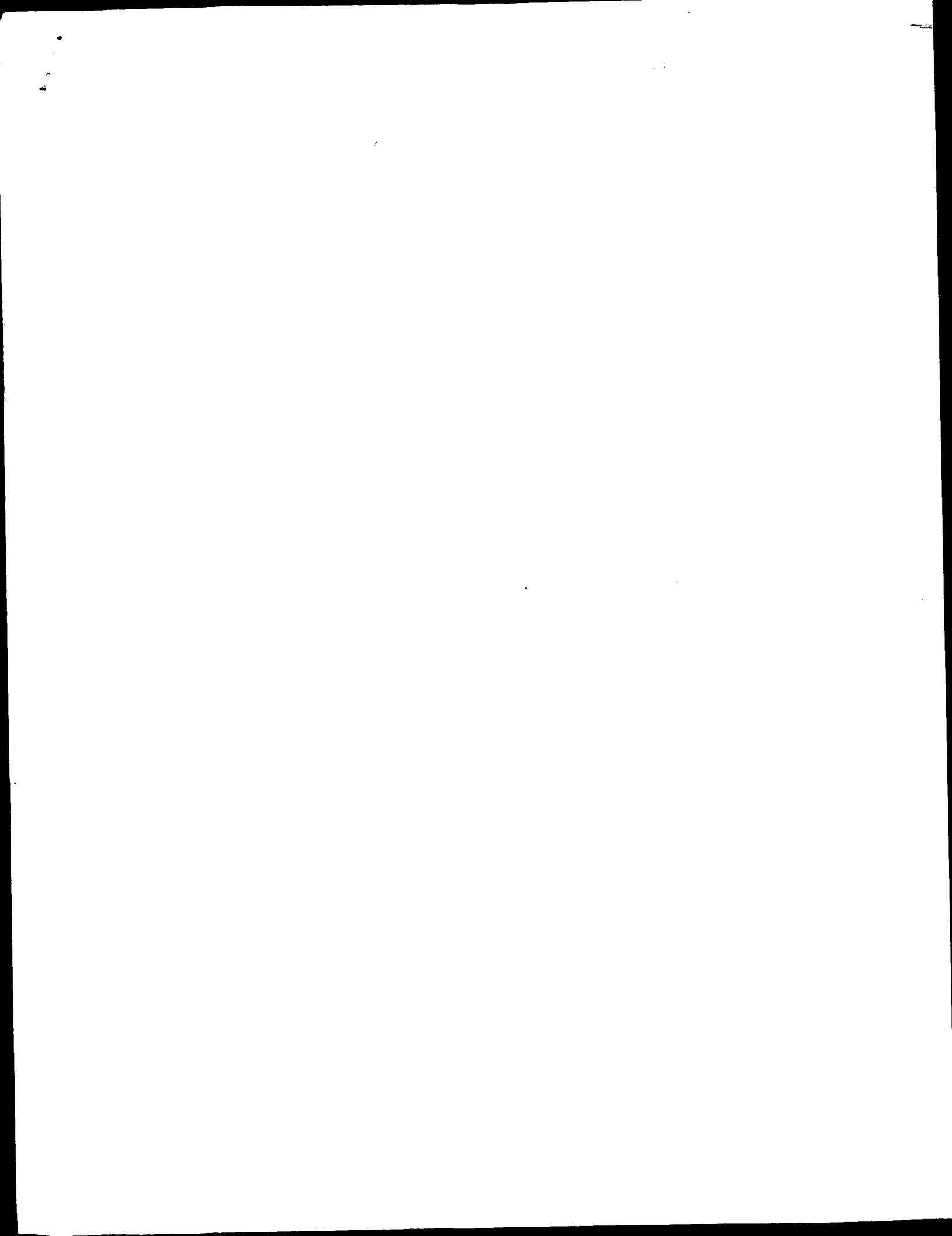
seq_documentation_block:
 ID AAE04211 standard; Protein; 184 AA.

AC AAE04211;

DT 09-AUG-2001 (first entry)

DE Human gene 14 encoded secreted protein HNSA27, SEQ ID NO:66.

XX Human; secreted protein; proliferative disorder; cancer; tumour;




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490 GAAGATTCAGAGCAACCTGATTTGCTACTCAGAAAAGTCATCAG 539
|||||
151 GUGUUGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 167
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540 TGCCATATCTGATTCGATTCATTCATTCCTGCTGAGAGATGACGG 589
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167 TAAATATATATATATATATATATATATATATATATATATATATAT 184
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590 AGAAC 594
|||||
184 TAAAT 185

seq_name: /cgn2_6/ptodata/2/pae/US093_COMB.pep:US-09-377-497-17

seq_documentation_block:
; Sequence 17, Application US/09377497
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: KATO, FUMITSUGU
; APPLICANT: HINO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-17

alignment_scores:
Quality: 803.00 Length: 194
Ratio: 4.412 Gaps: 0
Percent Similarity: 93.814 Percent Identity: 74.227

alignment_block:
US-09-821-726-17 x US-09-377-497-17 ..
Align seg 1/1 to: US-09-377-497-17 from: 1 to: 194

13 TCACTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 62
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1 SerValHisCysPheArgGluAspLysMetLysPheThrIleValPheAl 17
|||||
63 TGGACTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 112
|||||
17 aglyLeuLeuGlyValPheLeuAlaProAlaLeuAlaAsnTyrAsnIleA 34
|||||
113 GTGTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 162
|||||
34 snValAsnAspAspAsnAsnAsnAlaGlySerGlyGlnGlnSerValSer 50
|||||
163 GTCAACATGAACACAGCTGGCCACAGCTTGACATATACATGATGAA 212
|||||
51 ValAsnAsnGlnHisAsnValAlaAsnValAlaAsnAsnAsnGlyTyrP 67
|||||
213 CTCTGAGATGCCCTCTGGGACTATAGAACCTGCTTGTCTGTAACGAC 262
|||||
67 pserTyrPasnSerIleTyrPasnTyrGlyAsnGlyPheAlaIleThrArg 84
|||||
263 TCTTGAGAGAGAGATCATGATTCGTGCAAAATGAAGAGAGCCATG 312
|||||
84 eupheIleLysLysThrCysIleValHisLysMetAsnLysGlnValMet 100
|||||
313 CCTCCCTTCAGACCTTGTATGCTGGTGTCAAGAAAGAGCTTCAAGG 362

```

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101 ProSerIleGlnSerLeuAspAlaLeuValLysGlnLysLysLeuGlnI 117
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363 TAAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 412
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117 yLysGlyProGlyIleProProlLysGlyLeuMetTyrSerValAsn 134
|||||
413 CCACAGATGTCAGACACCTGAGCAAGTTTGAAATTCATTCATTCATG 462
|||||
134 roAsnLysValAspAspLeuSerLysPheGlyLysAsnIleAlaAsnMet 150
|||||
463 TGCAGAGGATTCACATATACATGCTGAGAGATTCAGAGCAACCT 512
|||||
151 CysArgGlyIleProThrTyrMetAlaGlnLysMetGlnGlnLysSer 167
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513 GATTTGCTACTCAGAAAAGCTGATGATGAGCCATATATCTGATTCCT 562
|||||
167 unphePheTyrSerGlyThrCysTyrThrThrSerValLeuThrIleVal 184
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563 ACATTCCTCTCTGAGAGGATGAGGAGGAGGAGGAGGAGGAGGAG 594
|||||
184 splLeuSerPheCysGlyAspThrValGlnAsn 194
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seq_name: /cgn2_6/ptodata/2/pae/US093_COMB.pep:US-09-377-497-69

seq_documentation_block:
; Sequence 69, Application US/09377497
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: KATO, FUMITSUGU
; APPLICANT: HINO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 69
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-69

alignment_scores:
Quality: 803.00 Length: 194
Ratio: 4.412 Gaps: 0
Percent Similarity: 93.814 Percent Identity: 74.227

alignment_block:
US-09-821-726-17 x US-09-377-497-69 ..
Align seg 1/1 to: US-09-377-497-69 from: 1 to: 199

13 TCACTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 62
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6 SerValHisCysPheArgGluAspLysMetLysPheThrIleValPheAl 22
|||||
63 TGGACTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 112
|||||
22 aglyLeuLeuGlyValPheLeuAlaProAlaLeuAlaAsnTyrAsnIleA 39
|||||
113 GTGTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 162
|||||
39 snValAsnAspAspAsnAsnAlaGlySerGlyGlnGlnSerValSer 55
|||||
163 GTCAACATGAACACAGCTGGCCACAGCTTGACATATACATGATGAA 212
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56 ValAsnAsnGlnHisAsnValAlaAsnValAlaAsnAsnAsnGlyTyrP 72

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213 CTCTGGAATGCGCTTGAGCATATAGACGCTTGTCTGTAACGAC 262
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72 pSerTrpAsnSerIleTrpAspTyrGlyAsnGlyPheAlaIaIaThrArgL 89
263 TCTTCGAGAGAGAGCATGATGATTCGTGCACAAATGAAGAAGAGCAG 312
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
89 eupheGlnLysThrCysIleValHisIlyMetAsnLysGluValMet 105
313 CCTCCCTTCAGGCGCTTGATGGCTGTGTCAGAGAAAGAGAGCTTAC 362
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106 ProSerIleGlnSerIleuAspAlaLeuValLysGluLysLysLeuGln 122
363 TAAGGCCCAAGGGGAGCCACCTCCCAAGAGCTGAGTACTGATGATCA 412
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 YLysGlyProGlyGlyProProLysGlyLeuMetLysSerValAsn 139
413 CCAAGAGAGTCGACACCTGGACAGATTTGCAAAATCCATGCTGCATG 462
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139 roAsnLysValAspAspLeuSerLysPheGlyLysAsnIleAlaAsnMet 155
463 TGCAAGGGGATTCACATACATGCTGAAGAGATTCAAGGAGCAACCT 512
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156 CysArgGlyIleProThrIleMetAlaGlnGluMetGlnGluAlaSer 172
513 GATTTCGTACTCAGAAAGTGCATGCCAATATCTGATGATTTCTTA 562
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172 uPhePheTyrSerGlyThrCysTyrThrThrSerValLeuTrpIleVal 189
563 ACATTTCCTTCTGTGAGGAGATPAGCGGAGAGAC 594
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189 splSerPheCysGlyAspThrValGluAsn 199

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seq_name: /cgn2_6/ptodata/2/paa/US098_COMB.pep:US-09-821-726-13

seq_documentation_block:

Sequence 13, Application US/09821726

GENERAL INFORMATION:

APPLICANT: MARTIN, TERENCE E.

APPLICANT: TOBACK, F. GARY

APPLICANT: POWELL, C. THOMAS

APPLICANT: AGARNAL, KAN

TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

FILE REFERENCE: 21459/90913

CURRENT APPLICATION NUMBER: US/09/821,726

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 185

TYPE: PRT

ORGANISM: Homo sapiens

US-09-821-726-13

alignment_scores:

Quality: 779.00 length: 185

Ratio: 4.451 Gaps: 0

Percent Similarity: 94.595 Percent Identity: 75.676

alignment_block:

US-09-821-726-17 x US-09-821-726-13 ..

Align seg 1/1 to: US-09-821-726-13 from: 1 to: 185

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40 ATGAAGTTCACAAATGCTTGTGAGCATTTGTGCTTCTTCTACATCC 89
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1 MetLysPheThrIleValPheAlaGlyLeuGlyValPheLeuAlaIa 17
90 TGCCCTTGTGACTATAGTATCAGTGTCAAGCAGCAGCAGCAGTGGTG 139
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 oAlaLeuAlaAsnTyrAsnIleAspValAsnAspAsnAsnAlaIaG 34

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140 GAAGTGGGCGACAGTCAGTGTGTCACAAATGACACAACTGGCCAAC 189
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34 LysArgGlyGlnGlnSerValSerValAsnAsnGlnHisAsnValAlaAsn 50
190 GTTACAAATTAACAATGATGATGAACCTCTGGAATGCCCTTGGAGCAT 239
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51 ValAspAsnAsnAsnGlnTyrPaspSerTrpAsnSerIleTrpAspTyr 67
240 AACTGGCTTGTGCTTAACCGAGCTTTTCGAGAAAGAGTATGATTTG 289
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 YAsnGlyPheAlaIaIaThrArgLeuPheGlnLysThrCysIleVal 84
290 ACAAAATGAAGAAGAGCCTCCCTCCCTTCACACCTTGTATGCGCTG 339
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 LysLysMetLysLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
340 GTCAAGAAAGAAAGCTTCAGGGTAAAGGCCGAGGGGAGCCACTCCCA 389
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 ValLysGluLysLysLysLeuGlnGlyLysGlyProGlyGlyProPro 117
390 GAGCCTGAGGTACTCAGTCACCCCAAGAGAGTCGACAACTGGACAAGT 439
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 sGlyLeuMetLysSerValAsnProAsnLysValAspAspLeuSerLys 134
440 TTGCAAAATTCATCGTTGCCATGTCAAGGGGATTCCAACATATACGCT 489
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGATTCACAGCAAGCAACCTGATTCGATCTCAGCAAAAGTCATCAG 539
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151 GluGluMetGlnGlnAlaSerLeuPhePheTyrSerGlyThrCysTyr 167
540 TGCAATATATCTGTGATTTCTTAACATTTCTCTGTGAGCAATATACGG 589
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167 rThrSerValLeuTrpIleValAlaAspLysSerPheCysGlyAspThrVal 184
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184 LuAsn 185

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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US98-16318-18

seq_documentation_block:

Sequence 18, Application PC/TUS9816318

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John M.

APPLICANT: Lavallie, Edward R.

APPLICANT: Radele, Lisa A.

APPLICANT: Evans, Cheryl

APPLICANT: Merberg, David

APPLICANT: Treacy, Maurice

APPLICANT: Agostino, Michael J.

APPLICANT: Steininger II, Robert J.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: G16051A

CURRENT APPLICATION NUMBER: PCT/US98/16318

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 18

LENGTH: 185

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US98-16318-18

alignment_scores:

Quality: 775.00 length: 185

Ratio: 4.429 Gaps: 0

Percent Similarity: 94.595 Percent Identity: 75.135

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90 TGCCCTCGTCGACATATGATGATCAGTGTCAACGACGACGCAACAGTGGTG 139
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17  cAlaLeuAlaAsnIlyrIasnlIleAsnValAsnAspAspAsnAsnAlaG 34
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140 GAAGTGGGCGACCACTCAGTCAAGTGTCCAACTTGAACACACAGTGGCCAA 189
    |||||.....:|||||.....:|||||.....:|||||.....:
34  IySerGlyGlnIleSerValSerValAsnAsnGlnHisValAlaAsn 50
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190 GTTGACATTAACAATGATGATGGAACTCCTGGAAATGCCCTGTGGACTATAG 239
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51  ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspIlyrI 67
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240 AACTGGCTTTGCTGTACACCAACCTTGAGAGAAAGTCATCATTTGTC 289
    |||||.....:|||||.....:|||||.....:|||||.....:
67  yAsnIlyPheAlaAlaTrnArgLeuPheGlnIlySlyThrCysIleValH 84
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290 ACAAAATACAGAAAGAGAGCCATGCCCTCCCTTCAAGCCCTTATGCGCTG 339
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84  IlyIleMetAsnIlySglIuValMetProSerIleGlnSerIleuAspAlaIleu 100
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340 GTCAAGGAAAGAAACCTTCAGGGTAAAGGCCCAAGGGGAGCCACCTCCAA 389
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101  ValIySglIyLysIleuGlnIyLysGlyProGlyGlyProProIy 117
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390 GAGCCTGAGGTACTCAGTCAACCCCAACAGAGTCGACAACTGGACAAGT 439
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117  sGlyIleuMetIySerValAsnProAsnIyValAspAspIleSerIySp 134
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440 TTGGAAATTCATCGCTTCGACGTGGAGGGGATTCACAACTACATGAGCT 489
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134  helIyLysAsnIleAlaAsnMetCysArgGlyIleProThrIyMetAla 150
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184 IuAsn 185

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seq_documentation_block:
: Sequence 105, Application US/09684524
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 62 Human Secreted Proteins

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PRIOR APPLICATION NUMBER: US 60/088,825
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PRIOR APPLICATION NUMBER: US 60/093,339
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30

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Ratio: 4.429
Percent Similarity: 94.595 Percent Identity: 75.135

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34 TySerGlyGlnGlnSerValSerValaAsnGlnHisAsnValaAsn 50

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51 ValaAspAsnAsnAsnGlyTTPasPserTTPasSerIleTTPasPtyG 67

240 AACTGCGTTTGCTGTAAACGAGACTCTTCAGAAAGAATCATGATGTC 28

67 yAsnGlyPheAlaIleThrIlePheLeuPheGlnIleTySerIleValaH 84

290 ACAAATTAACAACAGGAGGACATGCCCTGCCCTTCAAGCCTTGATGCCGT 339

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340 GTCAAGCAAAAGACTTCAGGGTAAGGGCCAGGGGGACCACTCCCA 389

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117 SGilyMeItySerValaSnProAsnIlyValaIlySpIlySerIlySp 134

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490 GAAGAGATTCAAGACGACCTGATTCGATACACAAAAGCTACATG 539

151 GlnGlnMetGlnIleValaSerLeuPhePheItySerGlyIlyThrCysIlyTh 167

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184 IlyAsn 185

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  GENERAL INFORMATION:
    APPLICANT: McCoy, Kenneth
    McCoy, John M.
    Lavalie, Edward R.
    Racie, Lisa A.
    Treacy, Maurice
    Spaulding, Vikki
    Agostino, Michael J.
    Howes, Steven H.
    Fechtel, Kim
  TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
  NUMBER OF SEQUENCES: 231
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genetics Institute, Inc.
    STREET: 87 Cambridgepark Drive
    City: Cambridge
    STATE: MA
    COUNTRY: U.S.A.
    ZIP: 02140
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible

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1      OPERATING SYSTEM: PC-DOS/MS-DOS
2      SOFTWARE: Patentin Release #1.0, Version #1.30
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5      :
6      APPLICATION NUMBER: US/09/746,783
7      :
8      FILING DATE: 21-Dec-2000
9      :
10     CLASSIFICATION: <unknown>
11     :
12     ATTORNEY/AGENT INFORMATION:
13     :
14     NAME: Milasincic, Debra J.
15     :
16     REGISTRATION NUMBER: 46,931
17     :
18     TELECOMMUNICATION INFORMATION:
19     :
20     TELEPHONE: (617) 227-7400
21     :
22     TELEFAX: (617) 742-4214
23     :
24     INFORMATION FOR SEQ ID NO: 146:
25     :
26     SEQUENCE CHARACTERISTICS:
27     :
28     LENGTH: 185 amino acids
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34     TOPOLOGY: linear
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Quality:	775.00	Length:	185
Ratio:	4.429	Gaps:	0
Percent Similarity:	94.595	Percent Identity:	75.135

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US-09-821-726-17 x US-09-746-783-146      ..
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390  GAGCCTGAGGTACTAGTCAACCCCAACAGAGTGCACACCTGGACAAGT  439
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: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnovers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerdler, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C56
CURRENT APPLICATION NUMBER: US/09/989,279
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-02
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Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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Align seg 1/1 to: US-09-989-279-211 from: 1 to: 185

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51 ValAspAsnAsnAsnGlyTyrPaspSerTyrPaspSerIleTyrPaspIyrG 67
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184 LuAsn 185

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seq_documentation_block:

Sequence 211, Application US/09989293A

GENERAL INFORMATION:

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07

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69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091633
71	PRIOR FILING DATE: 1998-07-02
72	PRIOR APPLICATION NUMBER: 60/091978
73	PRIOR FILING DATE: 1998-07-07

1 APPLICANT: Eaton, Dan L.
2 APPLICANT: Ferrara, Napoleone
3 APPLICANT: Fong, Sherman
4 APPLICANT: Geider, Hanspeter
5 APPLICANT: Gerritsen, Mary E.
6 APPLICANT: Goddard, Audrey
7 APPLICANT: Godowski, Paul J.
8 APPLICANT: Grimaldi, J. Christopher
9 APPLICANT: Gurney, Austin L.
10 APPLICANT: Kijavini, Ivar J.
11 APPLICANT: Napier, Mary A.
12 APPLICANT: Pan, James
13 APPLICANT: Paoni, Nicholas F.
14 APPLICANT: Roy, Margaret Ann
15 APPLICANT: Stewart, Timothy A.
16 APPLICANT: Thomas, Daniel
17 APPLICANT: Watanabe, Colin K.
18 APPLICANT: Williams, P. Mickey
19 APPLICANT: Wood, William I.
20 APPLICANT: Zhang, Zemin
21 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleid
22 FILE REFERENCE: P2730PIC55
23 CURRENT APPLICATION NUMBER: US/09/989,721
24 PRIOR FILING DATE: 2001-11-19
25 PRIOR APPLICATION NUMBER: 60/049787
26 PRIOR FILING DATE: 1997-06-16
27 PRIOR APPLICATION NUMBER: 60/062250
28 PRIOR FILING DATE: 1997-10-17
29 PRIOR APPLICATION NUMBER: 60/065186
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: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
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: APPLICANT: Goddard, Audrey
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: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavir, Ivar J.
: APPLICANT: Napier, Mary A.
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: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730PIC63
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PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

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Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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390 GACCTGAGTACTGATGATCAACCCCAACAGAGTGCACAACTGCAAGT 439
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-06-22

OM of: US-09-821-726-17 to: Issued_Patents_AA:* out_format: pfs
Date: Sep 4, 2002 5:05 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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Score list:

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Patent No. 6114514
GENERAL INFORMATION:
APPLICANT: SRIVASTAVA, RANJANA
APPLICANT: KUMAR, DEEPAK
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
FILE REFERENCE: U011469-7
CURRENT APPLICATION NUMBER: US/08/997,897C
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
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LENGTH: 430
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Patent No. 6242585
GENERAL INFORMATION:
APPLICANT: Srivastava, Ranjana
APPLICANT: Kumar, Deepak
APPLICANT: Srivastava, Brahm Shanker
TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS SPECIFIC DNA FRAGMENT
FILE REFERENCE: U 011876-4
CURRENT FILING DATE: 1996-09-18
PRIOR APPLICATION NUMBER: 08/997,897
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 430
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4)
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TELEFAX: 904-372-5800

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; HYPOTHETICAL: YES
; ANTI-SENSE: NO
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; INDIVIDUAL ISOLATE: PS63B
; IMMEDIATE SOURCE:
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Patent No. 5616495

GENERAL INFORMATION:

APPLICANT: Payne, Jewel M.

APPLICANT: Kennedy, M. Keith

APPLICANT: Randall, John Brooks

APPLICANT: Meier, Henry

APPLICANT: Wick, Heidi Jane

APPLICANT: Foncetrada, Luis

APPLICANT: Schaeff, Harry E.

APPLICANT: Schwab, George E.

TITLE OF INVENTION: No. 5616495el Bacillus thuringiensis Isolates

TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding

TITLE OF INVENTION: Hymenopteran-Active Toxins

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/304,626

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/887,980

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: M/SCJ 104

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 803 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: linear

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Bacillus thuringiensis

INDIVIDUAL ISOLATE: PS63B

IMMEDIATE SOURCE:

CLONE: E. coli NM522(pMVC1642) NRRL B-18961

US-08-304-626-10

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alignment_scores:
  Quality: 94.00      Length: 184
  Ratio: 0.931       Gaps: 10
  Percent Similarity: 54.891   Percent Identity: 25.543

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alignment_block:

US-09-821-726-17 x US-08-304-626-10 ..

Align seg 1/1 to: US-08-304-626-10 from: 1 to: 803

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51  AATTGCGCTTGTGACTCTTGCTGCTCTGACTCCTGCCCTTGCTG 100
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398  AspCysPheCysTrpPro.TyrGlyValIleLeuAsnTyrAsnLysAsnT 414
    ::::::::::::::::::::

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CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/693,018
 FILING DATE: 03-MAY-1991
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/565,544
 FILING DATE: 10-AUG-1990
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/084,653
 FILING DATE: 12-AUG-1987
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/830,050
 FILING DATE: 31-JAN-1992
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Lloyd, Jeff
 REGISTRATION NUMBER: 35,589
 REFERENCE/DOCKET NUMBER: MA20CCDD1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 803 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Bacillus thuringiensis
 INDIVIDUAL ISOLATE: P563B
 IMMEDIATE SOURCE:
 CLONE: E. coli NM522(PMYC 1642) NRRL B-18961
 OS-08-316-301A-12

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alignment_scores:
    Quality: 94.00      Length: 184
    Ratio: 0.931       Gaps: 10
    Percent Similarity: 54.891   Percent Identity: 25.543

Alignment_block:
US-09-821-726-17 x US-08-316-301A-12 ..

Align seg 1/1 to: US-08-316-301A-12 from: 1 to: 803

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398 ASPLYSPHCYSTIRPPro.TyrglyValIleLeuAsnTyraSLysasnt 414
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101 ACTATAGTATCAAGTGTCAACGACGACGCAACAGTGTGCA..... 141H
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414 hrPhearTYrGLYASPASnaSPProGLyeuSerGIYAspaValGlnLeu 430V
AGTGGCGACGAGTCGACGTGTCAACAATGAACAACACAGCGGGCAC.. 189S
:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
431 ProAlaPrOmetservAl...ValSaNaLaGlInhrGlnIntraAlaGlnTy 446E
:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|

190 .GTTGACATAAACAAATGGATGAACTCCGTGAATGCCCCCTGCG...GACT 235S
:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
446 rThrsAPcylgLuAsnIlelrPrtnrAspThrGLYArGserTrpLeucyst 463K
ATAGAAGCGCTTGCTGCATTACCCAGACCTCTCGAGAGAATGCATCAT 285S
|||::|::|::|::|::|::|::|::|::|::|::|::|::|
463 hrlEuargCLYrCYcsThrthrAsncYSphErProGLYAArgLYCySTyr 479F
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286 GTGCAC.....AAAATGAAGAAGAACCCATGCCC..... 315S
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480 AsnAsnSerThrGlyTyrGlyGluSerCysAsnGlnSerLeuProGlyGln 496
316 .TCGCTCAAGCCCTTGATGCGCTGCGTCAAGGAAAGAAAGACTTCAGGCTA 364
496 nLysIleHisAlaLeuTyrProPheThrGlnThrAsnValLeuGlyGln 513
365 AGGGCCAGGAGGAGCAGCTCCAGAGAGCCTGAGTACTGATCAAGCC 414
513 erGlyLysLeuGlyLeuLeuAlaSerHisIleProTyrAspLeuSerPro 529
415 AACGAGA...GTGCAACACTGGAGCAACTTGGAAAATCCATCGTGGCAT 461
530 AsnAsnThrIleGlyAspLysAspThrAspSerThrAsnIleValAla... 545
462 GTGCAAGGGATTCACACA..... 480
546 ...LysGlyIleProValGlnLysGlyTyrAlaSerSerGlyGlnLysV 561
481 .....TACATGGCTGAAGAGATTCAAGAGCAAACTGATTGCTACTCA 525
561 aLgIleIleArgGlnTyrPheLysnGlyAlaAsnValAlaGlnLeuSer 577

seq_name: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:US-08-611-928-10

seq_documentation_block:
; Sequence 10, Application US/08611928
; Patent No. 5824792
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel
; APPLICANT: Kennedy, M. Keith
; APPLICANT: Randall, John Brooks
; APPLICANT: Meier, Henry
; APPLICANT: Ullick, Heidi Jane
; APPLICANT: Foncerrada, Luis
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Schwab, George E.
; APPLICANT: Fu, Jenny
; TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611, 928
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,232
; FILING DATE: 24-NOV-1993
; APPLICATION NUMBER: US 07/887,980
; FILING DATE: 22-MAY-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/797,645
; FILING DATE: 25-NOV-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/703,977
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794

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; REFERENCE/DOCKET NUMBER: M/SCU104.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; INDIVIDUAL ISOLATE: PS63B
; IMMEDIATE SOURCE:
; CLONE: E. coli NM522(pMTC1642) NRRL B-18961
; US-08-611-928-10

alignment_scores:
Quality: 94.00 Length: 184
Ratio: 0.931 Gaps: 10
Percent Similarity: 54.891 Percent Identity: 25.543

alignment_block:
US-09-821-726-17 x US-08-611-928-10 ..
Align seg 1/1 to: US-08-611-928-10 from: 1 to: 803

51 AATGCTTGTGCTGACCTTGTGCTTCTGACCTGCTGCTGCTG 100
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398 AspCysPheCysTrpPro.TyrGlyValIleLeuAsnTyrAsnLysAsnT 414
101 ACTATAGTATCACTGTCACAGCAGCGCAACAGTGGTGA..... 141
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414 hrPheArgTyrGlyAspAsnAspProGlyLeuSerGlyAspValGlnLeu 430
142 AGTGGCAGCAGTCACTGAGTGAATGAACAACTGAGGAGGCAAC... 189
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431 ProAlaProMetSerVal...ValAsnAlaGlnThrGlnThrAlaGlnTyr 446
190 .GTGCAACATTAACATGATGATGAACTCTGGAATGCTCTGCG...GACT 235
:::|||||:::|||||
446 rThrAspGlyGlnAsnIleTrpThrAspThrGlyArgSerTrpLeuCysT 463
236 ATGAACTGCTTGTGCTGAACCAAGCTCTGCAAGAAAGATCAATGAT 285
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463 hrLeuArgGlyTyrCysThrThrAsnCysPheProGlyArgGlyCysTyr 479
286 GTGCAC.....AAATGAAGAAGAGCCATGCC... 315
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480 AsnAsnSerThrGlyTyrGlyGluSerCysAsnGlnSerLeuProGlyGln 496
316 .TCGCTCAAGCCCTTGATGCGCTGCTCAAGGAAAGAAAGACTTCAGGCTA 364
496 nLysIleHisAlaLeuTyrProPheThrGlnThrAsnValLeuGlyGln 513
365 AGGGCCAGGAGGAGCAGCTCCAGAGAGCCTGAGTACTGATCAAGCC 414
513 erGlyLysLeuGlyLeuLeuAlaSerHisIleProTyrAspLeuSerPro 529
415 AACGAGA...GTGCAACACTGGAGCAACTTGGAAAATCCATCGTGGCAT 461
530 AsnAsnThrIleGlyAspLysAspThrAspSerThrAsnIleValAla... 545
462 GTGCAAGGGATTCACACA..... 480
546 ...LysGlyIleProValGlnLysGlyTyrAlaSerSerGlyGlnLysV 561
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256 ACCAGACTCTTCGAGAGAGATGATGTCACCAAAATGAGAGG. 304
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681 snlys..Sercysglylyshismetlleargthrargthrlleglm 697
305 .....AAGCCATGCCCT..... 316
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697 etgluproglinphleglylalyalaprocyserproglutthrvalglinarlyls 713
317 .....CCCTCAAGCCCTTGATGCG 336
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714 LysCysargAlaarglyscysleuargserProserlleglnlysleuar 730
CTGG.....TCAAGAAAGAGAGCTTCAGGCTTAAGGCCAG 374
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730 gtrparglualargluserargsergluglnleuararglugs 747
375 GGGACCACTCCCAAGAGCTGAGCTACTGATCAACCCCAAGAGACTG 424
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747 erasp.....glygluglnpheproglycysargmet 757
425 ACAACCTGACAGATTGGAAATTCATCGTTGCCATGTCAGAGGAT 474
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758 ArgprotrpthrAlatrpserglucysThrlyscysglyglylyl 774
475 CCAACATACATGGCTG.....AAGAGATTCAAG 502
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774 eglngluargtyrmetthrValylslysargPheyls 786

seq_name: /cgn2_6/plodata/2/1aa/PCTUS_COMB.pep:PCT-US93-03164-10

seq_documentation_block:
; Sequence 10, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP 01
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-03164-10

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alignment_scores:
  Quality: 76.50      Length: 196
  Ratio: 0.890      Gaps: 13
  Percent Similarity: 43.878      Percent Identity: 22.959

alignment_block:
US-09-821-726-17 x PCT-US93-03164-10

Align seq 1/1 to: PCT-US93-03164-10 from: 1 to: 807

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75 .TGTCTTCCTGACTCTGCGCCCTTGCTGACTATAGTACGTCAACGAC 123
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625 pcys.....serValthrCys.....glylysglymetArg 636
124 GAGCGACACAGTGGTGAAG...TGGCGACAGACGACGACGTCAACAA 170
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636 hrArgglinarlymetleuylsleuAlaglueuglyaspCysasnglu 652
171 TGAACACAACTGGCCCAACTTTCACAAATACATGATGACACTCTGCA 220
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653 AspleugluginAlaglulys.....CysmetleuProgl 664
221 ATGCCCTCTGGGACTA.....TAGACTGCTTGTCTGTA 255
||||| :||| :||| :||| :||| :|||
664 ucysprolleaspCysgluLeuserglutrpserglutrpserglucysa 681
256 ACCGACTCTTCGAGAGAGATGATGTCACCAAAATGAGAGAGG. 304
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714 LysCysargAlaarglyscysleuargserProserlleglnlysleuar 730
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seq_name: /cgn2_6/plodata/2/1aa/6A_COMB.pep:US-08-930-996A-4

seq_documentation_block:
; Sequence 4, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: Fluhr, Robert
; APPLICANT: Eshed, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND

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? TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BROWDY AND NEIMARK
? STREET: 419 Seventh Street, N.W., Suite 300
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/930,996A
? FILING DATE: 09-DEC-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US96/05272
? FILING DATE: 15-APR-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: IL 113,373
? FILING DATE: 13-APR-1995
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1240 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-930-996A-4

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  Quality: 76.50      Length: 196
  Ratio: 0.781       Gaps: 9
  Percent Similarity: 50.000   Percent Identity: 23.469

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alignment_block:
  US-09-821-726-17 x US-08-930-996A-4 ..

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Align seg 1/1 to: US-08-930-996A-4 from: 1 to: 1240

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72 TGGTGTCTTCTGACTCTGCCCCCTGTGACTATAGTATCAAGTCAAG 121
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246 uGnGluIle.....GlySerIleAspLeuValA 256
122 ACGACGCAACAGTGTGAGTGGGAGCATGTCAGTGTCAACAAT 171
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256 spAspSnaIleuAsnGlnIleuGlnValLysLeuLysGlnArgLeuLysGln 272
172 GAACACAACTGGCCCAAGCTTGACAAT.....AACAAATGATGAACTC 215
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273 LysLysPheLeuIleValLeuAspAspValTrpAsnAspAsnTyrAsnG 289
216 CTGGATGCGCTC.....TGGGACTATGAAGTGGCT 247
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289 uTrpAspGlnLeuArgAsnValPheValGlnGlyAspIleGlySerLysI 306
248 TTGCTGTACAGCACTCTTCGAGAAGATGATCATGATGATGACAAATG 297
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306 LeIleValThr.....ThrArgLysAspSerValAlaLeuMetMet 319
298 AAGAAGCAAGCCATGCC.....TCCTTCAGGCCCTTGATGC 335
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320 GlyAsnGlnGlnIleSerMetGlyAsnLeuSerThrGlnAlaSerTyr 336
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336 rIeuPheIlnArgHisAlaIaPheGlnAsnMetAspPrometGlyHis.... 351

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386 CCAAGAGCTGAGTACTAGTCAACCCCAACAGAGTCGACACCTGAC 435
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352 .....SerGluLeuGlu 355
436 AAGTTTGAAGAAATCATCTTCCATGTGCAAGGAGTTCACACATACAT 485
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356 GluValGlyArgGlnIleAlaIaLysCysLysGlyLeuPro.....Le 370
486 GCGTGAAGAGATTCAGAGCAACCACTGATTTGCTCTCAGAA..... 528
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370 uAlaLeuLysThrLeuAlaIleLysMetLeuArgSerLysSerGluValGluG 387
529 .....AAGTCATCAGTGGCCAAATATCTCTGATTCCTT 561
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seq_documentation_block:
? Sequence 2, Application US/08896449A
? Patent No. 6040143
? GENERAL INFORMATION:
? APPLICANT: Venta, Patrick J
? APPLICANT: Yuzhaslyan-Gurkan, Vilma
? APPLICANT: Schall, William D
? APPLICANT: Brewer, George J
? TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
? STREET: 5445 Corporate Drive
? CITY: Troy
? STATE: Michigan
? COUNTRY: USA
? ZIP: 48098
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/896,449A
? FILING DATE: 18-JUL-1997
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, Deann F.
? REFERENCE/DOCKET NUMBER: 2115-001226
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 248-641-1600
? TELEFAX: 248-641-0270
? TELEX: 287637
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2813 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-896-449A-2

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alignment_scores:
  Quality: 76.50      Length: 195
  Ratio: 0.922       Gaps: 11
  Percent Similarity: 42.564   Percent Identity: 23.590

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alignment_block:
  US-09-821-726-17/rev x US-08-896-449A-2 ..

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Align seg 1/1 to: US-08-896-449A-2 from: 1 to: 2813

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424 ..CGACTGTGTGGGTTGACTGAGTACCTCAGCCTTGGAGGCGCTC 377
2217 roArgLeuCysGluGlyAsnThrSerSerCysGlyAspGlnPro..... 2231
376 CCCCTGGGCCCTTACCTGAAGCTTCTTTCCTTGACCAAGCATCAAG 327
2232 .....SerGluGlyCysPheCysProAsnGlnValMe 2243
326 GCTTGAGGAGGAGGCGATGCTTCCTTTCATTTGTGCACATGCAATCA 277
2243 tLeuGluGly...SerCysValProGluGluAlaCysThrGlnCysIleS 2259
276 CTTCCTCT.....CGAAGATCTGGTTACAGCAAGC 245
2259 erGluAspGlyValAlaRHisGlnPheLeuGluThrTrpValProAlaHis 2275
244 CAG.....TTCTATAGTCCAGAGGCGCATTCACAGGAG 213
2276 GlnProCysGlnIleCysThrCysLeuSerGlyArgLysValAsnCysTh 2292
212 TTCCATCCATGTTATGTGCAACGTTGGCCACGTTGTTCATGTGTG.. 165
2292 tLeuGlnProCysProThrAlaLysAlaProThrCysGlyProCysGluV 2309
164 .....ACACTCACTGACTGCTGCCCA..... 144
2309 aAlaAlaArgLeuAlaArgGlnAsnAlaValGlnCysCysProGluTyrGluCys 2325
143 .....CTTCACCACTGTTCCCGTCGTCGTT 118
2326 ValCysAspLeuValSerCysAspLeuProProValProPro..... 2339
117 GACACTGATACTATATGTCAGCAAGGCGAGTGCAGAGACACCAAGAA 68
2340 .....CysGluAspGlyLeuGlnMetThrLeuThrA 2350
67 GTCCAGCAAAAGGCAATGTGAACTTCATCTTGCT 33
2350 snProGlyGluCysArgProAsnPheThrCysAla 2361
```




```

|||||
117 yLysGlyProGlyGlyProProProLysGlyLeuMetTySerValAsn 134
413 CCACAGAGCGACACATGGACAACTTGGAAATCCATCGTGGCAG 462
134 romslnysvalaspaspleuserLysPheGlyLysasnillealasnMet 150
463 TGCAGGGGATTCCACATACATAGCTGGAAGATTCAAGAGCAAACT 512
151 CysArgGlyIleProThrThrMetAlaGluMetGlnGluAlaSerle 167
513 GATTGCTACTCGAAGAAAGTCAGTCGCAATATCTCTGGATTCTTA 562
167 uphpeThySerGlyThrCysTyThrThrSerValIleuTrpIleValA 184
563 ACATTCCTCTCTGGAGGAATAGCGGAGAC 594
184 spliserPheCysGlyAspThrValGluAsn 194
seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-991-150-211

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seq_documentation_block:
: Sequence 211, Application US/09991150
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guiney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC48
: CURRENT APPLICATION NUMBER: US/09/991,150
: CURRENT FILING DATE: 2001-11-16
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 211
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-991-150-211

```

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alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429         Gaps: 0
  Percent Similarity: 94.595   Percent Identity: 75.135

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alignment_block:

US-09-821-726-17 x US-09-991-150-211

Align seg 1/1 to: US-09-991-150-211 from: 1 to: 185

40 ATGAAGTTCACAATTCCTTTCGTGAGACTTCTTGATGTCCTTCTGACAC 89

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|||||
1 MetLysPheThrIleValPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
90 TGCCCTTCTGACTATATCACTAGCTGTCACAGACAGCGCAACGTGTG 139
17 calaleuValasnTyAsnIleValasnValasnAspAspAsnAsnAlaG 34
140 GAAGTGGCGACAGTCAGTGTGATGTCACAAATCAACAACTGGCCAAC 189
34 LysSerGlyGlnGlnSerValSerValasnAsnGlnIleAsnValAlaAsn 50
190 GTTGCAATTAACAATGGATGGAACTCCTGGAATGCCCTGGGACTATAG 239
51 ValaspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrl 67
240 AAGTGGCTTCTGCTTAACCCAGACTCTGCGAAGAACATCATGCTTGGC 289
67 yasnGlyPheAlaIleThrAlaGluPheGlnLysLysThrCysIleValH 84
290 ACAAAATGAAGAGAGAACCCATGCCCTCCCTTCACAGCCCTGATGCGCTG 339
84 lslYsMetAsnLysGluValMetProSerIleGlnSerIleAspAlaLeu 100
340 GTCAAGGAAAGAAAGCTTCACGGTAAAGGCCCAAGGACCACTCCCAA 389
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyLysProPropoly 117
390 GAGCCTGAGTACTGCTGACGCAACCCCAACAGAGTCGACCACTGGACAGT 439
117 sGlyLeuMetLysSerValAsnProAsnLysValaspAspLeuSerLysP 134
440 TTGGAATTCATCGTTCGATGTGCAAGGGGATTCACATACATAGCTGT 489
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTTCTGACTCAAAAAGTCATCAG 539
151 GluGluMetGlnGluAlaSerLeuPhePheTySerGlyThrCysTyTrpH 167
540 TGCCAAATTAATCTGATTCATTCATTCCTTCTGGAGGAATACCGG 589
167 rThSerValLeuTrpIleValaspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
184 lUasn 185

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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-720-533-49
seq_documentation_block:
: Sequence 49, Application US/09720533
: GENERAL INFORMATION:
: APPLICANT: INCYTE PHARMACEUTICALS, INC.
: APPLICANT: Lal, Preeti
: APPLICANT: TANG, Y. Tom
: APPLICANT: GORGONE, Gina A.
: APPLICANT: CORLEY, Neil C.
: APPLICANT: GUEGLER, Karl J.
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: AKERLOW, Ingrid E.
: APPLICANT: AU-YOUNG, Janice
: APPLICANT: YUE, Henry
: APPLICANT: PATTERSON, Chandra
: APPLICANT: REDDY, Roopa
: APPLICANT: HILMAN, Jennifer L.
: APPLICANT: BANDMAN, Olga
: TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
: FILE REFERENCE: PF-0541 PCT
: CURRENT APPLICATION NUMBER: US/09/720,533
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
: PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
: NUMBER OF SEQ ID NOS: 268

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; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

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alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429        Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135

```

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alignment_block:
US-09-821-726-17 x US-09-720-533-49  ..

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Align seg 1/1  to: US-09-720-533-49  from: 1  to: 185

```

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40 ATGAAGTTCAACAATGCTTCTGCTGACTTCTGTGTCCTCTGACTCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlyValPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATGATGTCACAGACGACGCGACAGTGCTG 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 cAlaLeuAlaAsnTyraSnIleAsnValAsnAspAsnAsnAlaG 34
140 GAAGTGGGCGACGACGTCAGTCAAGTGTCAACATGACACAACTGGCCAA 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LySerGIyGInGInSerValSerValAsnAsnGInIhIsnValAlaAsn 50
190 GTTGACAATACACAATGATGATGACCTCTGGAATGCCCTCGGAGCATATG 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ValAspAsnAsnAsnGlyTrrPaspSerTrrPaspSerIleTrrPaspIyG 67
240 AACTGCTTTGCTGTAAACGACACTCTTCGAGAAGAAGTCATGCATTGTC 289
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yAsnGlyPheAlaAlaThrArgLeuPheGInIhIsnLysThrCysIleValH 84
290 ACAAAATGAAGAAGAACCATGCTCCCTCCCTTAAAGCCCTTGATGCGTGC 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 IsLyMetLysnLysGluValMetProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAAGCTTCAGGGTAAGGGCCGAGGGGACCACTGCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValLyGluLysLysLeuGInGlyLysGlyProGlyGlyProProProLy 117
390 GAGCTTGAGTACTGACTCAACCCCAACAGAGTGCACAACTGGACAACT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sGlyLeuMetTySerValAsnProAsnLysValAspAspLeuSerLySp 134
440 TTGGAATTCATCGATGTCATGTCGAAGGGCATTCACACATACATGCGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyMetAla 150
490 GAAGAGATTCAGAGCAAACTGATTTGTACTACAGAAAAGTGCATCGAC 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GluGluMetGInGInLysLeuPhePheTySerClyThrCysTyrrH 167
540 TGCCAAATATGCTGATTTTAACTTTCTCTCTGAGAGCAATAGCGG 589
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 rThrSerValLeuTrrPleValAspLysPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

```

```

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-119-480-148
seq_documentation_block:
; Sequence 148, Application US/10119480

```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-119-480-148

```

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alignment_scores:
  Quality: 775.00      Length: 185
  Ratio: 4.429        Gaps: 0
  Percent Similarity: 94.595  Percent Identity: 75.135

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alignment_block:
US-09-821-726-17 x US-10-119-480-148  ..

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Align seg 1/1  to: US-10-119-480-148  from: 1  to: 185

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```

40 ATGAAGTTCAACAATGCTTCTGCTGACTTCTGTGTCCTCTGACTCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlyValPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATGATGTCACAGACGACGCGACAGTGCTG 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 cAlaLeuAlaAsnTyraSnIleAsnValAsnAspAsnAsnAlaG 34
140 GAAGTGGGCGACGACGTCAGTCAAGTGTCAACATGACACAACTGGCCAA 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LySerClyGInGInSerValSerValAsnAsnGInIhIsnValAlaAsn 50
190 GTTGACAATACACAATGATGATGACCTCTGGAATGCCCTCGGAGCATATG 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ValAspAsnAsnAsnGlyTrrPaspSerTrrPaspSerIleTrrPaspIyG 67
240 AACTGCTTTGCTGTAAACGACACTCTTCGAGAAGAAGTCATGCATTGTC 289
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yAsnGlyPheAlaAlaThrArgLeuPheGInIhIsnLysThrCysIleValH 84
290 ACAAAATGAAGAAGAACCATGCTCCCTCCCTTAAAGCCCTTGATGCGTGC 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 IsLyMetLysnLysGluValMetProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAAGCTTCAGGGTAAGGGCCGAGGGGACCACTGCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValLyGluLysLysLeuGInGlyLysGlyProGlyGlyProProProLy 117
390 GAGCTTGAGTACTGACTCAACCCCAACAGAGTGCACAACTGGACAACT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sGlyLeuMetTySerValAsnProAsnLysValAspAspLeuSerLySp 134
440 TTGGAATTCATCGATGTCATGTCGAAGGGCATTCACACATACATGCGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyMetAla 150
490 GAAGAGATTCAGAGCAAACTGATTTGTACTACAGAAAAGTGCATCGAC 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



```

17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAsnAlaG 34
140 GAAGTGGGAGCAGTCAAGTCAAGTCAACATGAACACAGTGGCCAA 189
134 lYserGIyngInserValSerValAsnSngIuhIsaValAlaAsn 50
190 GTTGACAAATAACAATGAGTGAACCTCTGGAATGCCCTGGAGATTA 239
51 ValAspAsnAsnAsnGlyTrrPaspSerTrrPaspSerIleTrrPasp 67
240 AACGCGCTTGCTGTACACAGACTCTCGAGAGAGAAAGTCAATGTGC 289
67 yAsnGIyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleVal 84
290 ACAAAATGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 339
84 lYsMetAsnLysGlnValMetProSerIleGlnSerIleuAspAlaLeu 100
340 GTCAAGAGAAAAGAGCTTCAAGGTTAAGGGCCAGAGGGGAGACCTCC 389
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyProProGly 117
390 GAGCTGAGTCACTCAACCCCAACAGAGTGCAGAACCTGAGCAAGT 439
117 sGIyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLys 134
440 TTGGAATATCCATGCTGCATGTCAGAGGAGATTCACATACATAGCT 489
134 heGlyLysAsnIleAlaAsnMetCysArgLysIleProIleTrrYrMetAla 150
490 GAAGAGATTCAAGAGCAAACTGATTTGCTACTCAGAAAAGTGCATCAG 539
151 GluIleuMetGlnGlnIleAsnLeuPhePheTyrSerGIyThrCysTyrTh 167
540 TGCCATATATCTGATTCCTTAACATTTCTCTGAGAGAAATACCG 589
167 rThSerValLeuTrrPileValAspIleSerPheCysGIyAspThrValG 184
590 AGAAC 594
184 LuAsn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-164-148

seq_documentation_block:
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31

```

```

; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
US-09-821-726-17 x US-10-216-164-148 ..
Align seg 1/1 to: US-10-216-164-148 from: 1 to: 185

40 ATGAAGTTACAAATGCCCTTTCGACTTCTGTGCTCTCTCTGACTGCC 89
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlyValAlaPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATGATGATGTCACAGCAGCAGCAACAGTGTG 139
17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAlaG 34
140 GAAGTGGGAGAGTCAAGTCAAGTCAACATGAACACAGTGGCCAA 189
34 lYserGIyngInserValSerValAsnSngIuhIsaValAlaAsn 50
190 GTTGACAAATAACAATGAGTGAACCTCTGGAATGCCCTGGAGATTA 239
51 ValAspAsnAsnAsnGlyTrrPaspSerTrrPaspSerIleTrrPaspTyrGI 67
240 AACGCGCTTGCTGTACACAGACTCTCGAGAGAGAAAGTCAATGTGC 289
67 yAsnGIyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleVal 84
290 ACAAAATGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 339
84 lYsMetAsnLysGlnValMetProSerIleGlnSerIleuAspAlaLeu 100
340 GTCAAGAGAAAAGAGCTTCAAGGTTAAGGGCCAGAGGGGAGACCTCC 389
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyProProGly 117
390 GAGCTGAGTCACTCAACCCCAACAGAGTGCAGAACCTGAGCAAGT 439
117 sGIyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLys 134
440 TTGGAATATCCATGCTGCATGTCAGAGGAGATTCACATACATAGCT 489
151 GluIleuMetGlnGlnIleAsnLeuPhePheTyrSerGIyThrCysTyrTh 167
540 TGCCATATATCTGATTCCTTAACATTTCTCTGAGAGAAATACCG 589
167 rThSerValLeuTrrPileValAspIleSerPheCysGIyAspThrValG 184

```

590 AGAAC 594
 |||||
 184 Luasn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-165-148

seq_documentation_block:

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: Sequence 148, Application US/10216165
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C7
: CURRENT APPLICATION NUMBER: US/10/216,165
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining prior Application data removed - See file wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 148
: LENGTH: 185
: TYPE: PR1
: ORGANISM: Homo Sapien
: US-10-216-165-148

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alignment_scores:

Quality: 775.00 Length: 185
 Ratio: 4.429 Gaps: 0
 Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:

US-09-821-726-17 x US-10-216-165-148 ..

Align seg 1/1 to: US-10-216-165-148 from: 1 to: 185

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40 ATGAAGTTCACAAATGGCTTTGGCTGCTTCTCTCTCTGACTCC 89
|||||
1 MetlyspherthriLevalPhealaglyLeuleuclyValPheleualapr 17
TGCCTTGCTGATATGATATGATGCTGACAGAGAGCAAGCAGTGTG 139
|||||
17 OAlaleuAlasntyrAsnIleAsnValAsnAspAsnAsnAlag 34
140 GAAGTGGGACGACGTCAGTGAAGTGTCAACAATGAAACAGAGTGGCCAC 189

```

```

|||||
34 IySerGlyInGInserValSerValAsnAsnGluHisnValAlaAsn 50
GTTGACAAATACAAATGATGACAACTCTCGAATGCCCTCGGACTATAG 239
|||||
51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTrpG 67
AAGTGGCTTTGCTGTACACGACTCTTCGACAGAGAATGATCATTTGGC 289
|||||
67 yAsnGlyPheAlaIaIaThrArgLeuPheGlnIlystysThrCysIleValH 84
IstysMetAsnIlysgluValMetProserIleGlnSerIleAsnAspAla 100
340 GTCAAGGAAGAAACACCTTCAGGGTAAAGGCCAGGGGACCACTCCCA 389
|||||
101 ValIlysgluIlysglyLeuGlnIlysglyProglyProglyProgly 117
390 GAGCCTGAGGTACTGACGTCACCCACAGAGTGCACAACTGACAGAGT 439
|||||
117 sGlyLeuMetIlySerValAsnProAsnIlyValAspAsnIlyserIysP 134
440 TTGAAATATCATCGTTGCCATGTGCAAGGGGATTCACAAATACATGCT 489
|||||
134 heGlyIysAsnIleAlaIaAsnMetCysArgglyIleProThrIyMetAla 150
490 GAAGATTCAGAGAGCAACCTGATTCGTAATCTAGAAAAGTGCATGAG 539
|||||
151 GluGluMetGlnGluIaSerLeuPhePheIyThrCysTyrTh 167
540 TGCCAATATATCTGTGATCTTAACATTTCTCTGTGAGGAATAGCGG 589
|||||
167 rThrSerValLeuTrpIleValAspIleSerPheCysIlyspThrValG 184
590 AGAAC 594
|||||
184 Luasn 185

```

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-166-148

seq_documentation_block:

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: Sequence 148, Application US/10216166
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C9
: CURRENT APPLICATION NUMBER: US/10/216,166
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910

```

```
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO 148
;; LENGTH: 185
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-216-166-148
```

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alignment_scores:
    Quality: 775.00      Length: 185
    Ratio: 4.429         Gaps: 0
    Percent Similarity: 94.595      Percent Identity: 75.135
```

alignment_block:

US-09-821-726-17 x US-10-216-166-148

Align seg 1/1 to: US-10-216-166-148 from: 1 to: 185

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40 ATGAAGTTCACAATTCCTTGGCTGACTTCTTGGTGTCTTCTGACTCC 89
|||||.....:|||||.....:|||||.....:|||||.....:
1 MetLysPheThrIleValPheAlaGlyLeuGlyValPheLeuAlaPr 17
TGCCTTCTGCTATAGTATAGTGTCAAGCAGCAGCGCAACAGTG 139
|||||.....:|||||.....:|||||.....:|||||.....:
17 CAlaLeuAlaAsnTyraIleAsnValAsnAspAsnAsnAlaG 34
GAAGTGGCAGCAGTCAAGTGTCAACAATGAACACAGCTGGCCAA 189
|||||.....:|||||.....:|||||.....:|||||.....:
34 LySerGlyGlnGlnSerValSerValAsnAsnGlnHisValAlaAsn 50
GTTGACAAATACAAATGATGATGAACTCTGGAATGCCCTGGAGCTATAG 239
|||||.....:|||||.....:|||||.....:|||||.....:
51 ValAspAsnAsnAsnGlyTyrPaspSerTyrPaspSerIleTyrPaspTyrGcl 67
AAGTGGCTTGTGTTAACCAGACTCTTGAGAGAAGAGTACATGCTGCG 289
|||||.....:|||||.....:|||||.....:|||||.....:
67 yAsnGlyPheAlaAlaTyrArgLeuPheGlnLysLysThrCysIleValH 84
ACAAATGAAGAAGAGAGAGCCATGCCCTTCAAGCCCTTGATGCGCTG 339
|||||.....:|||||.....:|||||.....:|||||.....:
84 IsLysMetAsnLysGlnValMetProSerIleGlnSerLeuAspAlaLeu 100
GTCAAGAAAAAGAGCTTCAGGGTAAGGGCCAGGGGAGCACCCTCCAA 389
|||||.....:|||||.....:|||||.....:|||||.....:
340 GTCAAGAAAAAGAGCTTCAGGGTAAGGGCCAGGGGAGCACCCTCCAA 389
|||||.....:|||||.....:|||||.....:|||||.....:
101 ValLysGlyLysLysLeuGlnGlyLysGlyProGlyGlyProProLys 117
GAGCCTGAGGTAAGTCAAGCCCAAGAGTGCAGCAAGTGCAGCAAGT 439
|||||.....:|||||.....:|||||.....:|||||.....:
117 sGlyLeuMetLysSerValAsnProAsnLysValAspAspLeuSerLysP 134
TTGGAATTCATCGTTCATGTCAGAGGAGATTCAAATACATGAGCT 489
|||||.....:|||||.....:|||||.....:|||||.....:
440 TTGGAATTCATCGTTCATGTCAGAGGAGATTCAAATACATGAGCT 489
|||||.....:|||||.....:|||||.....:|||||.....:
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
GAGAGGATTCAGAGCAACCGATTTGCTACTCAGAAAGATGCATCAG 539
|||||.....:|||||.....:|||||.....:|||||.....:
151 GlnGlnMetGlnGlnAlaSerLeuPhePheThrCysTyr 167
TGCCCAATTAATCTTGATTTTAATCTTCTGCTGGAGCAATAGCGG 589
|||||.....:|||||.....:|||||.....:|||||.....:
540 TGCCCAATTAATCTTGATTTTAATCTTCTGCTGGAGCAATAGCGG 589
|||||.....:|||||.....:|||||.....:|||||.....:
167 rThSerValLeuTyrPheValAspIleSerPheCysGlyAspThrValG 184
AGAAC 594
|||||
184 LuAsn 185
```

seq_name: /cgn2_6/plodata/2/paa/us10_NEW.COMB.pep:US-10-216-167-148

seq_documentation_block:

Sequence 148 Application US/10216167

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gueney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin I.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3530P1C4

CURRENT APPLICATION NUMBER: US/10/216,167

PRIOR FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063549

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/064103

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/069873

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079728

PRIOR FILING DATE: 1998-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 246

SEQ ID NO 148

LENGTH: 185

TYPE: PRT

ORGANISM: Homo Sapien

US-10-216-167-148

alignment_scores:

Quality: 775.00 Length: 185

Ratio: 4.429 Gaps: 0

Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:

US-09-821-726-17 x US-10-216-167-148

Align seg 1/1 to: US-10-216-167-148 from: 1 to: 185

```
40 ATGAAGTTCACAATTCCTTGGCTGACTTCTTGGTGTCTTCTGACTCC 89
|||||.....:|||||.....:|||||.....:|||||.....:
1 MetLysPheThrIleValPheAlaGlyLeuGlyValPheLeuAlaPr 17
TGCCTTCTGCTATAGTATAGTGTCAAGCAGCAGCGCAACAGTG 139
|||||.....:|||||.....:|||||.....:|||||.....:
17 CAlaLeuAlaAsnTyraIleAsnValAsnAspAsnAsnAlaG 34
GAAGTGGCAGCAGTCAAGTGTCAACAATGAACACAGCTGGCCAA 189
|||||.....:|||||.....:|||||.....:|||||.....:
34 LySerGlyGlnGlnSerValSerValAsnAsnGlnHisValAlaAsn 50
```



```

190 GTTGCAATTAACAATGATGGAAGTCTGGAATGCCCTGGAGCATATAG 239
|||||.....:|||||
51 ValaspsasnasnsglyTrpaspserTrpaspserIletrpaspTyrGI 67
240 AACGGCTTGTCTGTAACCCAGACTCTTCGAGAAAGATGATGCTTGTGC 289
:::|||||.....:|||||
67 yasnlglyPheAlaIatThrArgLeuPheGlnLysLysThrcysIleValH 84
290 ACAAATGAGAGAGAGAGCCATGCCCTCCCTTCGAAGCCCTGATGCCCTG 339
|||||.....:|||||
84 IsLysMetAsnLysGluValMetProserIleGlnSerLeuAspAlaLeu 100
340 GTCAAGGAGAGAGAGCTTCAGGGTAAAGGCCCAAGGGAGCCACCTCCCA 389
|||||.....:|||||
101 ValLysGluLysLysLeuGlnGlyLysGlyProGlyLysPropProly 117
390 GAGCCTGAGTACTGAGCAACCCCAAGACAGTCGAGCAACCTGAGCAAGT 439
|||||.....:|||||
117 sGlyLeuMetLysIserValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATAATCCATCGTTGCCATGTGCAAGGGAGATTCCACATACATGCT 489
|||||.....:|||||
134 heGlyLysAsnLleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAAGGAGCAACCTGATTGCTACTCAGAAAAAGTGCATCAG 539
|||||.....:|||||
151 GluGlnMetGlnGluAlaSerLeuPhePheThrcysGlyThrcysTyrTh 167
540 TGCCAATATATCTGATTCATTAACTTCTCTCTGAGAGAAATAGCGG 589
|||||.....:|||||
167 rThSerValLeuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-168-148

seq_documentation_block:
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gertlisen, Maty
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Collin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216.168
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

```

```

; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-216-168-148

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

alignment_block:
US-09-821-726-17 x US-10-216-168-148 ..

Align seg 1/1 to: US-10-216-168-148 from: 1 to: 185

40 ATGAAGTTCACAATTGCTTGTGCTGAGCTTCTGTGCTGCTGCTGCTGCTG 89
|||||.....:|||||
1 MetLysPheThrIleValAlaPheAlaGlyLeuGlyValAlaPheAlaIaPr 17
90 TGCCCTGCTGCTATAGTATGATGATGATGATGATGATGATGATGATGATG 139
|||||.....:|||||
17 oAlaLeuAlaAsnTyrAsnLleAsnValAsnAspAspAsnAsnAlaG 34
140 GAAGTGGCAGCAGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 189
|||||.....:|||||
34 LysSerGlyGlnGlnSerValSerValAsnAsnGlnHisAsnValAlaAsn 50
190 GTTGACATTAACAATGATGATGATGATGATGATGATGATGATGATGATG 239
|||||.....:|||||
51 ValAspAsnAsnAsnGlyTrpaspserTrpaspserIletrpaspTyrGI 67
240 AACTGCTTGTGCTGTAACCAAGCTCTGAGAGAAAGTCAATGATGCTGCT 289
|||||.....:|||||
67 yasnlglyPheAlaIatThrArgLeuPheGlnLysLysThrcysIleValH 84
290 ACAAATGAGAGAGAGAGCCATGCCCTCCCTTCGAAGCCCTGATGCCCTG 339
|||||.....:|||||
84 IsLysMetAsnLysGluValMetProserIleGlnSerLeuAspAlaLeu 100
340 GTCAAGGAGAGAGCTTCAGGGTAAAGGCCCAAGGGAGCCACCTCCCA 389
|||||.....:|||||
101 ValLysGluLysLysLeuGlnGlyLysGlyProGlyLysPropProly 117
390 GAGCCTGAGTACTGAGCAACCCCAAGACAGTCGAGCAACCTGAGCAAGT 439
|||||.....:|||||
117 sGlyLeuMetLysIserValAsnProAsnLysValAspAspLeuSerLysP 134
440 TTGGAATAATCCATCGTTGCCATGTGCAAGGGAGATTCCACATACATGCT 489
|||||.....:|||||
134 heGlyLysAsnLleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
490 GAAGAGATTCAAGGAGCAACCTGATTGCTACTCAGAAAAAGTGCATCAG 539
|||||.....:|||||
151 GluGlnMetGlnGluAlaSerLeuPhePheThrcysGlyThrcysTyrTh 167
540 TGCCAATATATCTGATTCATTAACTTCTCTCTGAGAGAAATAGCGG 589
|||||.....:|||||
167 rThSerValLeuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 LuAsn 185

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-216-160-148

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seq_documentation_block:
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-216-160-148

```

```

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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alignment_block:

US-09-821-726-17 x US-10-216-160-148 ..

Align seg 1/1 to: US-10-216-160-148 from: 1 to: 185

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40 ATGAAGTTCAAAATGCTTGGCTGAGCTCTTGGTCTTCCGACTCC 89
|||||.....|.....|.....|.....|.....|.....|
1 MetLysPheThrIleValPheAlaGlyLeuLeuClYValPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATCAGTGTCAACGACGACGCAACAGTGTG 139
|||||.....|.....|.....|.....|.....|.....|
17 cAlaLeuAlaAsnTyraSniIleAsnValaAsnAspAsnAsnAlaG 34
140 GAAATGGGGCAGCTGAGTGTCAACAATGACACACAGTGGCCAAAC 189
|||||.....|.....|.....|.....|.....|.....|
34 LySerGlyGlnGlnSerValSerValaAsnAsnGlnIleHisValaAlaAsn 50
190 GTTGACATATAACAATGATGGAATGCTCTGGAATGCCCTTGGAATATAG 239
|||||.....|.....|.....|.....|.....|.....|
51 ValaSpAsnAsnAsnGlnYTrpAspSerTrpAsnSerIleTrpAspTyrG 67
240 AACTGGCTTGTCTGTACACAGACTCTTCGAGAAAGATCATGCTTGTGC 289
|||||.....|.....|.....|.....|.....|.....|
67 yAsnGlyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleValH 84
290 ACAAAATTAAGAAGAGCCATGCCCTCCCTTCAAGCCCTTGATGCCGTG 339
|||||.....|.....|.....|.....|.....|.....|
84 IlysMetAsnLysGlnValaMetProSerIleGlnSerIleAsnAlaLeu 100
340 GTCAAGAAAAGAAAGCTTCAAGGTAAGGGCCAGGGGACCACTCCCAA 389
|||||.....|.....|.....|.....|.....|.....|
101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyPropropGly 117
390 GAGCTGAGTGTCTGACGACACCCACACAGAGTGTGACAACTGGACAACT 439
|||||.....|.....|.....|.....|.....|.....|
117 sGlyLeuMetTySerValaAsnProAsnLysValaAspAspLeuSerLysP 134
440 TTGGAATAATCAATGCTTGCATGTGCAAGGAGGATTCACATATACATGCT 489
|||||.....|.....|.....|.....|.....|.....|
134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150

```

```

490 GAAGATTTCAAGAGCAACCTGATTTCGTACTCAGAAAAATGCATCAG 539
|||||.....|.....|.....|.....|.....|.....|
151 GluGlnMetGlnGlnAlaSerLeuPhePheIleArgLysThrCysTyrTh 167
540 TGCCATATACTGTGATTTTCAACATTTCTTGTGAGAGGAAATACCG 589
|||||.....|.....|.....|.....|.....|.....|
167 ThrSerValLeuTrpIleValaAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
184 LuAsn 185

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seq_name: /cgn2_6/pilotdata/2/paa/US10_NEW_COMB.pep:US-10-218-849-148

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seq_documentation_block:
; Sequence 148, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-218-849-148

```

```

alignment_scores:
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135

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alignment_block:

US-09-821-726-17 x US-10-218-849-148 ..

Align seg 1/1 to: US-10-218-849-148 from: 1 to: 185

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40 ATGAAGTTCAAAATGCTTGGCTGAGCTCTTGGTCTTCCGACTCC 89
|||||.....|.....|.....|.....|.....|.....|
1 MetLysPheThrIleValPheAlaGlyLeuLeuClYValPheLeuAlaPr 17
90 TGCCCTTGCTGACTATAGTATCAGTGTCAACGACGACGCAACAGTGTG 139
|||||.....|.....|.....|.....|.....|.....|
17 cAlaLeuAlaAsnTyraSniIleAsnValaAsnAspAsnAsnAlaG 34
140 GAAATGGGGCAGCTGAGTGTCAACAATGACACACAGTGGCCAAAC 189
|||||.....|.....|.....|.....|.....|.....|
34 LySerGlyGlnGlnSerValaAsnAsnGlnIleHisValaAlaAsn 50
190 GTTGACATATAACAATGATGGAATGCTCTGGAATGCCCTTGGAATATAG 239
|||||.....|.....|.....|.....|.....|.....|
51 ValaSpAsnAsnAsnGlnYTrpAspSerTrpAsnSerIleTrpAspTyrG 67
240 AACTGGCTTGTCTGTACACAGACTCTTCGAGAAAGATCATGCTTGTGC 289
|||||.....|.....|.....|.....|.....|.....|
67 yAsnGlyPheAlaIaThrArgLeuPheGlnLysLysThrCysIleValH 84

```

```
290 ACAAATGACAGAGAGACCATGCCCTCCCTTCAAGCCCTTGATGCGCTG 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 lslYmeTAsnIlySgluValmetProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAACGCTTCAGGCTTAAGGCCCGGAGGACCACTCCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValYsgIuIySlySleuGInGlyLysGlyProGlyProProProly 117
390 GAGCCTGAGTACTAGTCAACCCCAACAGAGTGCACATCGGACAGT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sglYeuMetIySerValAsnProAsnIySValAspAspLeuSerIySp 134
440 TTGGAATTCATCGCTTCCATGTGCAGAGGATTCACATACATAGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgIlyIleProThrTyMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTCGACTACAAAAGTCATCAG 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GluGluMetGInGluAlaSerLeuPhePheIySerGlyThrcysTyrrh 167
540 TGCCAAATATCTGTGATTTCTTAACATTTCTTGTGAGGAATAGCG 589
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 rThSerValleuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 IuAsn 185
```

seq_name: /cgn2_6/plodata/2/paa/US10_NEW_COMB.pep:US-10-218-930-148

seq_documentation_block:

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; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C13
; CURRENT APPLICATION NUMBER: US/10/218,930
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148
```

alignment_scores:

```
Quality: 775.00 Length: 185
Ratio: 4.429 Gaps: 0
Percent Similarity: 94.595 Percent Identity: 75.135
```

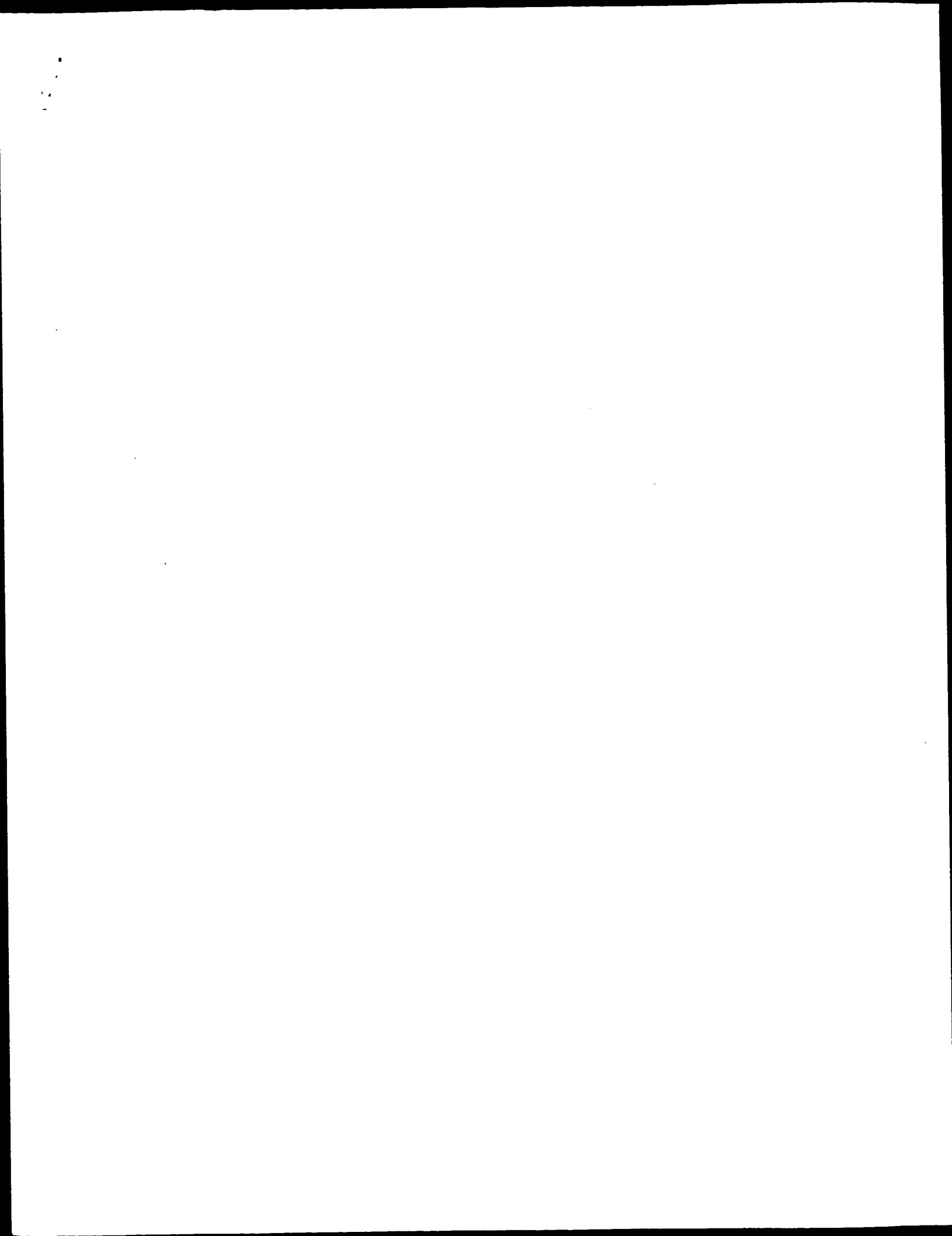
alignment_block:

US-09-821-726-17 x US-10-218-930-148 ..

Align seg 1/1 to: US-10-218-930-148 from: 1 to: 185

```
40 ATGAAGTTCACAAATTCGCTTGTGAGACTTCTTGCTGCTCTCTACATCC 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetLysPheThrIleValIlePheAlaGlyLeuGlyValIlePheValAlaPr 17
90 TGCCCTTGCTGACTATAGTATCAGTGTCAACGACGCAACAGTGTGTG 139
```

```
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 oAlaLeuAlaAsnTyfAsnIleAsnValAsnAspAspAsnAsnAlaG 34
140 GAAGTGGGACAGCAGTCACTGAGTGTCAACATGAAACCAACGTGGCCAA 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 IySerGlyGInGInSerValSerValAsnAsnGluHisValAlaAsn 50
190 GTTGCACATTAACATGATGATGAACTCTCGAATGCCCTTGGGACTATAG 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ValAspAsnAsnAsnGlyTyfPaspSerTrpAsnSerIleTrpAspTyrgl 67
240 AACTGCGTTGGTGTAAACCACTCTTCGAAACAATCATGATTTGTGC 289
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yAsnIyPheAlaIleAlaThrArgLeuPheGlnIySlyfThrcysIleValH 84
290 ACAAATGACAGAGAGAGACCATGCCCTCCCTTCAAGCCCTTGATGCGCTG 339
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 lslYmeTAsnIySgluValmetProSerIleGInSerLeuAspAlaLeu 100
340 GTCAAGGAAAGAACGCTTCAGGCTTAAGGCCCGGAGGACCACTCCCAA 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ValYsgIuIySlySleuGInGlyLysGlyProGlyProProProly 117
390 GAGCCTGAGTACTAGTCAACCCCAACAGAGTGCACATCGGACAGT 439
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 sglYeuMetIySerValAsnProAsnIySValAspAspLeuSerIySp 134
440 TTGGAATTCATCGCTTCCATGTGCAGAGGATTCACATACATAGCT 489
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 heGlyLysAsnIleAlaAsnMetCysArgIlyIleProThrTyMetAla 150
490 GAAGAGATTCAAGAGCAACCTGATTCGACTACAAAAGTCATCAG 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 GluGluMetGInGluAlaSerLeuPhePheIySerGlyThrcysTyrrh 167
540 TGCCAAATATCTGTGATTTCTTAACATTTCTTGTGAGGAATAGCG 589
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 rThSerValleuTrpIleValAspIleSerPheCysGlyAspThrValG 184
590 AGAAC 594
|||||
184 IuAsn 185
```



OM of: US-09-82L-726-17 to: PIR_71:★ out_format : pfs
Date: Sep 4, 2002 5:07 PM
About: Results were produced by the GenCore software, version 4.5
Copyright (c) 1993-2000 CompuGen Ltd.

```

Command line parameters:
-MODEL=framer-n2p.model -DEV=xlp
-O=/cgn2_1/USFTQ_spool/US09821726/runatc_04092002_163854_17529/app_query.fasta.1.664
-DB_PIR_71 -GPM=Fastan -SUFFIX=fp -GAPOP=12.000 -GAEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-OCAPEXT=0.050 -XGAPOP=10.000 -XGAEXT=0.500 -GAPOP=6.000
-FCAPEXT=7.000 -YGAPOP=10.000 -YGAEXT=0.500 -DELOP=6.000
-DEEXT=7.000 -START=1 -MATRIX=blomsum62 -TRANS=human40.cgi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM_ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09821726 @CGN1.1.149
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPHY -WAIT -THREADS=1

```

```
Search information block:
Query: US-09-821-726-17
Query length: 597
Database: PIR_71:*
Database sequences: 283138
Database length: 9608934
Search time (sec): 48.240000
```

Sequence	Strd Orig	zScore	Escore	Len	Documentation
pir2:561046	+	148.09	0.5161	719	! ARPI protein - yeast (Saccharom
pir2:UC67210	+	89.50	1.58	568	! molluscan shell matrix protein
pir2:T35096	+	88.50	1.59	266	! hypothetical protein SCG6.36 -
pir2:T35118	+	85.50	1.35	144	! probable secreted protein - Str
pir2:T30918	+	84.50	4.77	409	! hypothetical protein D1007.14 -
pir2:S33793	+	83.50	140.36	5.37	! hypothetical protein - spoonwor
pir2:S38907	+	83.00	127.19	6.63	! probable phosphatidylserine de
pir2:G88087	+	83.00	135.33	6.44	! protein B0454.8 (imported) - Ca
pir2:T15880	+	83.00	128.44	7.19	! hypothetical protein D2021.1 -
pir2:T32205	+	82.50	123.11	7.82	! hypothetical protein T02H1.7 -
pir2:E81094	+	82.50	126.77	8.16	! hypothetical protein T02H1.7 -
pir2:T12687	+	81.50	124.66	8.44	! pyruvate dehydrogenase, E1 comp
pir4:OOHUP	-	81.00	113.92	12.25	! AR protein homolog - fruit fl
pir2:T07755	-	81.00	139.77	8.98	! hypothetical protein B-120 - hu
pir2:569652	-	81.00	134.10	9.83	! disease resistance protein homoc
pir2:T18827	+	81.00	122.77	11.77	! hypothetical protein YDH485c -
pir2:T02227	+	81.00	118.31	12.66	! protein-tyrosine kinase (EC 2.7
pir2:G61348	+	80.50	131.89	11.26	! NB-ILR type resistance protein
pir2:S70151	-	80.50	121.24	13.35	! valine--tRNA ligase (EC 6.1.1.9
pir2:T45025	-	80.00	127.15	13.44	! tau1 protein - Xanthomonas sp.
pir2:C98425	-	80.00	107.77	18.29	! mucin MUC5B, tracheobronchial
pir2:G98288	-	79.50	127.68	14.74	! quinolinate synthetase A XP1923
pir2:AA3060	-	79.50	127.68	14.74	! quinolinate synthetase A (import
pir2:JN0250	-	79.50	127.68	14.74	! dehydroshikimate dehydratase (E
pir2:A55071	-	79.00	124.53	17.14	! chitinase (EC 3.2.1.14) 2 prech
pir2:TC4566	+	78.50	117.75	21.12	! hydrogen peroxide-Inducible p
pir2:861847	+	78.50	117.47	21.22	! pyruvate dehydrogenase (lipoam
pir2:S20434	+	78.50	106.32	25.34	! fatty-acid synthase (EC 2.3.1.
pir2:T02628	+	78.00	130.20	19.16	! hypothetical protein A12925950
pir2:A85091	+	78.00	124.88	20.86	! hypothetical protein A14090010
pir2:T41551	+	78.00	117.71	23.38	! hypothetical protein SPC070.05c
pir2:T00078	-	78.00	113.11	25.16	! probable RNA-directed DNA pol
pir2:H82650	-	77.50	124.01	23.39	! quinolinate synthetase A XP1923
pir2:HT1607	-	77.50	117.01	26.13	! hypothetical protein PEB0705w -
pir2:887303	+	77.00	115.61	29.58	! hypothetical protein CAC3279 -
pir1:S20907	+	77.00	114.13	30.28	! endo-1,4-beta-xylanase (EC 3.2.
pir2:DT1613	-	77.00	111.76	31.45	! GAF domain protein (cyclic nt
pir2:T08179	-	76.50	116.79	32.11	! LR65 protein - Chlamydomonas re
pir2:JS0747	+	76.50	114.93	33.19	! regulatory protein Spl - rat
pir2:A38152	+	76.50	114.72	33.07	! F-spondin - rat
pir2:T06404	+	76.50	110.90	35.27	! resistance complex protein I2D

seq_name	pir2	seq_name	pir2	seq_name	pir2	seq_name	pir2
pir2:S50366	+	76.50	110.20	35.66	1341	!	probable membrane protein Y
pir2:TC04084	+	76.00	124.62	31.36	240	!	caffeoyl-coA O-methyltransferase
pir2:S55097	+	76.00	117.35	35.20	543	!	murJ
pir2:S55114	+	76.00	107.75	41.02	1587	!	RmlI protein - yeast (Sacch
pir2:T02211	-	75.50	120.75	36.89	335	!	1,3-beta glucanase (EC 3.2.1

```
seq_documentation_block:
```

AKP1 protein yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D1478; protein YDL167c
C:Species: Saccharomyces cerevisiae
C:Date: 15-Feb-1996 #sequence, revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S61046; S1139; S67719
R:Pohl, T.M.
Submitted to the EMBL Data Library on Feb-16-1996

Submitted to the EMBL Data Library, November 1995
A/Reference number: S61010

A;Accession: S61046
A;Molecule type: DNA

A;Residues: 1-719 <POH>
A;Cross-references: EMBL:267750. NID:a1061256. PIRN:CAA91579.1. PDB:a1061272

R; Wehner, E. P.; Rao, E.; Brendel, M.
Mol Genet 237 351-358 1993

A;Title: Molecular structure and genetic r

A;Reference number: S31138; MUID:93247548
A;Accession: S31139

A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA

A; Residues: 1-492, 'N', 494-719 <MEH>
Cross-references: EMBL: Y68830, NID: 0577600, DTD: 0040150 1, DTD: 000500

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

submitted to the Protein Sequence Database, July 1996
R;Pohl, T.M.

A;Reference number: 5677708
A;Accession: 5677719

A;Molecule type: DNA
A:Residues: 1-719 <PDB>

A; Cross-references: EMBL:27

A; Experimental source: Streptococcus pneumoniae

A;Gene: SGD:NRP1; ARP1
A;Cross-references: MIPS:YD

A;Map position: 4L

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alignment_scores:
  Quality: 94.5
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Ratio:	1.139
Percent Similarity:	52.86

alignment block:

US-09-821-726-17 x 561046

Align seg 1/1 to: S61046

103 TATAGTATCAGTGTCAAC

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508  |||::|||:::  |||
    TvrasnTleasnasn

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153 **СЛУЖБА СЛУЖБЕНИХ РАДОВА**

123 GICAGAGGAGGACACAA
:||| :: |||||

524 nSerASnASnASnAS

181

541 snGlySerIleAsnSerA

202 AATGGATGGAACCTCCTGG

558 ASNGLYASnASnSerAsn

252 TGTACCAGACTC...

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574 sglSerAsnMetProPheArgAlaGlyAspTrpLysCysSerThrCyst 591
284 TTGTGCACAAATGAAAGAGAACCATG.....CCC 315
591 htrYrHisAspHeaLalysAsnValAlaCysLeuArgCysGlyGlyPro 607
316 TCCTTCACGCGCTGTGCTGCTGCAAGGAAAGAGAGCTTCAGGGTAA 365
608 LysSerTlleSerGlyAspAlaSerGluThrAsnHisTyrIleAspSerSe 624
366 G.....GGCCGAGGGGACCACTCCCAAGACCTGAGTACTCATGCA 409
624 rThrPheGlyProAlaSerArgThrProSerAsnAsnIleSerValA 641
410 ACCCCGAC.....AGAGTCGACAACTGACCAAGTTT 441
641 snThrAsnGlyGlySerAsnAlaGlyArgThrAspGlyAsnAspAsnLys 657
442 GGAATAATCCATCGTGCATG 462
658 GLYArgAspIleSerLeuMet 664

```

seq_name: pir2:JC7210

seq_documentation_block:

molluscan shell matrix protein N66 - Pinctada maxima
 C:Species: Pinctada maxima
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: JC7210
 R:Kono, M.; Hayashi, N.; Samata, T.
 Biochem. Biophys. Res. Commun. 269, 213-218, 2000
 A:Title: Molecular mechanism of the nacreous layer formation in Pinctada maxima.
 A:Reference number: JC7210; MUID:20160475
 A:Accession: JC7210
 A:Molecule type: mRNA
 A:Residues: 1-568 <KON>
 A:Cross-references: DDBJ:AB032612
 C:Comment: This protein is rich in asparagine and glycine residues, it serves as a product layer. It is also important in calcification.
 C:Keywords: matrix protein

alignment_scores:
 Quality: 89.50 Length: 177
 Ratio: 1.053 Gaps: 8
 Percent Similarity: 48.023 Percent Identity: 23.164

alignment_block:
 US-09-821-726-17 x JC7210 ..

Align seg 1/1 to: JC7210 from: 1 to: 568

```

124 GACGGCAACAGTGTGGAATGGGACACACTGACGTGCTCAACATGA 173
392 AsnGlyAsnAsnGlyGlyAsnGly.....AsnAsnGly 402
174 ACACACAGTGGCCACCTGACATTAACATGATGACACTCTGCAATG 223
402 YAsnAsnGlyAspAsnGlyAsnGlyAspAsnGlyTyrAsnGlyAspAsnG 419
224 CC.....CTCTGGACTATAGACTGGCTTGGCT 252
419 LysAsnSerAspGlyArgLeuArgArgTrpAspLeuAlaAsn..... 432
253 GTACACGACTCTCTGAGAGAGAG.....TCATGCAATGT 287
433 ValArgArgMetHisAlaGluArgTyrHisPheSerGlyGlyCysTleVal 449
288 GCACAAATATGAGAAGAGCCATGCCCTTCATCAAGCCCTTGATGCGC 337
449 LlyLysAlaLalysArgLeuSer.....ArgIleLeuGluCysA 462
338 TGTCAAGGAAAGAGAGCTTCAG.....GGTAAAGGCCCA 372

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462 lAtYrArgHisLysLysValArgGluPheLysArgAsnGlyGluLys 478
373 GGGGG.ACCACCTCCCAAGACCTGAGGTACTGACGTCAACCCCAAGAG 421
479 GlyLeuAspValAspIleThrProGluMetValLeuProPheMetLysTyr 495
422 TCGA.....CAAC 429
495 rArgHisTyrTrpThrTyrGluGlySerLeuThrThrProProCysAsnG 512
430 CTGCACAAATTGGAAAAATCCATGCTGTCATGTCAGAGGGAT..... 473
512 luthrValLeuThrValAlaGluLysCysHisValAlaValSerArgArg 528
474 .....TCACATACATGCGCTGAGAGAGATTCACAGAGCAA 508
529 ValLeuAspAlaLeuArgAsnValGluGlyTyrGluAspGlyThrThr 545
509 ACCGTGATTTCGTAACACAGAAAGTGACATCAG 539
545 uSerLysTyrGlyThrArgArgProThrGln 555

```

seq_name: pir2:T35096

seq_documentation_block:

hypothetical protein SCAG6.36 - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 15-Sep-2000
 C:Accession: T35096
 R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
 submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21567
 A:Accession: T35096
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-266 <SEE>
 A:Cross-references: EMBL:AL096884; PIDN:CA851459.1; GSPDB:GN00070; SCOEDB:SC4G6.36
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC4G6.36
 C:Superfamily: Streptomyces coelicolor probable secreted protein SCC22.22c

alignment_scores:
 Quality: 89.00 Length: 173
 Ratio: 1.085 Gaps: 8
 Percent Similarity: 47.399 Percent Identity: 26.012

alignment_block:
 US-09-821-726-17 x T35096 ..

Align seg 1/1 to: T35096 from: 1 to: 266

```

28 GGTGAAGCAAGATGAGTTCACATTCGCTTGTGACACTTCTTGNGCT 77
125 GlyAspTyrLysLeuSerPheThrVal.....GlyThr 135
78 CTTCCTGACTCTCGCCCTTGCTGACTATAGTATCAGTGTCAACGACGAGC 127
135 rPheLeu.....AspG 139
128 GCACAGTGTGGAGAGTGGGACAGCTAGTG.....AGTGTCAACAT 171
139 LysAsnLeuGlyGlyGluGlySerLysAsnAlaLeuSerAlaLeuLysAla 155
172 GAACACACAGTGGCCACAGCTTACATATACATATGATGGAATCCTCGAA 221
156 AlaLeuAsnVal.....SerProGly 162
222 TGCCCTCTGGACTATAGAACTGGCTTGTCTGTAAACAGACTCTTGAGA 271
162 uAlaPheValAspTyrLysThrAlaLeuTyrSerThrLysTyrHisProG 179

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272 AGAAGTCATGCAATTGTGCACAAAATGAGAGAGAGCCATGCCCTCCCTT 321
    ::::|::|
179 LuGIuSerThrAspGluPheAlaLysAspSplyLeuLeuLysValAla 195
    ::::|::|
322 CAAGCCCTTGATCCCTGCTGCAAGAAAGACCTTCAGGT..... 363
    ::::|::|
196 AspSerValAspAlaLeuLysGlyAsnLysPheGluAspAlaValG1 212
    ::::|::|
364 .AAGGGCCGAGGGGAGC.....CACCTGCCA 388
    ::::|::|
212 ulysGly.ThrTyrAspAlaTlPAlaMetArgMetSerLysSerPheAsp 228
    ::::|::|
389 AGAGCCCTGAGTACTGATCAACCCCAAGAGAGTGCACAACCTGAGACAAG 438
    ::::|::|
229 LysAlaGluLysAlaGluSerThrProThrLleLysLleAsnAspLysVa 245
    ::::|::|
439 TTGGGAAATCCATGCTGCCATGTCGAAGGGATTCCAAACATACATGCG 488
    ::::|::|
245 LValGluThrProSerThrProAspAla.....TrpG 256
    ::::|::|
489 TGAAGATTCACAGAG 505
    ::::|::|
256 LulysAlaLeuLysAsp 261
    ::::|::|
seq_name: p1r2:T35118

```

```

seq_documentation_block:
probable secreted protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 08-Sep-2000
C:Accession: T35118
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21568
A:Accession: T35118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-409 <SEE>
A:Cross-references: EMBL:AL022268; PIDN:CA18335.1; GSPDB:GN00070; SCODEB:SC4H2.19C
A:Experimental source: strain A1(2)
C:Genetics:
A:Gene: SCODEB:SC4H2.19C
C:Superfamily: Streptomyces coelicolor probable secreted protein SC4H2.19C

```

```

alignment_scores:
Quality: 84.50      Length: 188
Ratio: 1.043      Gaps: 7
Percent Similarity: 43.085      Percent Identity: 21.277

```

```

alignment_block:
US-09-821-726-17 x T35118 ..

```

```

Align seg 1/1 to: T35118 from: 1 to: 409

```

```

97 GCTGATATAGTATCATGTCACGACGACGACGACATGCTGGAAGTGG 146
    ||::|::|
51 AlaSerAlaSerAlaSerAlaAlaAspAspGlyAsnGlyLleArgL1 67
147 GCAGCAGTCACTGATGTCACACATTAACACAAAGTGGCCAACTGGTGA 196
    ::::|::|
67 eProAspAspLleLysAspLysLysGlyLleAspValAspA 84
197 AT.....AACATGATGGAATCCTCTGGAAT..... 222
    ::::|::|
84 spTrpLysAsnGlyAlaTrpLysAsnTrpAsnLysAspSplyLeuArg 100
223 .....GCCCTGGGACTATAG 239
    ::::|::|
101 GluAlaGluAspPheValAsnProLleLleGluGlyLeuTrpAsp..... 115
240 AACTGGCTTTGCTGTAAACAGACTCTTGAGAAAGATCATGATTTGTC 289

```

```

115 ..... 115
290 ACAAAATGACAGAGAGACCATGCCCTCCCTTCAAGCCCTTGATCCGCTG 339
116 .....ProAspArgMetArgAspAlaGluGluProAspLleGlu 128
    ::::|::|
340 CTCGAAGAAAGAACAGCTTCAGAGT...AAGGGCCGAGGGGACACACCTCC 386
    ||| |::|::|
129 ValAspGluAsnAspLleSerGlyAspGlnGlyAlaThrAspProGluPr 145
    ::::|::|
387 CAAGACCTGACGTACTGATCAACCCCAACAGATC...GACACCTGG 433
    ::::|::|
145 AlaProValGluAlaGluAlaValProAlaLysThrLysAspAsnAlaA 162
    ::::|::|
434 ACAAGTTTGGAATAATCCATCGTGGCAGTCGACAGAGGATTCACAAATAC 483
    ::::|::|
162 lAThAlaGlyLysLeuLeuPheAspSerProLysGlySerMetValCys 178
    ::::|::|
484 ATGCGTGAAGAGATTCACAGGA.....GCAACCTGAT 515
    ::::|::|
179 SerAlaThrValValLysAspProAlaHisProGlyLysSerAsnMetVa 195
    ::::|::|
516 TTCGTACTCAGAAAGTGCATCATGTCACATATATCTC.....TGATTC 559
    ::::|::|
195 lTrpThrAlaGlyHisCysValHisAlaGlyLysSerGlyGlyTrpTyrA 212
    ::::|::|
560 TTAACATTTCCCTTC 573
    ::::|::|
212 rGAsnLleAlaPhe 216
    ::::|::|
seq_name: p1r2:T30918

```

```

seq_documentation_block:
hypothetical protein D1007.14 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
R:Davidson, S.; Rohlfing, T.
submitted to the EMBL Data Library, August 1999
A:Description: The sequence of C. elegans cosmid D1007.
A:Reference number: Z20934
A:Accession: T30918
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-186 <DAV>
A:Cross-references: EMBL:AF003151; PIDN:AAB54231.1
A:Experimental source: strain Bristol N2; clone D1007
C:Genetics:
A:Map position: 1
A:Introns: 15/2; 68/2; 87/2
A>Note: D1007.14

```

```

alignment_scores:
Quality: 83.50      Length: 43
Ratio: 2.694      Gaps: 1
Percent Similarity: 72.093      Percent Identity: 39.535

```

```

alignment_block:
US-09-821-726-17 x T30918 ..

```

```

Align seg 1/1 to: T30918 from: 1 to: 186

```

```

118 AACGACGACGACACAGTGGTGGAAAGTGGGACGACGATGATGATCTCA 167
    ||::|::|
34 AsnAsnAsnGlyAlaSerGlyLysSerTrpGlyAsnGlyAsnAlaAsnAs 50
168 CAATGACACAAACGTGGCCCAACGTTGACATTAACATGAGATGAGG..... 210
    ||::|::|
50 AsnAsnAsnAsnAsnAsnGlyGlySerAsnAsnGlyTrpGlyAsnA 67
211 ..AACTCTGGAATGCCCTCTGGGACTAT 237

```



```
seq_documentation_block:
  pyruvate dehydrogenase, E1 component NMB1341 (imported) - Neisseria meningitidis (strains)
C:Species: Neisseria meningitidis
```

[illegible]

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Lichtenthaler (1987). The total chlorophyll content was determined by the method of Arar and Cook (1980). The carotenoid content was determined by the method of Lichtenthaler and Weil (1983). The total phenolic content was determined by the method of Singleton and Rossi (1965). The total flavonoid content was determined by the method of Zhishen et al. (1999). The total protein content was determined by the method of Lowry et al. (1951). The total amino acid content was determined by the method of Kjedahl (1882). The total sugar content was determined by the method of Dubois and Gilles (1950). The total lipid content was determined by the method of Folch et al. (1957). The total nucleic acid content was determined by the method of Burton (1956). The total mineral content was determined by the method of Ashby et al. (1984). The total organic acid content was determined by the method of Saito et al. (1987). The total alkaloid content was determined by the method of Kato et al. (1989). The total saponin content was determined by the method of Kato et al. (1989). The total tannin content was determined by the method of Kato et al. (1989). The total terpenoid content was determined by the method of Kato et al. (1989). The total steroid content was determined by the method of Kato et al. (1989). The total glycoside content was determined by the method of Kato et al. (1989). The total alkaloid content was determined by the method of Kato et al. (1989). The total saponin content was determined by the method of Kato et al. (1989). The total tannin content was determined by the method of Kato et al. (1989). The total terpenoid content was determined by the method of Kato et al. (1989). The total steroid content was determined by the method of Kato et al. (1989). The total glycoside content was determined by the method of Kato et al. (1989).

OM of: US-09-821-726-17 to: SwissProt_40.* out_format : pfs
Date: Sep 4, 2002 5:15 PM
About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODE=frame+asp_model -DEV=xlp
-O=/cgn2.1/USPSPool/US09821726/turnal_04092002.163856.17658/app-query.fasta.1.664
-DB=SwissProt_40 -OFMT=fastan -SUFFIX=sp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-DELDP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORMEXT=HEAPSIZ=500 -MINLEN=200000000
-USER=US09821726.ecgn1.1.60 -NCPU=6 -ICPU=3 -LOGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

Query: US-09-821-726-17
Query length: 597
Database: SwissProt_40.*
Database sequences: 105224
Database length: 38719550
Search time (sec): 24.280000

score_list:

```
SwissProt_40:CLIP_HUMAN + 803.00 1426.14 4.9e-72 199 | 09ns71 homo sapiens (human)
SwissProt_40:CLIP_MOUSE + 627.00 1112.22 1.6e-54 184 | 09cr37 mus musculus (mouse)
SwissProt_40:NRL1_YEAST + 94.50 147.47 0.2252 719 | P32770 saccharomyces cerevisiae
SwissProt_40:CDNA_BACU + 94.00 145.54 0.2582 803 | 045755 bacillus thuringiensis
SwissProt_40:DVIL_MOUSE + 87.00 134.37 1.125 695 | P51141 mus musculus (mouse)
SwissProt_40:DVIL_MOUSE + 87.00 134.37 1.125 695 | 09wvd9 rattus norvegicus (rat)
SwissProt_40:CTNB_URECA + 83.00 126.59 2.88 818 | P35224 urochis caupo (inksee)
SwissProt_40:DSND_CLOPA + 83.00 135.21 2.63 296 | 046192 clostridium pasteurie
SwissProt_40:SVY_CAMJ + 80.50 120.65 5.80 870 | 09p964 campylobacter jejuni
SwissProt_40:CH12_COCJA + 78.50 117.18 9.15 860 | P54197 coccidioides immitis
SwissProt_40:VNF_CANPA + 78.50 106.09 11.61 2813 | 028295 canis familiaris (dog)
SwissProt_40:TI29_ARATH + 77.00 124.73 8.56 349 | P82281 arabidopsis thaliana
SwissProt_40:XTNA_RUMPL + 77.00 113.53 13.18 954 | P29126 rumibococcus thalana
SwissProt_40:Z335_HUMAN + 77.00 110.34 14.11 1342 | 09h422 homo sapiens (human)
SwissProt_40:MNS1_RHME + 76.50 121.35 12.26 376 | 030559 rhizobium meliloti (s
SwissProt_40:SP1_RAT + 76.50 114.43 14.22 788 | 001714 rattus norvegicus (rat)
SwissProt_40:PSPO_RAT + 76.50 114.20 14.29 807 | P35446 rattus norvegicus (rat)
SwissProt_40:YL78_YEAST + 76.50 109.45 15.83 1341 | 005854 saccharomyces cerevi
SwissProt_40:TI29_LYCES + 76.00 121.27 13.52 345 | 09thx6 lycopericon esculent
SwissProt_40:TRAB_HUMAN + 76.00 114.54 15.61 708 | 09ug10 homo sapiens (human)
SwissProt_40:GLT5_WHEAT + 76.00 112.95 16.15 839 | P10388 triticum aestivum (w)
SwissProt_40:RLR1_YEAST + 76.00 106.92 18.38 1597 | P53552 saccharomyces cerevi
SwissProt_40:PGMU_ACEXY + 75.50 115.92 16.68 555 | P38569 acetobacter xylinum
SwissProt_40:TRF1_SALSA + 75.50 113.88 17.42 690 | P80426 salmo salar (atlantic
SwissProt_40:FKN2_MOUSE + 75.00 105.20 20.54 1567 | 09j104 mus musculus (mouse)
SwissProt_40:CSP_PLAFL + 75.00 117.16 17.87 442 | P08307 plasmodium falciparum
SwissProt_40:MMQC_MYCTU + 75.00 108.24 21.63 1146 | 050585 mycobacterium tuberc
SwissProt_40:PMR2_HUMAN + 75.00 106.98 22.22 1311 | P51816 homo sapiens (human)
SwissProt_40:KGL1_ARATH + 74.50 111.59 22.15 728 | 039017 arabidopsis thaliana
SwissProt_40:ZFX_BOVIN + 74.00 109.82 25.31 800 | 062836 bos taurus (bovine)
SwissProt_40:TI2M_DICDI + 74.00 105.40 27.82 1282 | P90520 dictyostelium discoi
SwissProt_40:FLIZ_BACSU + 73.50 121.05 21.89 219 | P35536 bacillus subtilis (f)
SwissProt_40:CHM1_HUMAN + 73.50 117.10 23.82 334 | 075829 homo sapiens (pfig)
SwissProt_40:MIS_PIG + 73.50 112.01 26.57 575 | P79295 sus scrofa (pfig)
SwissProt_40:GCSB_FLAFL + 73.50 106.52 29.89 1034 | P43632 flavetia pringlei
SwissProt_40:GSP_FLAFL + 73.50 106.52 29.89 1034 | 048850 flavetia anomala
SwissProt_40:GSP_FLAFL + 73.50 106.52 29.89 1034 | 048852 flavetia trimetria
SwissProt_40:YK76_YEAST + 73.50 105.17 30.77 1195 | P36168 saccharomyces cerevi
SwissProt_40:WVF_PIG + 73.50 98.32 35.63 2482 | 028833 sus scrofa (pfig) von w
SwissProt_40:SPYA_FELCA + 73.00 114.20 27.89 414 | P41869 felis silvestris catu
```

```
SwissProt_40:MEIL_CAEEL + 73.00 112.97 28.64 472 | P34808 caenorhabditis ele
SwissProt_40:ARSH_FELCA + 73.00 111.79 29.37 535 | P33727 felis silvestris c
SwissProt_40:PMIL_YEAST + 73.00 107.83 31.97 817 | P33775 saccharomyces cere
SwissProt_40:RPC2_SCHPO + 73.00 104.51 34.33 1165 | 010233 schizosaccharomyc
SwissProt_40:AROC_METYA + 72.50 115.12 30.09 341 | 058496 methanococcus jann
```

seq_name: SwissProt_40:CLIP_HUMAN

seq_documentation_block:

ID CLIP_HUMAN STANDARD; PRT; 199 AA.

AC Q9NS71;

DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE CALL protein.

GN CALL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Stomach;

RX MEDLINE=20296773; PubMed=10835488;

RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.,

RT "Isolation of two novel genes' down-regulated in gastric cancer.";

RL Jpn. J. Cancer Res. 91:459-463(2000).

CC -I- TISSUE SPECIFICITY: Expressed in stomach. No expression is

CC detected in cancer tissue or gastric cancer cell lines.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation

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CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb.ch/announce/>CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: AB039886; BAA92433.1; -

DR MIM: 606402; -

DR DR MIM: 606402; -

SO SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;

alignment_scores:

Quality: 803.00 Length: 194
Ratio: 4.412 Gaps: 0
Percent Similarity: 93.814 Percent Identity: 74.227

alignment_block:

US-09-821-726-17 x CLIP_HUMAN

Align seg 1/1 to: CLIP_HUMAN from: 1 to: 199

```
13 TCACATTCATGCAATGTTGAACCAAGATGATGACAAATGCTTGC 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
6 SerValHisCysPheArgLysMetLysPheThrIleValAlaPhe1 22
22 TGGAATTCCTGTCGTCCTGCAATGCTCCCTGCTGCTGCTATGATCA 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
22 aglyLeuLeuGlyValPheLeuAlaProAlaLeuAlaAsnIlyrAsnIleA 39
113 GTGTACAGACAGACAGCAAGAGTGTGGAAGTGGCAGCAGTCAAGT 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
39 snValAsnAspAspAsnAsnAsnAlaGlySerGlyGlnGlnSerValSer 55
153 GTCAACATGACACACAGCTGCCAAGCTTGACAAATTAACATGATGAA 212
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
56 ValAsnGlnGluHisAsnValAlaAsnValAlaAspAsnAsnGlyTrpAs 72
213 CTCGCGAATGCTCTGCGACGACATAGAACGCTTGCTGCTGAACGAC 262
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
72 pSerTrpAsnSerIleTrpAspIlyrGlyAsnGlyPheAlaAlaThrArgL 89
```


1. *What is the purpose of this study?*

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DR SMART; SM00049; DEP: 1.
 DR SMART; SM00228; PDZ: 1.
 DR PROSITE; PS50186; DEP: 1.
 DR PROSITE; PS50106; PDZ: 1.
 DR Developmental protein.
 FT DOMAIN 251 323 PDZ.
 FT DOMAIN 425 499 DEP.
 FT DOMAIN 390 393 POLY-SER.
 FT CONFLICT 122 125 MISSING (IN REF. 2).
 FT CONFLICT 211 211 T -> N (IN REF. 2).
 SQ SEQUENCE 695 AA; 75350 MW; A9FMA49F95CE75P2 CRC64;

alignment_scores:

Quality: 87.00 Length: 112
 Ratio: 1.359 Gaps: 5
 Percent Similarity: 57.143 Percent Identity: 26.786

alignment_block:

US-09-821-726-17 x DVL_MOUSE ..

Align seg 1/1 to: DVL_MOUSE from: 1 to: 695

```

133 AGTGTGCAAGTGGCGACGAGTCAGTGTCAACATGACACACAGT 182
    ::::::::::::::::::::
596 Alaglyglyserglysergluser.....Asphisthrva 607
183 GCGCAAGCTTGACATACATGATGAACTCTGGAATGCCCTGGG 232
    | ::::::::::::::::::::
607 lProserglyserglyserthrltyr.....Trrg 618
233 ACTATGAACTGGCTTGTCTGTAACGAGCTTTCGAGAAGATGATGC 282
    ::::::::::::::::::::
618 lAtrg.....Provalserglneuserargglyser..... 629
283 ATTGTGCACAAATGAGAGGAGGAGCCCTCCCTCAAGCCCTTA 332
    ::::::::::::::::::::
630 ...ProargserglneuserAlaValAlaProgllyleuproProleu 645
333 TCGCGTGTCAAGGAAAGAGGCTTCAGGTAAGGCCCGGAGGACAC 382
    ::::::::::::::::::::
645 sProleuthrlysalatryAlaValAlaGlyglyProglglylPro 662
383 CTCCCAAGAGGCTGAGTACTCACTGATCAACCCCAACAGAGTGCAC 432
    | ::::::::::::::::::::
662 rovalarggluleuAla...AlaValProgllyleuthrlyserArg 677
433 GACAAGTTTGGAAATCCATCCTGTCGATGTCACAG 468
    ::::::::::::::::::::
678 GlnerPheglInylsAlaMetglYasnProCysglu 689

```

seq_name: SwissProt_40:DVL_RAT

seq_documentation_block:

ID DVL_RAT STANDARD: PRT: 695 AA.
 AC Q9WVB9; Q9WVB9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Segment polarity protein disvelled homolog DVL-1 (Disvelled-1)
 DE (DSH homolog 1) (Fragments).
 DE DVL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NX NCBI_TaxID=10116;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR KYOTO.
 RA de Lange R.P.J., Burr K., Clark J.S., Negri C.D., Brosnan M.J.,
 RA St Clair D.M., Shaw D.J., Dominiczak A.F.;
 RT "Does Disvelled-1 determine sensitivity to cerebral ischaemic insult
 in a rat model of stroke?";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).

```

DR EMBL; AF143548; AAD41492.2; -.
DR EMBL; AF143547; AAD41492.2; JOINED.
DR EMBL; AF143550; AAD41493.1; -.
DR EMBL; AF143549; AAD41493.1; JOINED.
DR InterPro: IPR000591; DEP.
DR InterPro: IPR001158; DIX.
DR InterPro: IPR001478; PDZ.
DR Pfam; PF00610; DEP: 1.
DR Pfam; PF00778; DIX: 1.
DR ProDom; PD003639; DIX: 1.
DR SMART; SM00021; DAX: 1.
DR SMART; SM00049; DEP: 1.
DR PROSITE; PS50186; DEP: 1.
DR PROSITE; PS50106; PDZ; PARTIAL.
KW Developmental protein.
FT DOMAIN 251 323 PDZ.
FT DOMAIN 425 499 DEP.
SQ SEQUENCE 695 AA; 75684 MW; BDEA252BA1E87601 CRC64;

```

alignment_scores:

Quality: 87.00 Length: 112
 Ratio: 1.359 Gaps: 5
 Percent Similarity: 57.143 Percent Identity: 26.786

alignment_block:

US-09-821-726-17 x DVL_RAT ..

Align seg 1/1 to: DVL_RAT from: 1 to: 695

```

133 AGTGTGCAAGTGGCGACGAGTCAGTGTCAACATGACACACAGT 182
    ::::::::::::::::::::
596 Alaglyglyserglysergluser.....Asphisthrva 607
183 GCGCAAGCTTGACATACATGATGAACTCTGGAATGCCCTGGG 232
    | ::::::::::::::::::::
607 lProserglyserglyserthrltyr.....Trrg 618
233 ACTATGAACTGGCTTGTCTGTAACGAGCTTTCGAGAAGATGATGC 282
    ::::::::::::::::::::
618 lAtrg.....Provalserglneuserargglyser..... 629
283 ATTGTGCACAAATGAGAGGAGGAGCCCTCCCTCAAGCCCTTA 332
    ::::::::::::::::::::
630 ...ProargserglneuserAlaValAlaProgllyleuproProleu 645
333 TCGCGTGTCAAGGAAAGAGGCTTCAGGTAAGGCCCGGAGGACAC 382
    ::::::::::::::::::::
645 sProleuthrlysalatryAlaValAlaGlyglyProglglylPro 662
383 CTCCCAAGAGGCTGAGTACTCACTGATCAACCCCAACAGAGTGCAC 432
    | ::::::::::::::::::::
662 rovalarggluleuAla...AlaValProgllyleuthrlyserArg 677
433 GACAAGTTTGGAAATCCATCCTGTCGATGTCACAG 468
    ::::::::::::::::::::
678 GlnerPheglInylsAlaMetglYasnProCysglu 689

```

seq_name: SwissProt_40:CTNB_URECA

```

seq_documentation_block:
ID CTNB_URECA STANDARD; PRT; 818 AA.
AC P35224;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Beta-catenin.
OS Urechis caupo (Innkeeper worm) (Spoonworm).
OC Eukaryota; Metazoa; Echinura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93305730; PubMed=8318544;
RA Rosenthal E.T.;
RT "Identification of homologues to beta-catenin/plakoglobin/armadillo
in two invertebrates, Urechis caupo and Trilipneustes gratilla."
RL Blochum. Biophys. Acta 1173:337-341(1993).
CC -1- FUNCTION: BINDS TO THE CYTOSOLIC DOMAIN OF THE CELL-CELL
ADHESION MOLECULE E-CADHERIN, AND PERHAPS TO OTHER (MEMBRANE)
PROTEINS. THE ASSOCIATION OF CATENINS TO CADHERINS PRODUCES A
COMPLEX WHICH IS LINKED TO THE ACTIN FILAMENT NETWORK, AND WHICH
SEEMS TO BE OF PRIMARY IMPORTANCE FOR CADHERINS CELL-ADHESION
PROPERTIES.
CC -1- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
CC -1- SIMILARITY: CONTAINS 7 ARM REPEATS.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L10355; AAA30330.1; -.
DR HSSP: Q02248; 2BCT.
DR InterPro: IPR000225; Armadillo.
DR Pfam: PF00514; Armadillo-seg; 12.
DR SMART: SM00185; ARM; 11.
DR PROSITE: PS50176; ARM_REPEAT; 9.
KW Cell adhesion; Cytoskeleton; structural protein; Repeat.
FT REPEAT 164 203 ARM 1.
FT REPEAT 248 287 ARM 2.
FT REPEAT 412 451 ARM 3.
FT REPEAT 454 495 ARM 4.
FT REPEAT 501 541 ARM 5.
FT REPEAT 543 582 ARM 6.
FT REPEAT 648 687 ARM 7.
SQ SEQUENCE 818 AA; 89070 MW; 1DF174BEF745CID CRC64;

```

alignment_scores:

Quality: 83.50 Length: 123
Ratio: 1.128 Gaps: 7
Percent Similarity: 60.163 Percent Identity: 26.829

alignment_block:

US-09-821-726-17 x CTNB_URECA ..

Align seg 1/1 to: CTNB_URECA from: 1 to: 818

```

115 GTCAAGGAGGAGGCGC..AACAGTGTGGAAGTGGGACAGCAGTCACTAGTAG 161
      ::::::::::::::::::::|
47 MetGlyAspSerIleGlnSerGlyAlaThrThiGlnAlaProProse 63
162 TGTCAACATGTAACACACAGTGGCAGCCTGACATTAACAATGATGTA 211
      ||::::::::::::::::::|
63 ValSerSerIleGlnGlyLeuAspAspMetAspThrIleGlnGlyMetA 80
212 ACTTCGGAATGCCCTGTGGACTATAGAACTGGCTTTGCTGTAACGAGA 261

```

```

      :::::  :::::|:::|  |:::|  |:::|
80 sptHrSerArgMetMetPheAspPheAspGlnGlyPheSer...ThrGln 95
262 CTCTTCGAGAGAGATCATGTCATGTCACAAATATAGACAGAACCAT 311
      ||  :::::|  ||  :::::|
96 AlaPheThrGlnGlnGln.....ValAspGlnMetAsnGlnGln..... 108
312 GCCCTCCCTTCAGGCCCTTGATCGCTGTCAGGAAGAAAGACCTTCAG 361
      ||  :::::|  ||  :::::|
109 .....Leu.AsnGlnThrArgSerGlnArg 116
362 GTAAGGCGC.....CAGCGGAGCACCCTGCC 387
      ||:::|  ||  :::::|
117 ValArgAlaAlaMetPheProGlnThrLeuGlnGlnGlyValGlnIleP 133
388 AAGAGCCTGAGTACTGATCAACACCCACAGAGCTGACACACCTGACAA 437
      |  :::|  ||  :::::|
133 O.....SerThrGlnLeuAspProGlnIleProThrAlaValGlnA 147
438 GTTGGAAATTCATCG 454
147 rgleuSerGluProSer 152

```

seq_name: SwissProt_40:DPSD_CLOPA

seq_documentation_block:
ID DPSD_CLOPA STANDARD; PRT; 296 AA.
AC Q46192;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative phosphatidylserine decarboxylase (EC 4.1.1.65).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1501;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 6013;
RA Meyer J.;
RL Submitted (NOV-1993) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: phosphatidyl-L-serine =
phosphatidylethanolamine + CO(2).
CC -1- COFACTOR: Pyruvoyl group (by similarity).
CC -1- PATHWAY: AMINOPHOSPHOLIPID BIOSYNTHESIS.
CC -1- SIMILARITY: TO THE C-TERMINAL OF YEAST PSD2.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z28353; CAA82212.1; -.
DR InterPro: IPR003817; PS_Dcarboxylase.
DR Pfam: PF02666; PS_Dcarboxylase; 1.
KW Phospholipid biosynthesis; Lyase; Decarboxylase; Pyruvate; zymogen.
FT SITE 255 256 CLEAVAGE (NONHYDROLYTIC)
FT MOD_RES 256 256 (BY SIMILARITY).
FT MOD_RES 256 256 CONVERTED TO A PYRUVOL GROUP
SQ SEQUENCE 296 AA; 34243 MW; A131FA6D2FB0472A CRC64;

alignment_scores:

Quality: 83.00 Length: 132
Ratio: 1.297 Gaps: 6
Percent Similarity: 48.485 Percent Identity: 27.273

alignment_block:

US-09-821-726-17 x DPSD_CLOPA ..

```

seq_name: SwissProt_40::VWF_CANFA
seq_documentation_block:
ID: VWF_CANFA          STANDARD:          PRT:      2013 AA.
AC: Q28295; Q28311; Q9T514;
DT: 01-NOV-1997 (Rel. 35, Created)
DT: 16-OCT-2001 (Rel. 40, Last sequence update)
DT: 01-MAR-2002 (Rel. 41, Last annotation update)
DE: Von Willebrand factor precursor (VWF).
GN: FBVWF OR VWF.
OS: Canis familiaris (Dog).
OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX: NCBI_TaxID=9615;
RN: [1]
RP: SEQUENCE FROM N.A.
RA: Stoy S.J., Shiduya H., Noneman D.J., Holzhauer J., Mohammed I.H.,
RA: Johnson G.S.;
RL: Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN: [2]
RP: SEQUENCE FROM N.A.
RA: Montgomery R.R., Fahs S., Montgomery M.W.;
RL: Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN: [3]
RP: SEQUENCE FROM N.A.
RA: Venta P.J., Li J., Yuzbasizyan-Gurkan V., Brewer G.J., Schall W.D.;
RL: "Complete sequence of the structural gene for canine von Willebrand
RT: factor and identification of a mutation causing Scottish terrier von
RT: Willebrand's disease.";
RL: Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN: [4]
RP: SEQUENCE OF 1234-1669 FROM N.A.
RC: TISSUE=Blood;
RA: Mancuso D.J., Christopherson P.A., Kroner P.A., Montgomery R.R.;
RT: "The canine von Willebrand factor gene: sequence and expression of
RT: a region encoding the glycoprotein Ib/IX binding domain.";
RL: Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC: -1- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS. IT
CC: PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
CC: NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF

```


Align seg 1/1 to: DPSD_CLOPA from: 1 to: 296

```

157 GTGATGTCACAAATGAACACAAAGCGCCACCTTGACATATACATGCG 206
    : : : : : : : : : : : : : : : : : : : : : : : : : :
116 lIelleVallyTrasnaSnlleasMetasnlleleleGlnVallySgl 132
    : : : : : : : : : : : : : : : : : : : : : : : : : :
207 ATGGAAGCTCCGTGAATGCCCTCTGAGCTATAGAACTGGCTTGTCTAA 256
    : : : : : : : : : : : : : : : : : : : : : : : : : :
132 YlleThr.....TyrlySleuasnaPlelleGlnasnsPserlies 147
    : : : : : : : : : : : : : : : : : : : : : : : : : :
257 CCACACTCTTCGAGACAGATCATCTTGACAAATATGACAGAGAA 306
    : : : : : : : : : : : : : : : : : : : : : : : : : :
147 erlystrhTyrglulysglYthrcysllellealargleucysProthr 163
    : : : : : : : : : : : : : : : : : : : : : : : : : :
307 GCCATGCCCTCCCTTCAGGCCCTTGATGCCGTGTCAGAGAAAAGAGCT 356
    : : : : : : : : : : : : : : : : : : : : : : : : : :
164 AspYrhtlsarphnehlSpheleuasPasnlylleCyslnserThrIL 180
    : : : : : : : : : : : : : : : : : : : : : : : : : :
357 TCAGGTAAGGGCCAGGGGACCACCTCCCAAGAGCCCTGAGTACTCAG 406
    : : : : : : : : : : : : : : : : : : : : : : : : : :
180 elysllellysglyAsn.....TyrTyserv 189
    : : : : : : : : : : : : : : : : : : : : : : : : : :
407 TCACACCC.....AACAGACTGCACACCTG..... 432
    : : : : : : : : : : : : : : : : : : : : : : : : : :
189 alasnProllealealeuaslnlyslleasnaslnleuphecysGlnasnllys 205
    : : : : : : : : : : : : : : : : : : : : : : : : : :
433 .....GACACGTTTGAAAA..... 447
    : : : : : : : : : : : : : : : : : : : : : : : : : :
206 ArgGlutrpserlterPheasnsersAspaspnheglYslleleutyrya 222
    : : : : : : : : : : : : : : : : : : : : : : : : : :
448 .TCATGCTGTCGATGTCAGAGGG.....ATTCCACATACATG 486
    : : : : : : : : : : : : : : : : : : : : : : : : : :
222 lglulleGlyalathrcysvalglyserllelleGlnThrTyrMet 237
    : : : : : : : : : : : : : : : : : : : : : : : : : :
seq_name: swissprot_40:svy_CAMJG

```

```

seq_documentation_block:
ID SVY_CAMJG STANDARD: PRG: 870 AA.
AC Q9PEP4:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS).
GN VALS OR C07075.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group.
OX Campylobacter.
RX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTC 11168;
RC MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kelley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltham T., Holtroyd S.,
RA Jagers K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RA Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -1- CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val) = AMP + diphosphate
CC + L-valyl-tRNA(Val).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.
CC -----
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```

CC -----
DR EMBL: AL139076; CAB73040.1; -.
DR HSSP: P96142; 1GAX.
DR InterPro: IPR002300; tRNA-synt_1a.
DR InterPro: IPR001412; tRNA-synt_1.
DR InterPro: IPR002303; tRNA-synt_val.
DR Pfam: PF00133; tRNA-synt_1.
DR PRINTS: PR00986; tRNA5SYNTHAL.
DR PROSITE: PS00178; AA-TRNA-LIGASE_1; 1.
KW Aminoacyl-tRNA synthetase; protein biosynthesis; ligase; ATP-binding;
KW complete proteome.
FT SITE 42 52 "HIGH" REGION.
FT SITE 527 531 "KMSKS" REGION.
FT BINDING 530 530 ATP (BY SIMILARITY).
SQ SEQUENCE 870 AA; 101810 MW; 53DA604A0DC724DA CRC64;

```

alignment_scores:
 Quality: 80.50 Length: 224
 Ratio: 0.767 Gaps: 13
 Percent Similarity: 46.875 Percent Identity: 20.536

alignment_block:

US-09-821-726-17 x SVY_CAMJG ..
 Align seg 1/1 to: SVY_CAMJG from: 1 to: 870

```

21 TTGCATTTGTTGAAGCCACAGATGATGATGCAATTCCTTTGC..... 62
    : : : : : : : : : : : : : : : : : : : : : : : : : :
402 Leutrprtrpglynlsglnleeroyaltyrtyrglysserhnlsgl 418
    : : : : : : : : : : : : : : : : : : : : : : : : : :
63 .TGACATTTTGTTGTTCTTCTGACTCCCTGCCCTTGCTAGTATGATTC 111
    : : : : : : : : : : : : : : : : : : : : : : : : : :
418 utrpalaserclnhsthrProlysthrCysPro.....L 430
    : : : : : : : : : : : : : : : : : : : : : : : : : :
112 AGTGTCAACGACGACGG.....CMACTGG 137
    : : : : : : : : : : : : : : : : : : : : : : : : : :
430 yscysGlnserGlnasnpheylsglnasprgluasprvalleuasprhtr 446
    : : : : : : : : : : : : : : : : : : : : : : : : : :
138 TGGAGG.....TGGGACAGACTGAGTACGTCACAAATGACACACA 178
    : : : : : : : : : : : : : : : : : : : : : : : : : :
447 PheSererGlyLeutrprala.MetSerThrleu..... 457
    : : : : : : : : : : : : : : : : : : : : : : : : : :
179 ACGTGCCCAACGTTGACAAATGACATGATGGAACCTCGGAAT..... 222
    : : : : : : : : : : : : : : : : : : : : : : : : : :
458 .....glytrpglyasnGlnasntprgly 465
    : : : : : : : : : : : : : : : : : : : : : : : : : :
223 .....GCCCTGTGGACTATAGA..... 240
    : : : : : : : : : : : : : : : : : : : : : : : : : :
466 LysasprlyslletrpserGlnlyAspleulysAspPheTyrProasnsE 482
    : : : : : : : : : : : : : : : : : : : : : : : : : :
241 .....ACTGACTTGTCT.....GTACACGACTCT 265
    : : : : : : : : : : : : : : : : : : : : : : : : : :
482 rleuLeullethrGlyPheasprlleuPhePheThrValalargmetm 499
    : : : : : : : : : : : : : : : : : : : : : : : : : :
266 TCGAAGAGAAAGTGCATGCTGTGACAAATGAGAAGAGAACCATGCC 315
    : : : : : : : : : : : : : : : : : : : : : : : : : :
499 etrPheGlnSerThrAsnvalleuhslslnleuProPheLysAspIle... 514
    : : : : : : : : : : : : : : : : : : : : : : : : : :
316 TCCCTTCAGAGCCCTTGATGCCCTGTGTCAGAGAAAGAAAGCTCAGGTA 365
    : : : : : : : : : : : : : : : : : : : : : : : : : :
515 .....TyrleuHslalaleuVallyAspsoludn..... 524
    : : : : : : : : : : : : : : : : : : : : : : : : : :
366 GGGGCCAGGGGGACCACTCCCAAGAGCTGAGGTACTCAGTCAACCCCA 415
    : : : : : : : : : : : : : : : : : : : : : : : : : :
525 .....GlyArglyMetSerlysserleuglyAsnValilleasprroA 539
    : : : : : : : : : : : : : : : : : : : : : : : : : :
416 ACAGATTCGACAACTGTGACAGATTTGGAATTCACATCTGGCAGTGC 465
    : : : : : : : : : : : : : : : : : : : : : : : : : :
539 sn.....GluserllelysglnutyserlalaAspilleuargPheThr 553
    : : : : : : : : : : : : : : : : : : : : : : : : : :
466 AAGGGATTCACACATACATGAGTGAAGAGATTCAGAGGACCAAC..... 510

```


FT	DISULFID	914	921	BY SIMILARITY.
FT	DISULFID	1060	1084	BY SIMILARITY.
FT	DISULFID	1071	1111	BY SIMILARITY.
FT	DISULFID	1089	1091	BY SIMILARITY.
FT	DISULFID	1153	1165	BY SIMILARITY.
FT	DISULFID	1149	1169	BY SIMILARITY.
FT	DISULFID	1126	1130	BY SIMILARITY.
FT	DISULFID	1196	1199	BY SIMILARITY.
FT	DISULFID	1234	1237	BY SIMILARITY.
FT	DISULFID	1272	1458	BY SIMILARITY.
FT	DISULFID	1669	1670	BY SIMILARITY.
FT	DISULFID	1686	1872	BY SIMILARITY.
FT	DISULFID	1879	1904	BY SIMILARITY.
FT	DISULFID	1899	1940	OR 1942 (BY SIMILARITY).
FT	DISULFID	1972	2123	BY SIMILARITY.
FT	DISULFID	1950	2085	BY SIMILARITY.
FT	DISULFID	1927	2088	BY SIMILARITY.
FT	DISULFID	1993	2001	BY SIMILARITY.
FT	DISULFID	2724	2774	BY SIMILARITY.
FT	DISULFID	2739	2788	BY SIMILARITY.
FT	DISULFID	2750	2804	BY SIMILARITY.
FT	DISULFID	2754	2806	BY SIMILARITY.
FT	DISULFID	?	2811	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. .)
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. .)
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. .)
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. .)
FT	CARBOHYD	857	857	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1231	1231	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1515	1515	N-LINKED (GLCNAC. .)
FT	CARBOHYD	1574	1574	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2223	2223	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2290	2290	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2357	2357	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2400	2400	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2546	2546	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2585	2585	N-LINKED (GLCNAC. .)
FT	CARBOHYD	2790	2790	N-LINKED (GLCNAC. .)
FT	CONFLICT	55	55	G -> E (IN REF. 2) .
FT	CONFLICT	70	70	V -> I (IN REF. 3) .
FT	CONFLICT	266	266	A -> G (IN REF. 2) .
FT	CONFLICT	280	280	I -> V (IN REF. 2) .
FT	CONFLICT	409	411	VCH -> ICO (IN REF. 2) .
FT	CONFLICT	994	994	G -> A (IN REF. 1) .
FT	CONFLICT	1021	1021	F -> L (IN REF. 2) .
FT	CONFLICT	2381	2381	L -> P (IN REF. 2) .
FT	CONFLICT	2406	2406	P -> L (IN REF. 2) .
SO	SEQUENCE	2813 AA;	309716 MW;	SDF93BEJZF80C CRC64;

alignment_scores:

Quality:	78.50	Length:	195
Ratio:	0.957	Gaps:	11
Percent Identity:	42.051	Percent Identity:	24.103

alignment_block:

```
US-09-821-726-17/rev x vWF_CANFA ..
```

Align seg 1/1 to: vWF_CANFA from: 1 to: 2813

```

484 TGTATGTTGGAGATCCSCTTGACA...TGCACAGATGAGATTTC.... 443
|||||.....|||:|||:|||||
2184 Cysatgthlhylyvalcyvalasprlrgratgylalaaprhcsyal 2200
      ::::|||||
442 CAAACTGTGCCA.....GGTGT. 425
      ::::::::::|
2200 ametserctyrproseledeualtlytlasnlnscysglinilniglcysr 2217
      ::::|||||
424 ..CGACTCTGTTGGAGTTGAGTAGTACSTCAAGSCTCTTGAGAGTGGTC 377
      |||||:||| |||:|||||
2217 rodltglelccysglugllyasnrlhtseretctcysgluaspnrro..... 2231

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107 LysalalysProgluLeuValProSerLeuLeuLysLeuAlaLeuAsnAs 123
333 TGCCCTGTCAGCAAGAAAGACTTCAGGGAGAGGCCAGGGGACAC 382
123 palamethritylaspilysalatrlyserglyAlaAsnly 138
383 CTCCCAAGACCTGAGTACTCACTCAACCCCAACAGAGTCGACAC 429
139 SerIleargPheSerSerLeuLeuSerArgAlaGluAsnGlu 152
430 CTGACACAGTTTGGAAATTCATCGT 455
153 GlyLeuSeraspGlyLeuSerLeuIleGluValLysGluLeuAs 169
456 TGCCATGTCAGAGGATTCACATCATGAGCAAGATTCACAA 501
169 pserIleSerLysGlyLysProIleSerTyrAlaAspIleLeu 186
502 .GGAGCAACCTGATTTCGTACTCAGAAAGTCATCATGCGCAATATA 549
186 IacGlyGlnSerAlaValLysPheThrTyrLeuAlaSerAla 199
550 CTCTGATTTCTTAACATTCCTCTCTGGAGCAATACCGAG 591
200 .IleArgLysCysGlyGlyAsnGluGlu 208
seq_name: SwissProt_40:XYNA_RUMFL

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seq_documentation_block:
ID XYNA_RUMFL STANDARD: PRT: 954 AA.
AC P29126:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Bifunctional endo-1,4-beta-xylanase XYLA precursor (EC 3.2.1.8).
GN XYNA.
OS Ruminococcus flavefaciens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Ruminococcus.
OX NCBI_TaxID=1265;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17.
RX MEDLINE=92261318; PubMed=1584021;
RA Zhang J.-X., Flint H.J.;
RT "A bifunctional xylanase encoded by the xyna gene of the rumen
RT cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
RT dissimilar domains linked by an asparagine/glutamine-rich sequence.";
RL Mol. Microbiol. 6:1013-1023(1992).
CC -1- FUNCTION: XYLANASE DOMAIN 1 RELEASES MORE XYLO-OLIGOSACCHARIDES
CC AND DOMAIN 2 MORE XYLOSE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC G (FAMILY 11 OF GLYCOSYL HYDROLASES).
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CELLULASE FAMILY
CC F (FAMILY 10 OF GLYCOSYL HYDROLASES).
CC -----
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CC -----
DR EMBL: Z11127; CA77476.1;
DR PIR: S18043; S18043.
DR PIR: S20907; S20907.
DR HSSP: P48793; IXND.
DR InterPro: IPR001000; Glyco_hydro_10.

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DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00331; Glyco_hydro_10; 1.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00134; GLHYDRLASE10.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F12; 1.
DR Xylan degradation; Hydrolyase; Multifunctional enzyme;
KW Repeat; Signal.
FT SIGNAL 1 27 OR 28, OR 29 (POTENTIAL).
FT CHAIN 28 954 BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA.
FT DOMAIN 28 244 XYLANASE DOMAIN 1.
FT DOMAIN 245 622 ASN/GLN/TRP-RICH (LINKER).
FT DOMAIN 623 954 XYLANASE DOMAIN 2.
FT ACT_SITE 122 122 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 223 223 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 774 774 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 884 884 NUCLEOPHILE (BY SIMILARITY).
SO SEQUENCE 954 AA; 111362 MW; 1033567D4B526BBD CRC64;

```

```

alignment_scores:
Quality: 77.00 Length: 46
Ratio: 2.406 Gaps: 2
Percent Similarity: 69.565 Percent Identity: 39.130

```

```

alignment_block:
US-09-821-726-17 x XYNA_RUMFL
Align seg 1/1 to: XYNA_RUMFL from: 1 to: 954

```

```

106 AGTATCATGTTCACAGCAGCAGCAGCTGTGAGTGGCAGCAGCTC 155
235 SerValSerValThrGlnGlyLysSerSeraspasnnglyGlnGlnG 251
156 AGTGTGTCAACATGACACAGCAGTGGCCAGTGTGACATTAACATG 205
251 nsnasnsprrpsnnglnnglnasn..AsnspnnglnnglnasnAsnA 267
206 GATGGAACCTCTGG.....AATGCCCTCTGGGAG 234
267 sptRpAsnAsntrpGlyGlnGlnAsnAsnAsprrpAsn 279

```

```

seq_name: SwissProt_40:Z335_HUMAN
seq_documentation_block:
ID Z335_HUMAN STANDARD: PRT: 1342 AA.
AC Q9H422; Q9H684;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 335.
GN ZNF335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagdley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA Coulson A.G., Franklin G.J., Deadman R., Dhami P., Dunn M.,
RA Ellington A.G., Fraser J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

```


OM of: US-09-821-726-17 to: SPTREMBL_19:* out_format: fts

Date: Sep 4, 2002 5:15 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

```
-MODEL=frame+np.model -DEV=xlp
-O=/cgn2.1/USPRO.spool/US09821726/runat_04092002_163855_17608/app.query.fasta_1.664
-DB=SPTREMBL_19 -OFMT=fasta -SUFFIX=sp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-REAPOP=6.000 -REAPEXT=7.000 -YGAPO=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=dlcosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pcr
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=fts
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09821726_@CGN1_1_265 -NGPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
```

Search information block:

```
Query: US-09-821-726-17
Query length: 597
Database: SPTREMBL_19:*
Database sequences: 56222
Database length: 172994929
Search time (sec): 82.480000
```

Score list:

Sequence	Strd	Orig	ZScore	Escore	len	Documentation
SP_rodent:Q9D077	+	252.50	476.77	1.7e-18	191	Q9D077 mus musculus (mouse). 11
SP_rodent:Q9C056	+	217.00	408.26	1.2e-14	184	Q9C056 mus musculus (mouse). 18
SP_organelle:Q9M78	+	97.50	165.16	0.1303	574	Q9M78 candida albicans (yeast). 1637
SP_mammal:Q9XSV8	+	90.50	141.22	0.9847	1637	Q9XSV8 bos taurus (bovine). 568
SP_invertebrate:Q76810	+	90.00	154.87	0.7506	373	Q76810 anopheles gambiae (afr
SP_invertebrate:Q9NL38	+	89.50	149.74	0.9514	578	Q9NL38 pinctada maxima. n66 m
SP_bacteria:Q9S253	+	89.00	156.27	0.8794	266	Q9S253 streptomyces coelicolor
SP_invertebrate:Q9VSD9	+	87.50	143.79	1.165	700	Q9VSD9 drosophila melanogaster
SP_organelle:Q9TJ56	+	87.00	149.73	1.55	348	Q9TJ56 leptocheilus munitus. n42
SP_bacteria:Q9R7U7	+	87.00	149.15	1.58	369	Q9R7U7 streptomyces coelicolor
SP_rodent:Q90UG5	+	87.00	142.81	1.87	695	Q90UG5 rattus norvegicus (rat). 285
SP_invertebrate:Q94477	+	86.00	149.76	1.89	409	Q94477 dictyostelium discoide
SP_bacteria:Q669974	+	84.50	143.28	3.02	1297	Q669974 streptomyces coelicolor
SP_invertebrate:Q952B0	+	84.50	131.88	4.12	1328	Q952B0 leishmania major. pos
SP_invertebrate:Q9NE64	+	84.50	124.32	5.05	2786	Q9NE64 leishmania major. pos
SP_invertebrate:Q01876	+	83.50	149.13	3.14	186	Q01876 caenorhabditis elegans
SP_bacteria:Q92RS8	+	83.50	146.41	3.38	245	Q92RS8 rhizobium meliloti (sinc
SP_invertebrate:Q01769	+	83.00	133.92	4.96	642	Q01769 caenorhabditis elegans
SP_invertebrate:Q09519	+	83.00	130.00	5.82	1168	Q09519 caenorhabditis elegans
SP_bacteria:Q9U712	+	82.50	131.75	6.12	410	Q9U712 neisseria meningitidis
SP_invertebrate:Q9W1W2	+	81.50	137.44	6.38	425	Q9W1W2 drosophila melanogaster
SP_bacteria:Q9LAA3	+	81.50	137.08	6.44	441	Q9LAA3 clostridium cellulosum
SP_bacteria:Q02056	+	81.50	136.72	6.51	707	Q02056 hordeum vulgare (barley)
SP_plant:Q02056	+	81.50	132.05	7.39	989	Q02056 mus musculus (mouse). ar
SP_rodent:Q9W1W9	+	81.50	128.74	8.08	2304	Q9W1W9 mus musculus (mouse). ar
SP_invertebrate:Q9W48	+	81.50	120.38	10.13	2422	Q9W48 drosophila melanogaster
SP_invertebrate:Q04603	+	81.50	119.88	10.27	227	Q04603 drosophila melanogaster
SP_plant:Q93572	+	81.00	142.31	6.17	227	Q93572 solanum tuberosum (potat
SP_plant:Q94GH5	+	81.00	140.24	6.53	280	Q94GH5 oryza sativa (rice). hyf
SP_plant:Q9SXY8	+	81.00	138.44	6.85	336	Q9SXY8 oryza sativa (rice). bet
SP_plant:Q9SXY7	+	81.00	138.38	6.86	338	Q9SXY7 oryza sativa (rice). bet
SP_fungi:Q03388	+	81.00	129.74	8.67	810	Q03388 saccharomyces cerevisiae
SP_invertebrate:Q023927	+	81.00	124.78	9.92	1338	Q023927 dictyostelium discoide
SP_plant:Q048991	+	80.50	139.89	7.27	263	Q048991 oryza sativa (rice). nbs
SP_human:Q9HAD6	+	80.50	125.09	10.68	1107	Q9HAD6 homo sapiens (human). m
SP_bacteria:Q056451	+	80.00	134.65	9.24	405	Q056451 xanthomonas sp. mercury
SP_mammal:Q9GLX9	+	80.00	127.84	11.11	807	Q9GLX9 bos taurus (bovine). vsg
SP_human:Q99552	+	80.00	113.14	16.55	3570	Q99552 homo sapiens (human). m
SP_bacteria:Q033798	+	79.50	138.81	9.11	241	Q033798 salmonella typhimurium.

```
seq_name: SP_rodent:Q9D077
seq_documentation_block:
ID Q9D077 PRELIMINARY: PRT: 191 AA.
AC Q9D077
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 1190003M12R1K. PROTEIN.
GN 1190003M12R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai T., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Botfield D., Bujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombearts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
RA Hayashizaki Y.
*Functional annotation of a full-length mouse cDNA collection.*
DR EMBL: AK004474; BAB23320.1;
DR MCD: MGI:1916138; 1190003M12R1K.
SO SEQUENCE 191 AA: 20772 MW: 7607DB4796A8B4D CRC64;

alignment_scores:
Quality: 252.50 Length: 204
Ratio: 1.913 Gaps: 7
Percent Similarity: 64.706 Percent Identity: 31.863

alignment_block:
US-09-821-726-17 x Q9D077
Align seg 1/1 to: Q9D077 from: 1 to: 191

1 ATGCGTACCTTCTGATTCATTCGATTCGTAAGCCAGATGAAGTTCAC 50
||||| ||||| : : : : :
1 MetPro.....LeuHisSerLeuGluAlaGAspAsnMetAlaGlyLe 14
51 AATGCGCTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 100
||||| : : : : :
14 uUaLaIProSeIleuValThrValPheLeuValIProAlaLeuAla. 30
101 ACTATAGTATCAGTGCACGACGACGACGAC.....AGTGGTGAAGT 144
: : : : :
31 .....LeuThrAsnThrSerAspSerTyrProLeuAspTylSerVal 44
145 GGGAGCAGATCAGTGCATGCAACATGAACACACGTCGCCACAGCTGA 194
||| ||||| : : : : :
```

```

620 CysnsmnncysrthrcyArqAlaIglYlnLeusercYstHraIaGlnPr 636
485 ATGTATCTTGGAATCCCGCTTCGCACATGGCAAGCATGATTTTCCAACCT 436
||||| ::||:::||:::||::|||
636 ocspProProlaIahiscYsAlatrPserAtrgTrpSerlaatPrsr. 652
435 GTCACAGTTTGCGACTGCTGTGGGGr.....TGA 407
||||| ||| |||
653 ..ProCysSerArgrSerCysGlyProAlaIglYlnInserArghearg 668
406 CTGATCACTCAGGCTCTTGg.....GAGCGTGtGCC 375
||||| ||||| ||||| |||
669 SererthrSerIglySertrPalaPrroGIucYsArqGlUGlInSercI 685
374 CCTGGGccCTTACCCTGAGcCTTCTTTCTTGACcAGcGATCAAGGc 325
||||| ||| ||::|||
685 nserclnPrrocYsProGInserrProcYsProProulcYsleuGInglYT 702
324 TTGA.....GGAGGGcARNGGCTTCTTCTCATTTGtGCA 287
::::: ||| ::||| ||| ::::: |||
702 hrarqProArgSerleugIlyAspSertrPleunGlnaspely...CysGln 717
286 CAATGC 281
|||||
718 Glncys 719
seq_name: sp_invertebrate.O76810
```

```
seq_documentation_block:
ID      076810      PRELIMINARY;      PRT;      373 AA.
```

DE 01-NOV-1998 (TREMBlrel_08, Created)
 DT 01-NOV-1998 (TREMBlrel_08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel_19, Last annotation update)
 DE ICHIT PROTEIN.
 GN ICHIT.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 OC Anophelinae.
 OX NCBI_Taxid=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUAKOKO; TISSUE=MAINLY MIDGUT;
 RX MEDLINE=99016033; Pubmed=9799221;
 RA Dimopoulos G., Sealey D., Wolf A., Kafatos F.C.;
 RT "Malaria infection of the mosquito Anopheles gambiae activates immune
 RT responsive genes during critical transition stages of the parasite
 RT life cycle.";
 RL EMBO J. 17:6115-6123(1998).
 DR EMBL: AJ010903; CAA09389.1; -;
 DR InterPro: IPR002557; Chitin_binding.
 DR Pfam: PF01607; Chitin_bind_2. 2.
 DR SMART: SM00494; ChEBD2. 2
 SQ SEQUENCE 373 AA; 40647 MW; CFAE3811FC224161 CRG64;

```
alignment_scores:
  Quality: 90.00      Length: 127
  Ratio: 1.698        Gaps: 4
Percent Similarity: 41.732  Percent Identity: 28.346
```

```
alignment_block:
US-09-821-726-17 x 076810 .
```

Align seg 1/1 to: 076810 from: 1 to: 373

```

92  CCCTTGTCACrTAATATCACTGTCACGACGACGGCA.....ACAGT 133
    |||      |||      ::|||::      |||||      ::|||
133  ProThrThrThrThrSerAlaProThrProSerGlnTyrPheAs 145
    ::|||::      |||||      ::|||
136  GGTGGAAAGTGGCAGCAGTCACTGAGTTCACCAATGAACCAACGTGG. 188
    ::|||      |||      |||||

```

```

149 pProThrIleThrThrThrProValTrpHisAspProThrTrpS 166
185 .....CCAAGCTTGACATPACATGATGGAGACCTCCGGATGGCCCT 229
    ||||| ||| ||| :::: ||||| |||||
166 eAlaProThrThrThrThrTrpSerAspAlaProProProThr 182
    ||||| ||||| ||||| ||||| ||||| |||||
230 GGGACCTAGACAGCGGCTTGCTGTACACAGACTCTGGAGAAAGTCA 279
    ||| :::: ||| :::: ||| :::: |||
183 ThrThrThrThrValTrpHisAspProThrAlaThrThrThrHi 199
    ||| :::: ||| :::: ||| :::: |||
280 TGCATTGTGCACAAATGAGAAGAGCAATGCCCTCCCTTCAAGCCT 329
    |||| ||| :::: ||||| ||||| |||
199 sAlaProThrThrThrThrTrpSerAspLeuProProProProt 216
    ||||| ||||| ||||| ||||| ||||| |||||
330 TGATGCCG.....TGTCAAGAGAAAAGATTCAGGGTAAGGGCC 370
    |||||
216 hrThrThrThrValTrpIleAsp..... 224
    |||||
371 CAGGGGGAGCCACCTCCCAAGAGCGCTGAGTCACTCAACCCCAACAGA 420
    ||| ||||| ||||| |||||
225 .....ProThrAlaThrThrThrThrHiAlaProThr 236
    ||||| ||||| ||||| ||||| ||||| |||||
421 GTCGACAACCTGACAAAGTTGGAAAAATCCA 451
    ::||| ||||| ::||| |||||
236 rThrThrThrTrpSerAspLeuProProPro 246

```

seq_name: sp_invertebrate:Q9NL38

```

seq_documentation_block:
ID      09NLU38      PRELIMINARY;      PRT;      568 AA.
AC      Q9NLU38;
DT      01-oct-2000 (TREMBLrel, 15, Created)
DT      01-oct-2000 (TREMBLrel, 15, last sequence update)
DT      01-DEC-2001 (TREMBLrel, 19, last annotation update)
DE      N66 MATRIX PROTEIN.
OS      Pinctada maxima.
OC      Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pterioidea;
OC      Pterioidea; Pteriliada; Pinctada.
OX      NCBI_TaxID=104660;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=NACREOUS LAYER.
RX      MEDLINE=20160475; Pubmed=10694502;
RA      Kono M., Hayashi N., Samata T.;
RT      "Molecular mechanism of the nacreous layer formation in Pinctada
RT      maxima.";
RL      Biochem. Biophys. Res. Commun. 269:213-218(2000).
DR      EMBL; AB032613; BAA90540.1; -.
DR      HSSP; P23589; 1DMY.
DR      InterPro; IPR001148; Carb_anhydrase.
DR      InterPro; IPR002952; Eggshell.
DR      Pfam; PF00194; carb_anhydrase; 1.
DR      PRINTS; PR01286; EGGSHELL.
DR      ProDom; PD000865; Carb_anhydrase; 2.
KW      Matrix protein.
SQ      SEQUENCE 568 AA: 62377 MW: 4AD9242A96EB42F CXC64;

```

[illegible]

```
alignment_block:
  00 00 00 17 00 00 00 00
```

Align seg 1/1 to: Q9NL38 from: 1 to: 568

```

124 GACGGCACAACGTGGTGAAGTGGGACGACGTCTAGTGTCAACCAATGA 173
      ::|||||:::|||||::|||
392 ASmGlyAsnAsnGlyIyAsnGly.....AsnAsnG 402
174 ACACACAGTGGCCACACAGTTGACACAAATACCAATGATGACGAACTCCGGAATG 223

```



```

KW      Hypothetical protein.
SQ      SEQUENCE   266 AA;  28612 MW;  837ADP6BBE1B18A CRC04;

alignment_scores:
    Quality:   89.00          Length:   173
    Ratio:     1.085         Gaps:     8
    Percent Similarity:  47.399      Percent Identity:  26.012

alignment_block:
US-09-821-726-17 x Q952S3      ..

Align seg 1/1   to: Q952S3   from: 1   to: 266

28  GGTGAAGCCAGATGAAGACTACACAAATTCGCTTGTGGACTTCTGGTCT  77
    |||:::  |||:::|||||:::
125  GLYASPTLYTLysLeuSerPheThrVal.....GLYTh  135
78  CTTCCTGACTCCCTCCCTGCTGCTACTAATAGTATCACTGTCACAGCAGCG  127
    |||||
135  rPheLeu.....AspG  139
128  GCACACAGCTGGTGAAGTGGCAGCAGCTCAGTG.....AGTGTCAACAAAT  171
    |||||  |||||:::|||||:::
139  LYSnLeuGLyGLyGLySerLysAsnAlaLeuSerAlaLeuGLyAla  155
172  GAACACACGTCGGCCCAACGTTGACAAATACATATGATGAGTACCTCTGSA  221
    |||||
156  AlAlaLeuAsnVal.....SerProG1  162
222  TGCCCTCTGGGACTATAGAACTGGCTTGTCTGTAAACAGACTCTTCGAGA  271
    ||:::  |||||:::|||||:::
162  uAlaPheValAspTyrLysThrAlaLeuTyrSerThrLysTyrHisProG  179
272  AGAATCTATGCATTGTGCACAAATATGAACAGAGAACCATGCCCTCCCTT  321
    :::::|||||  :::
179  LuGluSerThrAspGluPheAlaLysAspAspTyrLeuIleLysValAla  195
322  CAAGCCCTTGTAGCGCTGTCAGCAAGAAAGAGCTTCAGGCT.....  363
    :::::|||||:::|||||:::
196  AspSerValAspAlaLeuLysGLyAsnLysLysPheGlnAspAlaValG1  212
364  .AAGGCCCAAGGGGAC.....CACCTCCA  388
    |||||  |||
212  uLysLysLysThrTyrAspAlaTrpAlaMetArgMetSerLysSerPheAsp  228
389  AGAGCGCTGAGTACTACGTACGACCCCAACAGACAGTGCACACCTGGACA  438
    ::|||  |||||:::|||||:::
229  LysAlaGluGlyValGluSerThrProThrIleLysIleAsnAspLysVa  245
439  TTTCGAAATTCATCGTTGCCATGTGCAAGGGGATTCACACATCATGGC  488
    ::|||:::|||||  |||  |||
245  lValGluThrProSerThrProAspAla.....TrpG  256
489  TGAGAGACATCAAGGAG  505
256  lnlYsAlaLeuLysAsp  261

seq_name: sp_invertebrate:Q9VSD9

seq_documentation_block:
ID      Q9VSD9          PRELIMINARY:          PRT:          700 AA.
AC      Q9VSD9          :
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      UBIQUITIN-LIKE PROTEIN ACTIVATING ENZYME (SMT3 ACTIVATING ENZYME 2).
GN      OAR OR SAEZ OR CG7528.
OS      Drosophila melanogaster (Fruit fly)
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephyridioidea; Drosophilidae; Drosophila.
NCBI_Taxid=7227;

```


233 ACTATAGACTGGCTTTGCTGTACCAGACTCTTGAGAGACAGTCATCC 282

170 stentloetherinst.

170 stentloetherinst.

```

129 ValAspCuluaAsnPrLaseSerClYAspLoInClYalThAsPrProGluPr 145
130 ||| ||| : : : : : ||| : : ||| ||| |||
131 ValAspCuluaAsnPrLaseSerClYAspLoInClYalThAsPrProGluPr 145
132
133 387 CAGAGCCCTGAGGCTACTACGTCAACCCCAACAGAGTTC...GACAACTGG 433
134 | : : : : : : : : : ||| : : : ||| |||
135 145 oAlaProValaIGuaLaGuaLaValaProaLaLysTyrHisAspAsnLaIa 162
136 ||| ||| : : : : : ||| ||| |||
137 434 ACAAGTTTGGAAGAACCTATCGTCCATGTGGCAAGGAGATGCCAATAC 483
138 | : : : : : : : : : ||| ||| |||
139 162 lathrLaclYlysLeuPheAspSerProLysGlySerMetValGys 178
140 ||| ||| : : : : : ||| ||| |||
141 484 ATGCTCAAGAGATTCAAGA.....GCCAACTGAT 515
142 | : : : : : : : : : ||| ||| |||
143 179 SerLaIaThValaLysAspProaLaHisProGlyLysSerAsnMetVa 195
144 ||| ||| : : : : : ||| ||| |||
145 516 TTGCTATCTCAGAAAGTCAATCATGCTCCATATATCTC.....TGCATTG 559
146 | : : : : : : : : : ||| ||| |||
147 195 lTrpHrLaclYlscYsValHisLaclYlssSerGlylYlTrpYra 212
148 ||| ||| : : : : : ||| ||| |||
149 560 TTAACATTTCTCTTC 573
150 ||| ||| : : : : : ||| ||| |||
151 212 rGAsnTleLaPhe 216
152
153 seq_name: sp_plant:Q945S6
154
155 seq_documentation_block:
156 ID Q945S6 PRELIMINARY; PRT: 1297 AA.
157 AC Q945S6;
158 DT 01-DEC-2001 (TReMBLrel, 19, Created)
159 DT 01-DEC-2001 (TReMBLrel, 19, Last sequence update)
160 DT 01-DEC-2001 (TReMBLrel, 19, Last annotation update)
161 DE I2C-5.
162 I2C-5.
163 OS Lycopersicon pimpinellifolium (Culant tomato).
164 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
165 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
166 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
167 NX NCBI_TaxId=4084;
168 |||
169 SEQUENCE FROM N.A.
170 RP MEDLINE=2141641; PubMed=11523783;
171 RA Sela-Ibuurle M.B., Budai-Hadrian O., Pan Q., Carmel-Goren L.,
172 Vunsci R., Zamir D., Fluhr R.,
173 "Genome-wide dissection of Fusarium resistance in tomato reveals
174 multiple complex loci.",
175 Mol. Genet. Genomics 265:1104-1111(2001).
176 EMBL: AF408704; AAL01986.1; -.
177 SO SEQUENCE 1297 AA; 147917 MW; 76F5C20DE953181 CRC64;
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179 alignment_scores:
180
181 Quality: 84.50 Length: 214
182 Ratio: 0.918 Gaps: 11
183 Percent Similarity: 42.991 Percent Identity: 23.832
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185 alignment_block:
186 US-09-821-726-17 x Q945S6 ..
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188 Align seg 1/1 to: Q945S6 from: 1 to: 1297
189
190 22 TGCATTGGTGAAGCCAGATGAAGTTCACATTTGCTTCTGTGACTTCT 71
191 ||| ||| : : : : : ||| ||| |||
192 238 CysValSerCluValYraSpLaPhehrLlethr...LysGlyLeu 253
193 ||| ||| : : : : : ||| ||| |||
194 72 T.....GGTCTCTCTGACTCTCGCCCTTGTGACTATATATCA 112
195 ||| ||| : : : : : ||| ||| |||
196 253 uGlnGluLleGlyLysPhe..... 259
197 ||| ||| : : : : : ||| ||| |||
198 113 GTGTCAAGACGACGCAACAGTGGTGAAGTGGGACGACAGTCACTGACT 162
199 ||| ||| : : : : : ||| ||| |||
200 260 .....AspSerLysasp 263
201 ||| ||| : : : : : ||| ||| |||
202 163 GTCAACATGAACACAGCTGGCCAACTT..... 192

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264 ValHisAsnLeuAsnGlnLeuGlnValLysLeuLysGlnSerLeu 280
193 .....GACAA.....AACATGATGA 211
280 sglLysLysPheLeuIleValLeuAspValITrpsnGlnAsnTyrA 297
212 ACTCTGGAATGCCCTC.....TGGACTATAGAACT 243
297 snclutrpAsnAspLeuArgAsnIlePheValGlnGlnLysArgLys 313
244 GCGTTGCTGTAAACAAGACTCTTGAGAGAGACTCATGATGTGCACA 293
314 LysIleIleValThr.....ThrArgLysAspSerValAlaLeu 327
294 AATGAGAGAGAGCCATGCC.....TCCCTCAAGCCCTTG 311
327 tMetGlnAsnGlnGlnIleSerMetGlnAsnLeuSerThrGlnAlaSer 344
332 ATGCGCTGTCAAGAGAAAGACTTCAGGGTAAGGCCAGGGGAGCA 381
344 rPseLysPheLysArgHisAlaPheGlnAsnMetAspPrometGlnHis 360
382 CCTCCCAAGAGCCCTGAGCTACTGATCAACCCCAAGAGCTGCACA 421
361 Pro.....TCCCTCAAGCCCTTG.....GlnLeu 363
432 GGACAGATTGGAATATCATGCTTGCATGTCAGAGGGATTCACAT 481
363 uGlnGlnValGlnArgGlnIleAlaLysCysLysGlnLeuPro.... 378
482 ACATGCTGGAAGACTTCAGAGCAAACTGATTGCTACTCGAA... 528
379 ..LeuAlaLeuLysThrLeuAlaGlnMetLeuArgProLysSerGlnIle 394
529 .....AAGTCATCAGTGCATATATCTGATTTCT 561
395 AspGlnTrpLysCysIleLeuArgSerGlnIleTrpGlnLeu 408

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seq_documentation_block:
ID 0952B0 PRELIMINARY; PRT; 1328 AA.
AC 0952B0:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE POSSIBLE MAJOR AMPULATE SPIDROIN 2-LIKE PROTEIN (FRAGMENT).
GN L3747.01.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL596273; CAC44730.1; -.
FT NON_TER 1328 1328
SQ SEQUENCE 1328 AA; 138537 MW; 689EA0758A424434 CRC64;

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alignment_scores: 84.50 Length: 168
quality:

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Ratio: 1.225 Gaps: 9
Percent Similarity: 41.071 Percent Identity: 27.976
Alignment_block:
US-09-821-726-17/rev x 0952B0 ..
Align seg 1/1 to: 0952B0 from: 1 to: 1328

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213 SerSerProSerLysSerSerThrSerSerGlnProCysSerProPr 229
473 ATCCCTTGACAAAGGCAACGATGATTTCCAACTGTTCACAGTTGC 424
229 cArgGlnProArgAlaGlnArgTyrGlnCysLeuAsnCys.....CysA 244
423 GACTGTGTGGGGTGGTACTGAGTACTGAGCTCTGAGGAGGTGCCCC 374
244 rArgGlys.....GlySerCysAspSerValGly 253
373 CTGGGCCCTTACCT.....GAAGCTTCTTT 348
254 Leu...ProCysProValAsnAlaHisGlnHisArgSerArgGlnThrAl 269
347 TCCTTGACCAAGCATCAAGGCTTGAAGGAGGCA..... 311
269 aAlaGlnAlaAlaHisGlnArgCysHisAlaArgSerSerProAlaArg 286
310 ....TGCTTCCTCTCTCATTTTGTGCA..... 287
286 LArgGlnTrpLeuSerSerAlaAspCysAlaAlaThrAsnLysAspSerAla 302
286 .....CAATGCATGACTTCTTCTCGAAGAGTGTGTT 255
303 ProAlaAlaSerLysThrAlaThrValaAspSerProArgLeuGlnTrpLe 319
254 ACAGCA.....AGCAGTTCTATATGTCACAGAGGCAATT 220
319 uGlnGlnLeuProAlaThrProSerArgArgProSerProGlnGlnLeu 336
219 SCAGAGTTCATCATCATGTTGTAATTGTCAAGCTTGAGCAGTTGTTCAT 170
336 rSerSerGlnValArgCysArgSerThrArg.....ArgValArgHis 350
169 TGTTGACACTGACTGACTGCTGCCAC...TTCACACACTGTGGCGTGC 123
351 ArgArgArgGlnGlnSerProAlaHisAspArgGlnHisCysCysHisAs 367
122 TCGT 119
367 Patg 368

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:12 ; Search time 57.74 Seconds
(Without alignments)
77.837 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993
Sequence: 1 MKLTFVVGILGLAAPGFA.....TADILMLRMSFCGTVETTY 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	9.2	553	3	US-09-083-351-2
2	91	9.2	553	4	US-09-083-352-2
3	85.5	8.6	346	1	US-08-213-403-2
4	85.5	8.6	346	1	US-08-458-077-2
5	85.5	8.6	346	1	US-08-460-741-2
6	85.5	8.6	346	1	US-08-747-240-2
7	85.5	8.6	346	1	US-08-299-567-6
8	79	8.0	336	1	US-08-436-044-2
9	79	8.0	336	2	US-08-436-054-2
10	79	8.0	336	5	PCT-US95-08812-2
11	77.5	7.8	428	3	US-09-118-319-5
12	76	7.7	775	4	US-09-305-640-2
13	75	7.6	334	1	US-08-241-465B-19
14	75	7.6	334	1	US-08-241-465B-20
15	73	7.4	238	4	US-09-216-295-12
16	72	7.3	333	1	US-08-436-044-4
17	72	7.3	333	2	US-08-436-054-4
18	72	7.3	333	4	US-08-271-948-2
19	72	7.3	333	5	PCT-US95-08534-2
20	72	7.3	333	5	PCT-US95-08812-4
21	72	7.3	478	3	US-08-155-888-2
22	71	7.2	193	1	US-08-616-368A-1
23	71	7.2	193	4	US-08-616-368A-1
24	71	7.2	193	4	US-08-818-655-1
25	70	7.0	193	1	US-08-616-368A-8
26	70	7.0	193	1	US-08-616-368A-13
27	70	7.0	193	2	US-08-739-485-1

28	70	7.0	193	2	US-08-739-485-9	Sequence 9, Appl
29	70	7.0	193	4	US-09-054-298-8	Sequence 8, Appl
30	70	7.0	193	4	US-09-054-298-13	Sequence 13, Appl
31	70	7.0	193	4	US-08-818-655-8	Sequence 8, Appl
32	70	7.0	193	4	US-08-818-655-13	Sequence 13, Appl
33	70	7.0	312	1	US-08-525-505A-4	Sequence 4, Appl
34	70	7.0	314	1	US-08-525-505A-2	Sequence 2, Appl
35	70	7.0	992	1	US-08-127-499A-1	Sequence 1, Appl
36	70	7.0	992	1	US-08-482-847-1	Sequence 1, Appl
37	69.5	7.0	197	1	US-08-044-621D-29	Sequence 29, Appl
38	69.5	7.0	197	2	US-09-047-370-9	Sequence 9, Appl
39	69.5	7.0	197	2	US-09-216-295-16	Sequence 16, Appl
40	69.5	7.0	348	1	US-08-032-848C-13	Sequence 13, Appl
41	68	6.8	221	1	US-09-216-295-7	Sequence 7, Appl
42	68	6.8	239	4	US-09-216-295-5	Sequence 5, Appl
43	68	6.8	580	4	US-08-913-159-10	Sequence 10, Appl
44	68	6.8	1046	1	US-08-386-727-2	Sequence 2, Appl
45	68	6.8				

ALIGNMENTS

RESULT 1
US-09-083-351-2
Sequence 2, Application US/09083351
Patent No. 6087107
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patel, Shiva
TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR
TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,351
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UTA-029.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-351-2

Query Match 9.2%; Score 91; DB 3; Length 553;
Best Local Similarity 19.6%; Pred. No. 0.089;
Matches 38; Conservative 21; Mismatches 57; Indels 78; Gaps 9;

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Db      76 MYKPPSYALIT--MAIONAPDKKTLTGITOFIMDRFPFRDNKGQNSIRHNSL 132
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OY      58 -----DSNNSIMDYENS--FATRLFSKSCIVHRMKNDA 91
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Db      133 NECYKVPDRDKKPKGKGSYWTLPDDSYNM--FENGSEFLRRRRFRKKDAVKRKEKDRL 189
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OY      92 -----PSLDDLTMYKEQKGRGPGAPKDDMYSVNPRVEDLNFPGKIGMCRGIP 144
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OY      145 TYVABEIGPNQPL 158
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RESULT      2
US-09-083-352-2
Sequence 2, Application US/09083352
Patent No. 6207450
GENERAL INFORMATION:
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
APPLICANT: Stone, Edwin M.
APPLICANT: Nishimura, Darryl
APPLICANT: Patil, Shiva
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY, HONG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,352
FILING DATE: 22-MAY-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-029.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-083-352-2

Query Match      9.2%; Score 91; DB 4; Length 553;
Best Local Similarity 19.6%; Pred. No. 0.089;
Matches 39; Conservative 21; Mismatches 57; Indels 78; Gaps 9.

OY      14 LAADGAYIVYININGNDGNDVSGQASVINGVHVA-----MIDNNNGW----- 57
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Db      76 MYKPPSYALIT--MAIONAPDKKTLTGITOFIMDRFPFRDNKGQNSIRHNSL 132
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OY      58 -----DSNNSIMDYENS--FATRLFSKSCIVHRMKNDA 91
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      133 NECYKVPDRDKKPKGKGSYWTLPDDSYNM--FENGSEFLRRRRFRKKDAVKRKEKDRL 189
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OY      145 TYVABEIGPNQPL 158
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NECYSIMDYENS--FATRLFSKSCIVHRMKNDA 91

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OY      145 TYVAEIIIPGNQPL 158
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Db      234 -----PSPQPL 240

RESULT      3
US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457/el Cytokine Designated elx Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213.403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-213-403-2

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Best Local Similarity 23.1%; Pred. No. 0.19; Indels 49; Gaps 11;
Matches 40; Conservative 23; Mismatches 61;

OY      16  APGAATVTNNGNDGVNDSGOOSVSINGVNHYANLDNNNG-WDSWNSLMDYNSE-AAAT 73
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Db      195 APG-----SRGLSGSDGR-----HETVNGEEKSGPASAAGSSGDPPGFENR 238

OY      74  RLFSK-KSCIV-----HRNKDAMPSLDLDTMKVEQKGKGGGANP 113
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Db      239 ALFAAVAGACVFILLILIFVLTLKLKRKHKKHTOORAALSLSTLASPKGSSTAETE 298

OY      114 PKDLMTSVNTRVEDLNTFGP---KIAGMCRGIPTVAEIRPGPNP---LYSK 161
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Db      299 PSDLILRLRTIE---NNICPHYEKYSG-DYGHPIVIIVGEMP-PQSPANIITYK 345

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[illegible]

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-044-2

Query Match 8.0%; Score 79; DB 1; Length 336;
Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYNSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTWYKQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHVP 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335

RESULT 9
US-08-436-054-2
Sequence 2, Application US/08436054
Patent No. 5864020
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Matthews, William
TITLE OF INVENTION: HTK LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436, 054
FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/277722
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 902D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-436-054-2

Query Match 8.0%; Score 79; DB 2; Length 336;
Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYNSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTWYKQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHVP 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335

RESULT 10
PCT-US95-08812-2
Sequence 2, Application PC/TUS9508812
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: HTK LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08812
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 902PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-08812-2

Query Match 8.0%; Score 79; DB 5; Length 336;
Best Local Similarity 24.6%; Pred. No. 0.97;
Matches 34; Conservative 21; Mismatches 47; Indels 36; Gaps 9;

QY 49 ANIDNNNGDMSNLSMDYNSFAATRLFS--KKSCIV-----HRMKNK 88
DB 209 SSTDGNASAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITLVLLKTRRRHRKHS 263
QY 89 DAMPSLQDDLTWYKQKGGKGGAPPKDLMYSVNPTRVEDLNTFGP---KIAGMCRGIPT 145
DB 264 PQHTTTLSTLATPKRGNGNNGSEPSDV---IIPLRAD-SVFCPHYEKVSG-DYGHVP 318
QY 146 YVAEELPGNPQ--LYSK 161
DB 319 YIVQEMP-POSPANIYYK 335

APPLICANT: Junko SUZUKI
APPLICANT: Jun KONDO
APPLICANT: Atsuko KOHARA
APPLICANT: Akiko MORI
APPLICANT: Ei YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-1 PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-465B-20

Query Match 7.6%; Score 75; DB 1; Length 334;
Best Local Similarity 19.7%; Pred. No. 2.7;
Matches 29; Conservative 28; Mismatches 70; Indels 20; Gaps 4;

QY 21 YTVING--NDGNVDSGGSQSVSYNGVHNVANIDNNNGWDSNLDYENSEFAATRLFSK 78
Db 77 YTMISNGKLDG-----SMEDAGNNLETFKMGSGAEALAVNDFONGITGIRPAGG 128

QY 79 KSCIYHRMKNKDMPSLDLDTMWKEOKGK---PGGAPPKDLMSVNPTRVEDLNTFTGPK 135
Db 129 EKCYLEKQVARIPEVGAATVKOSISKLEKIMPEVKEENSLIWAADVPKDNLSLNSK 188

QY 136 IAGMCRGIPYVAEEIPGPNOPLYSKR 162
Db 189 VLELCGDLPIFWL-----KPTYPE 208

RESULT 15
US-09-216-295-12
; Sequence 12, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wenderoth, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIT-like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Fusarium equiseti

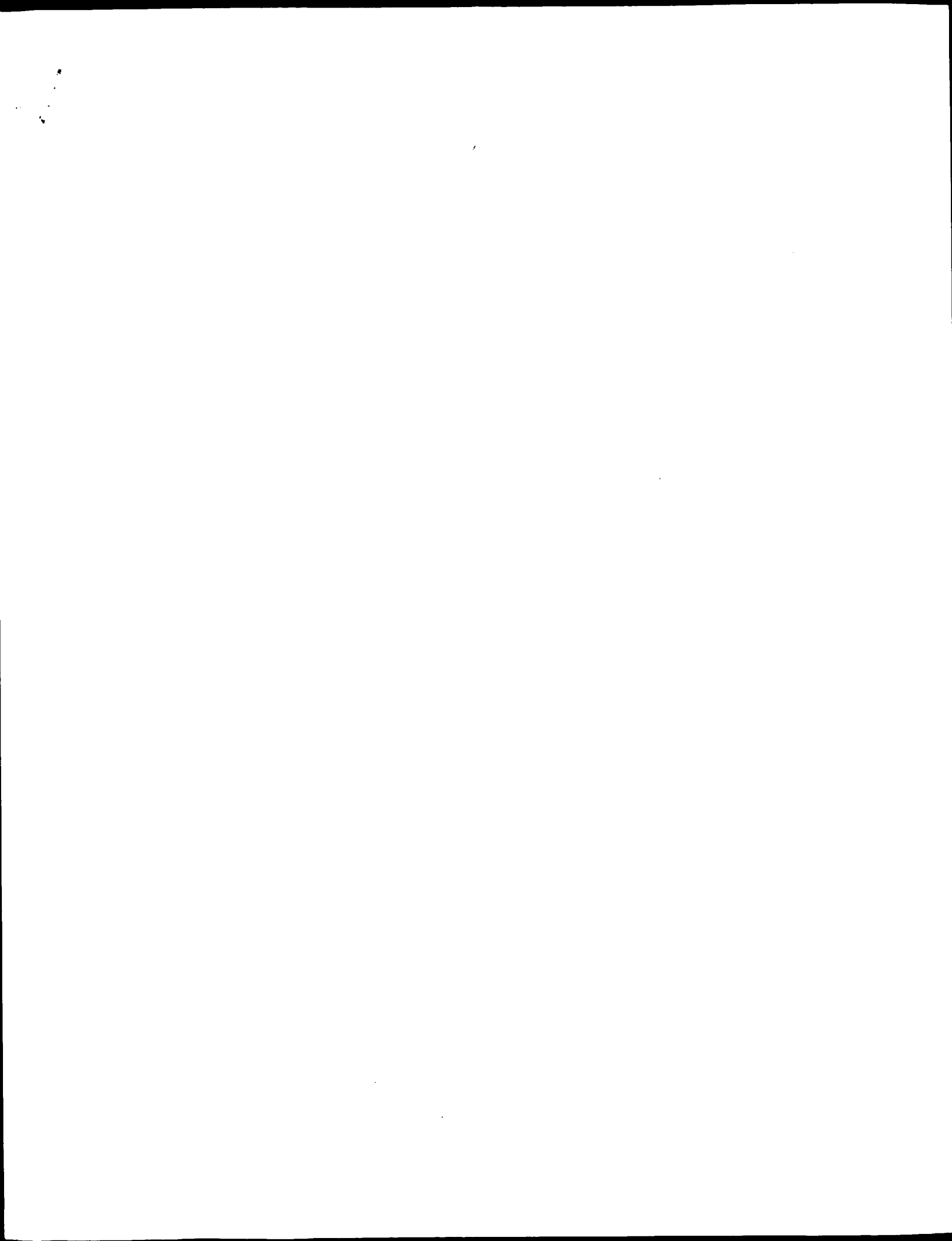
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Query Match 7.4%; Score 73; DB 4; Length 238;
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Matches 24; Conservative 11; Mismatches 26; Indels 28; Gaps 5;

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Db 1 MKSTLLAGAFAPLAFPAKDLCEOYGYLSSDGYSLNNVWCKD---SGTGDQCTHYNM--- 54

QY 48 VANIDNNNGWD-SWN-----SLMDYENS 69
Db 55 --NNANGAGWDVEMNWSGCKDNVKSYPNS 81

Search completed: September 4, 2002, 16:46:13
Job time: 334 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:21 ; Search time 704.77 Seconds
(without alignments)
91.894 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993
Sequence: 1 MKLTFVVGGLGLAAPGFA.....TADILILMSFGTSVET 184

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA_Main:*

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2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*

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22: /cgn2_6/ptodata/2/paa/US098_COMB.pep:*

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24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*

25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*

26: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	993	100.0	184	US-09-821-726-16	Sequence 16, App1
2	640	64.5	185	1 PCT-US98-16318-18	Sequence 18, App1
3	640	64.5	185	US-09-130-189-18	Sequence 18, App1
4	640	64.5	185	US-09-684-524-105	Sequence 105, App1
5	640	64.5	185	US-09-709-238-211	Sequence 211, App1
6	640	64.5	185	US-09-746-783-146	Sequence 146, App1
7	640	64.5	185	US-09-941-992-211	Sequence 211, App1

8	640	64.5	185	23	US-09-989-279-211	Sequence 211, App
9	640	64.5	185	23	US-09-989-293A-211	Sequence 211, App
10	640	64.5	185	23	US-09-989-721-211	Sequence 211, App
11	640	64.5	185	23	US-09-989-722-211	Sequence 211, App
12	640	64.5	185	23	US-09-989-723-211	Sequence 211, App
13	640	64.5	185	23	US-09-989-724-211	Sequence 211, App
14	640	64.5	185	23	US-09-989-725-211	Sequence 211, App
15	640	64.5	185	23	US-09-989-726-211	Sequence 211, App
16	640	64.5	185	23	US-09-989-727-211	Sequence 211, App
17	640	64.5	185	23	US-09-989-728-211	Sequence 211, App
18	640	64.5	185	23	US-09-989-729A-211	Sequence 211, App
19	640	64.5	185	23	US-09-989-730-211	Sequence 211, App
20	640	64.5	185	23	US-09-989-731-211	Sequence 211, App
21	640	64.5	185	23	US-09-989-732-211	Sequence 211, App
22	640	64.5	185	23	US-09-989-734-211	Sequence 211, App
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24	640	64.5	185	23	US-09-989-862-211	Sequence 211, App
25	640	64.5	185	23	US-09-990-427-211	Sequence 211, App
26	640	64.5	185	23	US-09-990-436-211	Sequence 211, App
27	640	64.5	185	23	US-09-990-437-211	Sequence 211, App
28	640	64.5	185	23	US-09-990-438-211	Sequence 211, App
29	640	64.5	185	23	US-09-990-439-211	Sequence 211, App
30	640	64.5	185	23	US-09-990-440-211	Sequence 211, App
31	640	64.5	185	23	US-09-990-441-211	Sequence 211, App
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33	640	64.5	185	23	US-09-990-443-211	Sequence 211, App
34	640	64.5	185	23	US-09-990-444-211	Sequence 211, App
35	640	64.5	185	23	US-09-990-456-211	Sequence 211, App
36	640	64.5	185	23	US-09-990-562-211	Sequence 211, App
37	640	64.5	185	23	US-09-990-711-211	Sequence 211, App
38	640	64.5	185	23	US-09-990-726-211	Sequence 211, App
39	640	64.5	185	23	US-09-991-073-211	Sequence 211, App
40	640	64.5	185	23	US-09-991-157-211	Sequence 211, App
41	640	64.5	185	23	US-09-991-163-211	Sequence 211, App
42	640	64.5	185	23	US-09-991-172-211	Sequence 211, App
43	640	64.5	185	23	US-09-991-181-211	Sequence 211, App
44	640	64.5	185	23	US-09-991-854-211	Sequence 211, App
45	640	64.5	185	23	US-09-992-521-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-16
Sequence 16, Application US/09821726
GENERAL INFORMATION:
APPLICANT: MARTIN, TERENCE E.
APPLICANT: TOBACK, F. GARY
APPLICANT: POWELL, C. THOMAS
APPLICANT: AGARWAL, KAN
TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
FILE REFERENCE: 21459/90913
CURRENT APPLICATION NUMBER: US/09/821,726
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 184
TYPE: PRT
ORGANISM: Mus sp.
US-09-821-726-16

Query Match 100.0%; Score 993; DB 22; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.2e-100;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLTFVVGGLGLAAPFAFATVNTINGNDGVDSGQSVSINGVHVNATIDNNNGDSW 60
DB 1 MKLTFVVGGLGLAAPFAFATVNTINGNDGVDSGQSVSINGVHVNATIDNNNGDSW 60
QY 61 NSLWDYENSFAATRLFSKSCIVHRNKKDAMPSTLDDITDVTWKQKGGKPGGAPPKDLMS 120

D6	61	NSLMWYENSPATRLFSKKSCTVHRMKNKDMPSLQDDLPYWKBEKGKGGPGGAPPKDLMTS	120
QY	121	VNPFVEEDLNTFFGPKIAGCMCRGIEPTYYAEELIGPNOPLYSKCYTADILMLRMSFCGT	180
D6	121	VNPFVEEDLNTFFGPKIAGCMCRGIEPTYYAEELIGPNOPLYSKCYTADILMLRMSFCGT	180
QY	181	VETTY 184	
D6	181	VETTY 184	

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RESULT 2
PCT-US98-16318-18
: Sequence 18, Application PC/TUS9816318
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John M.
: APPLICANT: LaVallie, Edward R.
: APPLICANT: Racie, Lisa A.
: APPLICANT: Evans, Cheryl
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Agostino, Michael J.
: APPLICANT: Steinhinger II, Robert J.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
: FILE REFERENCE: G16051A
: CURRENT APPLICATION NUMBER: PCT/US98/16318
: CURRENT FILING DATE: 1998-08-06
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO. 18
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US98-16318-18

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[illegible]

RESULT 3
US-09-130-189-18
Sequence 18, Application US/09130189
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Racine, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberly, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steinhinger II, Robert J

```

1  APPLICATION:  Genetics Institute, Inc.
2  TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
3  FILE REFERENCE:  G16051A
4  CURRENT APPLICATION NUMBER:  US/09/130.189
5  CURRENT FILING DATE:  1998-08-04
6  NUMBER OF SEQ ID NOS:  30
7  SOFTWARE:  PatentIn Ver. 2.0
8  SEQ ID NO 18
9  LENGTH:  185
10  TYPE:  PRT
11  ORGANISM:  Homo sapiens
12  US-09-130-189-18

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[illegible]

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RESULT      4
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.,
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIORITY APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,653
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-684-524-105

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Best Local Similarity	63.8%	Pred. No. 1.6e-61		
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QY	1	MKLTMPVGLGLGLAPGFA-YTVININGNCGANDSGGQGSYSVINGVHANYANDNNNGMS	59	
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QY	60	WNSLMDYENEFATRLFSKSCIVHNRHNRKAMPSTLDDLTMYEOK--GKPGCAPKDL	117	
	: : : : : : :			
Db	60	WNSLMDYGNCFATRLFLQKRTCIYHMKNEVMSIQLDLAEKRLQCKGPGPPKGL	119	
QY	118	MYSNPTPRVDDLTMTFGPKITGMGRGIPTYAAELPGNDQLYSKCKYTADILWILMSPC	177	
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DB 120 MTSVNPKNVDLSKFGKNIANNCRGIPITYMAEMQEASLFFYSGTCYTTSLMIVDISFC 179
QY 178 GTSTV 182
I : :
DB 180 GDTVE 184

RESULT 5
US-09-709-238-211
Sequence 211, Application US/09709238
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,030
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-10

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PRIOR APPLICATION NUMBER: US 60/090,254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 60/090,355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: US 60/090,429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: US 60/090,444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,461
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,472

QY 118 MVSUNFREDINTGPKIAGCGRIPYVAEIPGPNOLYSKCYADILILRMSPC 177
DB 120 MVSVMNKNKJDLKFKGNIANMCRGIPYMADEMQEASLFFYSGTCYTSVIMIVDISPC 179
QY 178 GTSVE 182
DB 180 GDVE 184

RESULT 7
US-09-941-992-211
Sequence 211, Application US/09941992
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C1
CURRENT APPLICATION NUMBER: US/09/941,992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.58; Score 640; DB 23; Length 185;

Best Local Similarity 63.88; Pred. No. 1.0e-61;

Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLMEVVGILGLAAPFA-YTVINNGDNGVSGGOOSVINGVHNVANIIDNNNGWDS 59
DB 1 MKFTTVAGLLGVFLAPALANTININVN-DDNNNGSGGOOSVYNNEHNVANVVDNNNGWDS 59

QY 60 WNSLMDYENSFAATRLFSKSCIVHRNKNKDAMPSLODLTMVKEQK--GKPGGAPPKDL 117
DB 60 WNSLMDYGNCFATRLFOKKTCTVHKNNKRYMPSISGLALVKEKKLQKGGPPPKGL 119
QY 118 MYSVNPTRVEDLNTFFGKRIAGMCRGIPITYVAEPIPGBNOPLYSKKCYTADIIMILMASC 177
DB 120 MYSVNPKNKVDLSKFGKNINAMCRGIPITYVAEEMOEASLFFYSGTCYTSVLMIVDISFC 179
QY 178 GTSYE 182
DB 180 GDIVE 184

RESULT 8

US-09-989-279-211

Sequence 211, Application US/09989279

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Collin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC56

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

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PRIOR APPLICATION NUMBER: 60/087106

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PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

Query Match	64.5%;	Score 640;	DB 23;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 1.6e-61;		

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54	PRIOR FILING DATE: 1998-07-02
55	PRIOR APPLICATION NUMBER: 60/091978
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59	PRIOR APPLICATION NUMBER: 60/092182

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; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match      64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3.

OY      1 MKLTMTFVLLGLLGAAPGFA-YTVNININGNDGHWVDSGQOOSVSIINGVHVAINDNNNGMS 59
DB      1 MKFTTFACLLGFLAPALANINYN-DNNNAGSGQOOSVSNBHNVAANDNNNGMS 59
OY      60 WNSLMDYENSFATRLFSKSCIVHRMKNKAMPSLQDDLTWYKEOK--GKGPGAPPKDL 117
DB      60 WNSIDYDNGFATRLFKOKTCIVHRMKNKEXPISQSDALVKEKKLQKGGPGPPKDL 119
OY      118 MVSVPTRPREDINTFGPKIAGCMCRGIPPTVVAEIIQGPNOPLYSKCYTADILWLMSPC 177
DB      120 MTSVPMKRVKDDLSFGCKNIANMCRGIPPTVMAEEMQEASLFYSGCYTTSVLMIVDISFC 179
OY      178 GTSVE 182
DB      180 GDTVE 184

RESULT 10
US-09-989-721-211
; Sequence 211, Application US/09989721
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C55
; CURRENT APPLICATION NUMBER: US/09/989,721
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519

PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMEVYGLGLIAPGFA-YVNVINGNDGNDGSGQGSVSTNGVHNVANDNNNGWDS 59
DB 1 MKFTVFAGLGLVFLAPALANNVNNV-DNNNAGSGQGSVSNNEHNVANDNNNGWDS 59

QY 60 WNSLWDYENSPFAATRLFSKSCIVHRNKNKDAMPLODLDTMYEOK--GKPGGAPPKDL 117
DB 60 WNSTWIDYGNFGAATRLFOKKTICIVHKKNKEVMSIQSLDALVEKKLQGGPGGPKGL 119

QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPFYVAEIPGPNOPLYSKCYTADILMLMSKFC 177
DB 120 MYSVNPKNVDLSFKGKNINAMCRGIPYMAEEMQASLFFYSGTCYTSVLMIVISFC 179

QY 178 GTSYE 182
DB 180 GDYVE 184

RESULT 12
US-09-989-723-211
Sequence 211, Application US/09989723
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5%, Score 640, DB 23, Length 185,
Best Local Similarity 63.8%, Pred. No. 1,6e-61,
Matches 118, Conservative 24, Mismatches 39, Indels 4, Gaps 3;

QY 1 MKLTFVYVGLGLAPGPA-YTVNINMGDGVDSGOOSVSIINGVHVANIDNNNGWDS 59
DB 1 MKFTTFACLLVFLAPALANNINVN-DDNNNAGSGQSVSVNNEHVANNVNNNGWDS 59
QY 60 WNSLDYENSFAATRLFSKSCIVHRMKNKAMPISLQDIDTMKEOK--GKGGGAPPKDL 117
DB 60 WNSIMWYGNCFATRLFCRKTCTVHRMKNKEXPISIOSLDALVEKRLKGKGGGPPKGL 119
QY 118 MYSVNTREDDINTGPKTJAGMCRGIPYVAEIIPGPNOLFSKRCYADILMIIRMSFC 177
DB 120 MYSVNNKVDLSKRCGNIAANMCRGIPYMAEDMEASLFEYSGCYTTSVMIYDISPC 179

QY 178 GTSVE 182
DB 180 GDIVE 184

RESULT 13
US-09-989-724-211

Sequence 211, Application US/09989724
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C67
CURRENT APPLICATION NUMBER: US/09/989,724
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12


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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C71
CURRENT APPLICATION NUMBER: US/09/989,725
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-11
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PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25

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;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5%; Score 640; DB 23; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 KKLMEVYGLGLAAGFA-YTVNINGNDGNDGSGQSVSINGVHNANIDNNNGMDS 59
Db 1 MKETIVEGGLGLVLAALANYNINNV-DNNNAGSGQSVSNNEHNANVDNNNGMDS 59
QY 60 WNSLMDENSEFAATRLFSKSCSYHRNKNKAMSLDLDITMYEOK--GKPGGAPPKDL 117
Db 60 WNSLMDGNGFAATRLFSKSCSYHRNKNKAMSLDLDITMYEOK--GKPGGAPPKDL 119
QY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYVAERIPGPNOPLYSKCYTADILMLMSFC 177
Db 120 MYSVNPVKVDLDLSEKGNKIANMCRGIPTYVAERIPGPNOPLYSKCYTADILMLMSFC 179
QY 178 GTSYE 182
Db 180 GDTVE 184

RESULT 15
US-09-989-726-211
;; Sequence 211, Application US/09989726
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Bolstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gertsens, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC60
;; CURRENT APPLICATION NUMBER: US/09/989,726
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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Page 18

PRIOR APPLICATION NUMBER: 60/088826
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 64.5%; Score 640; DB 23; Length 185;

Best Local Similarity 63.8%; Pred. No. 1,6e-61;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTFFVYGLGLIAPGFA-YVYVINGNDGCVNDGSGQGSVSINGVHYVNAVNDNNNGMDS 59
118 MYSVNPTRVEDLNTFGPKIAGMCRGIPYVAEPIGPNQLYSKKCTATLILMLMSFC 177
120 MYSVNPKNVDLDSKFGKRNIAVMCRGIPYVAEEMQEASLFTYSOTCTYSVLMIVDISFC 179
QY 178 GTSVE 182
Db 180 GDTVE 184

Search completed: September 4, 2002, 16:59:21
Job time: 1042 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:04:24 ; Search time 166.13 Seconds
(Without alignments) 272.394 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993
Sequence: 1 MKLTMEVYGLGLAAGFA.....TADILILRMSFCGSVETY 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 763338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 763338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.0	64.5	185	5	US-09-991-150-211
2	64.0	64.5	185	5	US-09-720-533-49
3	64.0	64.5	185	6	US-10-119-480-148
4	64.0	64.5	185	6	US-10-216-159A-148
5	64.0	64.5	185	6	US-10-216-162-148
6	64.0	64.5	185	6	US-10-216-163-148
7	64.0	64.5	185	6	US-10-216-164-148
8	64.0	64.5	185	6	US-10-216-165-148
9	64.0	64.5	185	6	US-10-216-166-148
10	64.0	64.5	185	6	US-10-216-167-148
11	64.0	64.5	185	6	US-10-216-168-148
12	64.0	64.5	185	6	US-10-216-169-148
13	64.0	64.5	185	6	US-10-218-849-148
14	64.0	64.5	185	6	US-10-218-930-148
15	64.0	64.5	185	6	US-10-219-003-148
16	64.0	64.5	185	6	US-10-218-612-148
17	64.0	64.5	185	6	US-10-218-956-148
18	64.0	64.5	185	6	US-10-219-010-148
19	64.0	64.5	185	6	US-10-218-765-148
20	64.0	64.5	185	6	US-10-218-784-148
21	64.0	64.5	185	6	US-10-219-061-148
22	64.0	64.5	185	6	US-10-219-062-148
23	64.0	64.5	185	6	US-10-219-063-148
24	64.0	64.5	185	6	US-10-219-064-148
25	64.0	64.5	185	6	US-10-219-065-148
26	64.0	64.5	185	6	US-10-219-066-148

27	64.0	64.5	185	6	US-10-219-070-148	Sequence 148, App
28	64.0	64.5	185	6	US-10-219-071-148	Sequence 148, App
29	64.0	64.5	185	6	US-10-219-072-148	Sequence 148, App
30	64.0	64.5	185	6	US-10-219-073-148	Sequence 148, App
31	64.0	64.5	185	6	US-10-219-074-148	Sequence 148, App
32	64.0	64.5	185	6	US-10-219-075-148	Sequence 148, App
33	64.0	64.5	185	6	US-10-219-077-148	Sequence 148, App
34	64.0	64.5	185	6	US-10-219-464-148	Sequence 148, App
35	64.0	64.5	185	6	US-10-219-465-148	Sequence 148, App
36	64.0	64.5	185	6	US-10-219-466-148	Sequence 148, App
37	64.0	64.5	185	6	US-10-219-467-148	Sequence 148, App
38	64.0	64.5	185	6	US-10-219-470-148	Sequence 148, App
39	64.0	64.5	185	6	US-10-219-471-148	Sequence 148, App
40	64.0	64.5	185	6	US-10-219-474-148	Sequence 148, App
41	64.0	64.5	185	6	US-10-219-475-148	Sequence 148, App
42	64.0	64.5	185	6	US-10-219-476-148	Sequence 148, App
43	64.0	64.5	185	6	US-10-219-478-148	Sequence 148, App
44	64.0	64.5	185	6	US-10-219-479-148	Sequence 148, App
45	64.0	64.5	185	6	US-10-219-480-148	Sequence 148, App

ALIGNMENTS

```
RESULT 1
US-09-991-150-211
: Sequence 211, Application US/09991150
: GENERAL INFORMATION:
: APPLICANT: Askenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C48
: CURRENT APPLICATION NUMBER: US/09/991,150
: PRIOR APPLICATION DATE: 2001-11-16
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 211
: LENGTH: 185
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-991-150-211
```

Query Match 64.5%; Score 64.0; DB 5; Length 185;

Best Local Similarity 63.8%; Pred. No. 6,8e-60;

Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

```

Db 1 MKLTMEVYGLGLAAGFA-...TVTNINGNDGVSQGSISNGVYRVANIDNNNGDS 59
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
      1 MKTTFVAGLGLVFLPALANTNINVN-DDNNNGSGQGSVSYNNEHNVANVDNNGMDS 59
```

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OY 60 WNSLWDYENSEFAATRLFSKSCIVHRNKKDAMPSLDLDTMVEOK--GKPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGSAATRLFLQKTCIVHKNNKEVMPISQSLDLVKEKKLQGGPGGPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEETGPNQPLYSKKCYTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYAAEEMQEAASLEFFSGTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDYVE 184

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: Pf-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

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Query Match 64.5%; Score 640; DB 5; Length 185;
Best Local Similarity 63.8%; Pred. No. 6, 8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTMFVGLGLLAAPGFA-YTVNINGNDGNDGSGQSVSINGYHNVANDNNNGMS 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKFTIVFAGLLGVFLAPALANYINVN-DDNNAGSGQSVSNNEHNVANDNNNGMS 59
OY 60 WNSLWDYENSEFAATRLFSKSCIVHRNKKDAMPSLDLDTMVEOK--GKPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGSAATRLFLQKTCIVHKNNKEVMPISQSLDLVKEKKLQGGPGGPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEETGPNQPLYSKKCYTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYAAEEMQEAASLEFFSGTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDYVE 184

```

RESULT 3
US-10-119-480-148

```

; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

```

```

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6, 8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

OY 1 MKLTMFVGLGLLAAPGFA-YTVNINGNDGNDGSGQSVSINGYHNVANDNNNGMS 59
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MKFTIVFAGLLGVFLAPALANYINVN-DDNNAGSGQSVSNNEHNVANDNNNGMS 59
OY 60 WNSLWDYENSEFAATRLFSKSCIVHRNKKDAMPSLDLDTMVEOK--GKPGGAPPKDL 117
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 WNSLWDYNGSAATRLFLQKTCIVHKNNKEVMPISQSLDLVKEKKLQGGPGGPPKGL 119
OY 118 MYSVNPTRVEDLNTFGPKIAGMCRGIPTYAAEETGPNQPLYSKKCYTADILMILRMSFC 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 MYSVNPKNVDLSKFGKNIANMCRGIPTYAAEEMQEAASLEFFSGTCYTTSVLMIVDISFC 179
OY 178 GTSVE 182
    |:||
Db 180 GDYVE 184

```

```

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

```

```

RESULT 6
US-10-216-163-148
: Sequence 148, Application US/10216163
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530P1C3
: CURRENT APPLICATION NUMBER: US/10/216,163
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17

```

PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6.8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMFVGLGLLAAPGA-YTVNINGNDGNVDGSGQGSVINGVHNVANIDNNNGWDS 59
1 MKLTTFAGLGLVFLAPALANYINVN-DNNNAGSGQGSVNNHNVANVDNNNGWDS 59
DB 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSLQDIDITWKEOK--GKGPGAPPKDL 117
118 MYSVNPTRVEDLTFPGKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
120 MYSVNPKNVDLSKFGKNIANMCRGIPTYMAEMQASLFFSGCYTTSVLMIVDISFC 179
QY 178 GTSVE 182
1 : : :
DB 180 GDTVE 184

RESULT 7
US-10-216-164-148
Sequence 148, Application US/10216164
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C5
CURRENT APPLICATION NUMBER: US/10/216,164
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-164-148

Query Match 64.5%; Score 640; DB 6; Length 185;
Best Local Similarity 63.8%; Pred. No. 6.8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMFVGLGLLAAPGA-YTVNINGNDGNVDGSGQGSVINGVHNVANIDNNNGWDS 59
1 MKLTTFAGLGLVFLAPALANYINVN-DNNNAGSGQGSVNNHNVANVDNNNGWDS 59
DB 60 WNSLMDYENSFATRLFSKSCIVHRNKKDAMPSLQDIDITWKEOK--GKGPGAPPKDL 117
118 MYSVNPTRVEDLTFPGKTAGMCRGIPTYVAEIPGPNQPLYSKCYTADILMLRMSFC 177
120 MYSVNPKNVDLSKFGKNIANMCRGIPTYMAEMQASLFFSGCYTTSVLMIVDISFC 179
QY 178 GTSVE 182
1 : : :
DB 180 GDTVE 184

RESULT 8
US-10-216-165-148
Sequence 148, Application US/10216165
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C7
CURRENT APPLICATION NUMBER: US/10/216,165
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26

```

RESULT      9
US-10-216-166-148
: Sequence 148, Application US/10216166
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3530P1C9
: CURRENT APPLICATION NUMBER: US/10/216,166
: PRIOR FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See File Wrapper or PALM.

```

```

RESULT 10
US-10-216-167-148
? Sequence 148, Application US/10216167
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Desnoyers, Luc
? APPLICANT: Gerritsen, Marc
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Smith, Victoria
? APPLICANT: Stephan, Jean-Philippe F.
? APPLICANT: Watanabe, Colin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? TITLE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P3530P1C4
? CURRENT APPLICATION NUMBER: US/10/216,167
? CURRENT FILING DATE: 2002-08-09
? PRIOR APPLICATION NUMBER: 10/119,480
? PRIOR FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/062287
? PRIOR FILING DATE: 1997-10-17
? PRIOR APPLICATION NUMBER: 60/063549
? PRIOR FILING DATE: 1997-10-28
? PRIOR APPLICATION NUMBER: 60/064103
? PRIOR FILING DATE: 1997-10-31
? PRIOR APPLICATION NUMBER: 60/069873
? PRIOR FILING DATE: 1997-12-17
? PRIOR APPLICATION NUMBER: 60/078910
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: 60/079294
? PRIOR FILING DATE: 1998-03-25
? PRIOR APPLICATION NUMBER: 60/079656
? PRIOR FILING DATE: 1998-03-26
? PRIOR APPLICATION NUMBER: 60/079728
? PRIOR FILING DATE: 1998-03-27
? Remaining Prior Application data removed - See file Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 246
? SEQ ID NO 148
? LENGTH: 185

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
us-10-218-930-148

Query Match          64.5%; Score 640; DB 6; length 185;
Best Local Similarity 63.8%; Pred No. 6.8e-60;
Matches 118; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY      1 MKLTFEYVGLGILGAAPFA-YTVNINGNNGDGVDSGGQSVSINGVHNVINIDNNNGMDS 59
        ||| : |||| - || : || : ||||| | : ||||| : ||||| |
Db       1 MKFLFYAGLLGYFLAPALANYINVN-DDNNNAAGSGQSVSNHEHNVANVDNNNGMS 59

QY      60 WNSLTDENSFATYRLFSSKSCIVHRMKMDAMPISLDITPTWKEOK--GKGPGCAPPKDL 117
        ||| : ||| | | ||||| : ||||| : ||||| | : ||||| | |||
Db       60 WNSLTWDGCFATRLFOKKTCIVHRMKNEVPSTSIDALVKEKKLKÖGCGPGBPCKGL 119

QY      118 MYSNVPTREVDLNTFGPKTAGMCRGIPITYVAEEIPGPNOPIYSKCTADIIWLTMSPC 177
        ||||| : ||| : || ||||| : ||| : || ||| : ||| : |||
Db       120 MYSNENNKVDLSLKEFGKNITANCMRCGIPTYMAEMEQEASLEFFYSOTCTTTSVLMIYDISFC 179

QY      178 GTSVS 182
        | : ||
Db       180 GDIVE 184
```

```

RESULT 15
US-10-219-003-148
: Sequence 148, Application US/10219003
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Geriltsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P353091C12
: CURRENT APPLICATION NUMBER: US/10/219,003
: PRIOR FILING DATE: 2002-08-12
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/069873
: PRIOR FILING DATE: 1997-12-17
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: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: PRIOR APPLICATION NUMBER: 60/081819
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/081955
: PRIOR FILING DATE: 1998-04-15
: PRIOR APPLICATION NUMBER: 60/082804
: PRIOR FILING DATE: 1998-04-22

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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090691
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PRIOR APPLICATION NUMBER: 60/095302
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PRIOR FILING DATE: 1998-08-17
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PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
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PRIOR APPLICATION NUMBER: 60/099812
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PRIOR APPLICATION NUMBER: 60/099816
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PRIOR APPLICATION NUMBER: 60/100038
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PRIOR APPLICATION NUMBER: 60/100385
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PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922

PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
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PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
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PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
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PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31

Thu Sep 5 11:23:30 2002

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Page 9

PRIOR APPLICATION NUMBER: 60/1664418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/1663641
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/1594455
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/1594555
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/1598355
PRIOR FILING DATE: 1999-12-07

Query Match	64.5%	Score 640;	DB 6;	Length 185;
Best Local Similarity	63.8%;	Pred. No. 6.8e-60;		
Matches 118; Conservative	24;	Mismatches 39;	Indels	

Matches 110; Conservative 24; Mismatches 39; Indels 4; Gaps 3;

QY 1 MKLTMFVGLGLLAPGFA-YTVNINGNDGVDGSGQQSVSINGVHNVANIDNNNGWDS 59

Db 1 MKETTFEAGLLGVFLAPALANYINVN - DDNNAGSGGQSVSYNNEHNVANVDNNGWDS 59

1. ENFALVEGELV LAFALANININVN - DDNNNAGSGGQSSVSYNNEHNVANVDNNNGWDS 59

QY 60 WNSLWDYENSFAATRLFSKSKSCI VHRMKNKDAMPSLQDDLTWYKEQ - GKPGGAPPKDL 11

Db 60 WNSIWDCNGFAATRLFQKKTCTIVHKMKEVMPISQSLDALVKEKKLOGKGGPPPKGT, 11

118 MYSVNPTRVEDLNTFGPKTAGMCRGIIPTVAEEIPGPNOLYSKKCYTADIIWIPMSEC 17

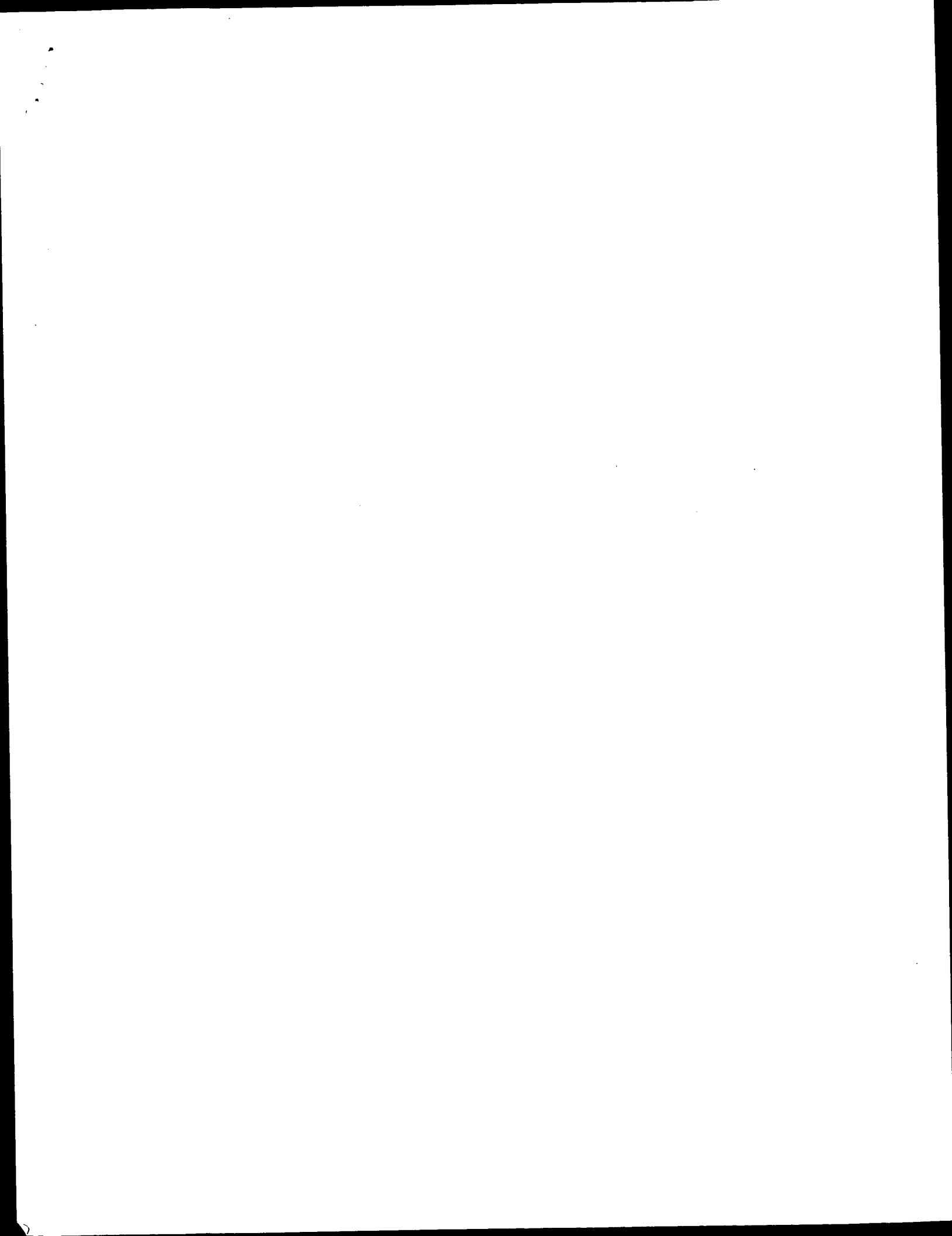
[illegible]

420 MLCVNFNVDELSTFGNNIANNMCRGIPITYMAEEMQEASLFFYSGTCYTTSVLWIVDISFC 17

QY	178	GTSVE	182
----	-----	-------	-----

Db 180 GDTVE 184

Search completed: September 4, 2002, 17:04:24
Job time: 1155 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:37 ; Search time 75.48 Seconds
(Without alignments) 234.240 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTFVVGGLGLAAGFA.....TADILMLRSMFCGTSVETY 184

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Length	DB ID	Description
1	89	9.0	345	2	Stral/Epig2 protei
2	88.5	8.9	442	2	hypothetical prote
3	86.5	8.7	658	2	hypothetical threo
4	85.5	8.6	335	2	chondromodulin-1 p
5	85.5	8.6	346	2	elk ligand - human
6	85.5	8.6	539	2	phosphoenolpyruvat
7	85	8.6	345	2	LEKK-2 - rat
8	84	8.5	643	2	hypothetical gene
9	83.5	8.4	782	2	rhodopyr-associat
10	81	8.2	617	2	lipoprotein (limpor
11	80.5	8.1	547	2	hypothetical prote
12	80.5	8.1	728	2	diacylglycerol kin
13	80.5	8.1	2295	2	H71621
14	80	8.1	3194	2	D71917
15	79.5	8.0	539	2	probable membrane
16	79.5	8.0	1215	2	phosphoenolpyruvat
17	79	8.0	186	2	chitinase A (limpor
18	79	8.0	336	2	hypothetical prote
19	78	8.0	338	2	hepatoma transmemb
20	78	7.9	338	2	gene h744 protein
21	78	7.9	362	2	hypothetical prote
22	77.5	7.8	642	2	regulatory protein
23	77.5	7.8	407	2	hypothetical prote
24	77.5	7.8	419	2	hypothetical prote
25	77.5	7.8	459	2	hypothetical prote
26	77.5	7.8	1109	2	hypothetical prote
27	76.5	7.7	363	2	beta-cysteine-rich
28	76.5	7.7	493	1	cellulase (EC 3.2.
29	76.5	7.7	504	2	mucin (clone pGM31

ALIGNMENTS

30	76	7.7	631	2	T07670	probable protein k
31	76	7.7	1278	2	A71609	probable secreted
32	75.5	7.6	194	2	S41761	cysteine-rich prot
33	75.5	7.6	397	2	S64841	hypothetical prote
34	75.5	7.6	421	2	E64819	Yb1 protein - Esc
35	75.5	7.6	421	2	E80741	hypothetical prote
36	75.5	7.6	421	2	E85591	hypothetical prote
37	75	7.6	331	2	AG2679	conserved hypothet
38	75	7.6	352	2	E97461	hypothetical prote
39	75	7.6	423	2	T51794	MYB DNA-binding-11
40	74.5	7.5	404	2	S50648	hypothetical prote
41	74.5	7.5	624	2	B82108	flagellar hook-ass
42	74.5	7.5	747	2	S46608	YTA11 protein - ye
43	74.5	7.5	1045	2	S23570	pol polyprotein ho
44	74.5	7.5	1362	2	A75207	amylopolylalanase P
45	74	7.5	241	2	S71473	endo-1,4-beta-xyla

RESULT 1
148780
Stral/Epig2 protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: 148780; A55507; A55062; S52670

R:Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schunbaur, B.; Doll

Dev. Biol. 170, 420-433, 1995

A:Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryona

A:Reference number: 148780; MUID:95377533

A:Accession: 148780

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-345 <RES>

A:Cross-references: EMBL:148781; NID:9747858; PIDN:CAA8695.1; PID:9747859

R:Biochem. J. 269, 26606-26609, 1994

A:Title: cDNA cloning and characterization of a ligand for the Cck5 receptor protein-

A:Reference number: A55062; MUID:95014510

A:Accession: A55062

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-89, 'T', '91-345 <SHA>

A:Cross-references: GB:012983; NID:9575928; PIDN:AAA3231.1; PID:9575929

C:Genetics:

A:Gene: EPLG2

Query Match 9.0%; Score 89; DB 2; Length 345;
Best local similarity 23.1%; Pred. No. 1.2;
Matches 40; Conservative 26; Mismatches 57; Indels 50; Gaps 10;

16 AAGFATVYININDGNVGS-----GGQSVSINGVHNVANINDNNQMSNMSLMDYENSFA 71
195 AAG-----RSGQSDSOKKHETVQKSGPAGAGGSGDSDFNSKVAL-----FA 241
72 ARLFLSKSCIV-----HRMKNKAMPSTLQDDTWTWKQKGGPGCAP 113
242 AV-----GAGCVFLILLIIFLVTLKLKRHRKHHTQQRALALSLTSLASKGSGTAGTE 297
114 PKDLWVSNPRFVEDLNFGP---KIAGMCGIPTTYAAELPGPNQD--LYSK 161
298 PSDIILPLRTE---NNYCPHYEKVSG-DYGHPIYIVQEMP--PQSPANIYYK 344

[illegible]

```

Oy      52  ---DNNGWDSWNSLMDYENSFAAT-RLFESKSCITYHRNMKKDAMPSLQDLDTFVKEOKGK 107
          ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : |
Db      380 NSSNNNSSGNTSDSTICYAAVFMAAGKFYSOHSCDLASGNKSQAQEGONOFLSMVESE----- 436

Oy      108 GPGGAPPKDLMT---YSVNPTFR 125
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      437 -----AKNLNKTNYNSANOSQ 452

RESULT      4
JT0569
chondromodulin-I precursor - bovine
M:Alternate names: 18k glycoprotein, cartilage; SCGP; small cartilage-derived glycopr
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
R:Hitrakl, Y.; Tanaka, H.; Inoue, H.; Kondo, J.; Kamizono, A.; Suzuki, F.
Biochem. Biophys. Res. Commun. 175, 971-977, 1991
A>Title: Molecular cloning of a new class of cartilage-specific matrix, chondromoduli
A:Reference number: JT0569; MUID:91222210
A:Accession: JT0569
A:Molecule type: mRNA
A:Residues: 1-335 <HIN>
A:Cross-references: GB:M65081; NID:g162840; PIDN:AAA30445.1; PID:g162841
A>Note: Part of this sequence, including the amino end of the mature protein, was det
R:Name, P.J.; Treep, J.T.; Young, C.N.
submitted to the Protein Sequence Database, October 1990
A:Reference number: A33138
A:Accession: A33138
A:Molecule type: protein
A:Residues: 215-220, 'W', 222, 'NE', 225-335 <NEA>
A>Note: 221-Val was also found
R:Name, P.J.; Treep, J.T.; Young, C.N.
J. Biol. Chem. 265, 9628-9633, 1990
A:Title: An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary st
A:Reference number: A36431; MUID:90277643
A:Accession: A36431
A:Molecule type: protein
A:Residues: 215-220, 'MNE', 224-225, 227-256, 'D', 257-335 <NE2>
A>Note: 221-Val was also found
A:Note: This sequence has been revised in reference A36535
R:Name, P.J.; Treep, J.T.; Young, C.N.
J. Biol. Chem. 265, 22056, 1990
A:Reference number: A36535
A:Contents: annotation, sequence revision
C:Comment: This protein stimulates DNA synthesis of cultured growth-plate chondrocyte
C:Keywords: extracellular matrix; glycoprotein; transmembrane protein
F:43-59/Domain: transmembrane #status predicted <TM>
F:215-335/Product: chondromodulin-I #status experimental <MAT>
F:223,236/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:248/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:283-287,284-324/Disulfide bonds: (or 283-324, 284-287) #status experimental
F:294-318,298-314/Disulfide Bonds: #status experimental

Query Match      8.6%; Score 85.5; DB 2; Length 335;
Best Local Similarity 22.3%; Pred.No.2.4;
Matches 33; Conservative 29; Mismatches 70; Indels 37; Gaps 7;

Oy      7  VVGLIGLIAAPG-----ATTVING--NDGNDGSGSOOSVSINGVHNANION 53
          ||| ||| | | | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      52  VLLILGAIGAIFYEFKGSDNHYYHYTMSINGKLQDS-----SMETDAGNNLETFEM 103

Oy      54  NNNGDSNNNSLMDYNENSAFARTLFESKSCITYHRNMKKDAMPSLQDLDTFVK-----EQGR- 107
          ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : | |||
Db      104 GSAGEAEAVNDPFGNGITGIRFAGGEKCIKAQYKAIIPE---EVGMTKGSSISELEGKI 160

Oy      108 GPGGAPPKDLMTYSNPTRVEDLTGPKIAGMCRGIFTTYAEELPGCNPLYSKK 162
          ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : | ||| : : : | |||
Db      161 MPVYEENKSLTWAGDPVKDNSFLSKVLLETGDDPIFWL-----KPTYKE 208

```

RESULT 5
S46993
elk ligand - human
C:Species: Homo sapiens (man)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May-1999
C:Accession: S46993
R:Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlic
EMBO J. 13, 3757-3762, 1994
A:Title: Molecular characterization of a family of ligands for eph-related tyrosine kinase
A:Reference number: S46993; MUID:94349923
A:Accession: S46993
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-346 <BEC>
A:Cross-references: GB:009304; NID:9538366; PIDN:AAA53093.1; PID:9538367

Query Match 8.6%; Score 85.5; DB 2; Length 346;
Best Local Similarity 23.1%; Pred. No. 2.5;
Matches 40; Conservative 23; Mismatches 61; Indels 49; Gaps 11;

OY 16 APGFAYTVNINGNDGNGVSGQSVSINGVHNVANINDNNNG-MDSNLSLDYENSF-AAT 73
DB 195 APG-----SRGSLGDSGDK-----HEIVNQEKGKGPASGSGSDPDGCFNSKY 238
OY 74 RLFSK--KSCIV-----HRMKNKAMPSLDIDITVMEKQKGGPGAP 113
DB 239 ALFAVAGACVIFLLIIFLTVLLKLRKRKHQOORAAALSLTLASPKGSGTAGTE 298
OY 114 PKDLMSVNTFRVEDLNTFGP---KIAGMCRGIPTYVAEIRPGNP--LYSK 161
DB 299 PSDIILPLRTE-----NNYCPHYEKVSG-DYGHPIYIVDEMP-POSPANIYK 345

RESULT 6
AF0998
phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Salmonella enterica subsp. enter
C:Species: Salmonella enterica subsp. enterica serovar typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF0998
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
Lh, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Ouali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0998
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-539 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08114.1; PID:916505093; GSPDB:GN00176
C:Genetics:
A:Gene: STY4296
C:Superfamily: phosphoenolpyruvate carboxykinase (ATP)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 8.6%; Score 85.5; DB 2; Length 539;
Best Local Similarity 23.4%; Pred. No. 4.4;
Matches 47; Conservative 32; Mismatches 65; Indels 57; Gaps 11;

OY 1 MKLTMEV--GLGLLAAGFAVTVNINGDGNV-----DGSQGSSTINGVHNVANID 52
DB 210 MKKGMFSVNNYLLPLKGLASMHCSANV-GEKDAVAVFGTGTTLSTDPKRRLLIG-D 267
OY 53 NNNKGSNLSLDYENS-FAATRLFSKRS--CIYHRMKNKDAMP----- 93
DB 268 DEHGMD-DGVNFEFGGCAKTIKLSKEAPEYIHAIRDALLENVYVREGTVDPPDGS 326
OY 94 -----LQDLDTVMEKQKGP-----GAPPPDLMSVNTFRVEDLNT 131

DB 327 KRENTVSVPIYHIDINYPVSKAGHATKVIPLFADAFGLPVSRL-TANQTOYHPLSG 385
OY 132 FGEKTAGMCRGI-----PTYVA 148
DB 386 FTAKLAGEGRGVTEPTPTFSA 406

RESULT 7
158406
LEKR-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: 158406
R:Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hol
Oncogene 9, 3241-3248, 1994
A:Title: LEKR-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily con
A:Reference number: 158406; MUID:95022634
A:Accession: 158406
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-345 <RES>
A:Cross-references: EMBL:007560; NID:9563118; PIDN:AAA53092.1; PID:9563119
C:Genetics:
A:Gene: Epl92

Query Match 8.6%; Score 85; DB 2; Length 345;
Best Local Similarity 23.1%; Pred. No. 2.8;
Matches 40; Conservative 24; Mismatches 59; Indels 50; Gaps 10;

OY 16 APGFAYTVNINGNDGNGVSGQSVSINGVHNVANINDNNKDSNLSLDYENSF 71
DB 195 APG-----RGSGGDSGKHETVNOEKGPGAGSGSGDDTDFNSKVAL-----FA 241
OY 72 ATRLFSSKSCIV-----HRMKNKAMPSLDIDITVMEKQKGGPGAP 113
DB 242 AV-----GAGCVIFLLIIFLTVLLKLRKRKHQOORAAALSLTLASPKGSGTAGTE 297
OY 114 PKDLMSVNTFRVEDLNTFGP---KIAGMCRGIPTYVAEIRPGNP--LYSK 161
DB 298 PSDIILPLRTE-----NNYCPHYEKVSG-DYGHPIYIVDEMP-POSPANIYK 344

RESULT 8
S17997
hypothetical gene COX1 intron 3 protein - yeast (Kluyveromyces marxianus var. lactis)
C:Species: mitochondrion Kluyveromyces marxianus var. lactis, Candida sphaerica
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 08-Dec-2000
C:Accession: S17997
R:Hardy, C.M.; Clark-Walker, G.D.
Curr. Genet. 20, 99-114, 1991
A:Title: Nucleotide sequence of the COX1 gene in Kluyveromyces lactis mitochondrial D
A:Reference number: S17993; MUID:92035081
A:Accession: S17997
A:Molecule type: DNA
A:Residues: 1-643 <HAR>
A:Cross-references: EMBL:X57546
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC2
A:Introns: 68/1; 235/3
C:Superfamily: DNA endonuclease I-SceII; COI intron 9 protein homology; cytochrome-c
F:1-324/Region: cox1 exons 1 to 3 encoded
F:325-643/Region: cox1 intron encoded

Query Match 8.5%; Score 84; DB 2; Length 643;
Best Local Similarity 26.9%; Pred. No. 7.6;
Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps 4;
OY 24 NINGNDGNGVSGQSVSINGVHNVANINDNNKDSNLSLDYEN--SFAATRLFSKRS 80

DB 347 NNNNNNNNNRPGSPYIGNMTAGMKNKYNNSYNNSNNNNNTYNNKLTITGNTLIS--- 403
 QY 81 CTVHRMKNKAMPLODLDTWYKEGKGPGCAPPKDLMSVNPTRVED 128
 DB 404 ---NLMNKYNTNTM-ITKMK-----IPNNIMYIMINGILLTD 437

RESULT 9

S27833
 Rhoptry-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)
 N:Alternate names: protective antigen
 C:Species: Plasmodium falciparum
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000
 C:Accession: A45514; S27833
 R:Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H.; Mol: Biochem. Parasitol. 41, 125-134, 1990
 A:Title: Characterisation and sequence of a protective rhoptry antigen from Plasmodium falciparum
 A:Reference number: A45514; MUID:90348711
 A:Accession: A45514
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-782 <RI2>
 A:Cross-references: GB:M32853; NID:g160656; PID:g160657
 C:Superfamily: Plasmodium falciparum rhoptry-associated protein 1

Query Match 8.4%; Score 83.5; DB 2; Length 782;
 Best Local Similarity 24.0%; Pred. No. 11;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;

QY 26 NNDGQVSGQSVSINGVHNANIDNNNGMSWNS---LMDYSEFAATRLFSKSC 81
 DB 18 NVADGIVNAGDNNYKGTI--INNDNFDDYNTWINKKEFLNSEDDESSSFLFNKSS 75
 QY 82 IVHRMKNKAMPLODLDTWYKEGKGPGCAPPK-----DLMTSVNPTRV 126
 DB 76 V-----DGGNINULTPTSTSKSK-KGHRGSRVRSASAAILEDDSKDMEFKASPSV 129
 QY 127 EDLNTFGPKIAGMCRGIPITYVAEIP 152
 DB 130 KTSTPGTQTGLKSSSPSTKSSP 155

RESULT 10

H90551
 Lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CT1P)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C:Accession: H90551
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: H90551
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-617 <KUR>
 A:Cross-references: GB:A1445566; PID:g14089734; PIDN:CAC13493.1; GSPDB:GN00153
 A:Experimental source: strain UAB CT1P
 C:Genetics:
 A:Gene: MYPU_3200
 A:Genetic code: SGC3

Query Match 8.2%; Score 81; DB 2; Length 617;
 Best Local Similarity 23.4%; Pred. No. 14;
 Matches 37; Conservative 21; Mismatches 52; Indels 48; Gaps 9;

QY 31 NVDSGOOSVSIINGVHNANIDNNNGMSW---NSLMDYSEFAATRLF----- 76
 DB 352 NITSSGINAKKLNIIHAAAN--GSVDWTSMDIRYNNSAFESSHVGILRSYDSPHSRTY 409
 QY 77 -----SKKSCIVHRMKNKAMPLODL---DTWYKEG-KGPK---GGAPPDLMYSVN 122

DB 410 VSGNEQEKKII-----DDEPKMEDVYWSNQTWYQKDSKHPIFEYEGSS---LVAIK 459
 QY 123 PTRVEDLNTFGPKIAGMCRGIPITYVAEELPGNPOLYS 160
 DB 460 TTSKRDKATI-----KLEMYEANIPIGTNRKWS 489

RESULT 11

T25478
 hypothetical protein B054.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T25478
 R:Graves, T. submitted to the EMBL Data Library, November 1996
 A:Description: The sequence of C. elegans cosmid B054.
 A:Reference number: Z20040
 A:Accession: T25478
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-547 <GRRA>
 A:Cross-references: EMBL:U80031; PIDN:AB37615.1; GSPDB:GN00023; CESP:B0554.2
 A:Experimental source: strain Bristol N2; clone B0554
 C:Genetics:
 A:Gene: CESP:B0554.2
 A:Map position: 5
 A:Introns: 103/2; 217/2; 339/2; 458/2

Query Match 8.1%; Score 80.5; DB 2; Length 547;
 Best Local Similarity 20.9%; Pred. No. 13;
 Matches 38; Conservative 25; Mismatches 74; Indels 45; Gaps 7;

QY 30 GNVDSGOOSVSIINGVHN-VANIDNNNG-----WDSNLSMDYEN 68
 DB 225 GSTTTTSMKISCAIAGYITMDVNNGLPAENDVVPQTVAINAECSSVDSIWNYYT 284
 QY 69 SFAATRLFSKSKSCIVHRMKNKAMPLODLDTWYKEGKGPGK-----GAPKDLMSY 121
 DB 285 VVACQTVKVPWTSATCOOIKDPGSPVTRSCSPALTYGMDDGMNPEYQIVYTTDFWTTA 344
 QY 122 NPTREVEDLNTFGPKIAGMCRGIPITY-VAEELPGNPOL-----YSKKCYTADI 168
 DB 345 TPGTMDSVSTW--KIT--CSGIAGYNQIMELDGTTLLENAGNPNPQTYTINAVCSADM 400
 QY 169 LW 170
 DB 401 IW 402

RESULT 12

S71467
 diacylglycerol kinase (EC 2.7.1.107) ATDGK1 - Arabidopsis thaliana
 N:Alternate names: protein F13624.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
 C:Accession: S71467; T43617
 R:Katagiri, T.; Mizoguchi, T.; Shinozaki, K. Plant Mol. Biol. 30, 647-653, 1996
 A:Title: Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in Arabidopsis thaliana
 A:Reference number: S71467; MUID:96189276
 A:Accession: S71467
 A:Molecule type: mRNA
 A:Residues: 1-728 <KAT>
 A:Cross-references: EMBL:D63787; NID:g1374771; PIDN:BA009856.1; PID:g1374772
 R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voelt, M.; Robben, J.; Volckaert, G.; submitted to the Protein Sequence Database, December 1999

A:Reference number: Z23009
 A:Accession: T43617
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-508, 'N', 510-728 <BEV>

A:Cross-references: EMBL:AL133421
A:Experimental source: cultivar Columbia; BAC clone F13G24
C:Genetics:
A:Map position: 5
A:Introns: 390/3: 513/1: 538/3: 578/3: 633/3: 679/3
A:Note: F13G24.120
C:Keywords: calcium binding; EF hand; phosphotransferase; zinc finger

Query Match 8.1%; Score 80.5; DB 2; Length 728;
Best Local Similarity 24.1%; Pred. No. 19;
Matches 34; Conservative 27; Mismatches 57; Indels 23; Gaps 7;

QY 27 GMDG--NDGSGGQSV-----SINGVH-----NVANIDNNNGWMSLMDYENSFATR 74
DB 275 GNSGNCDESESTADTGTPTVGAHVLNLSISVNGSDSSGDSKLEKPSKRTG 334
QY 75 LFSKKSCTIVHRMKNKAMPISLDDLT-----MKKQKGGPGGAPPKDLMYSVNPTRVE 127
DB 335 SFGQKE--YHAIKSKLAKELADLPDARPLLVFTNKRSGAQKQSLRQLHLHLPVOVF 392
QY 128 DINTF-GPKIA-GMCKGIPRY 146
DB 393 ELSSVQGEVGLFLFRKVPHP 413

RESULT 13

B71621
Probable membrane associated protein PFB0190C - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: B71621
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pierla, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: B71621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 12295 <GAR>
A:Cross-references: GB:AE001379; GB:AE001362; NID:g3845118; PIDN:AACT1827.1; PID:g384511
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0190C

Query Match 8.1%; Score 80.5; DB 2; Length 2295;
Best Local Similarity 24.8%; Pred. No. 82;
Matches 30; Conservative 10; Mismatches 44; Indels 37; Gaps 3;

QY 24 NINGNONGNVGSGGQSVSING-----VHRVANIDNNNGWMSLMDYENSFATR 74
DB 540 NISGDEVDGDEGDGDDGADDSVDTNHNKNDKESSESDVWNLMSYKRLANDE 599
QY 75 LFSKKSCTIVHRMKNKAMPISLDDLT-----MKKQKGGPGGAPPKDLMYSVNPTRVE 127
DB 600 NFKK-----YKYLTKNLNDFLNMSSEK-----EDINSYKN 631
QY 135 K 135
DB 632 K 632

RESULT 14

D71917
toxin-like outer membrane protein jhp0556 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71917
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557
A:Accession: D71917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3194 <ARN>
A:Cross-references: GB:AE001488; GB:AE001439; NID:g4155100; PIDN:AMD06134.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0556

Query Match 8.1%; Score 80; DB 2; Length 3194;
Best Local Similarity 31.4%; Pred. No. 1,4e+02;
Matches 43; Conservative 17; Mismatches 49; Indels 28; Gaps 9;

QY 8 VGLGLAAPGPATVYVING--NDGNVDS--GQGSYSI-----NGVHRVANIDNNNGWMS 60
DB 2066 VYLCITANAKRKNITITGTIGSGNMGSGGSANVSFESATNLVNOANID--AQGTD-- 2122
QY 61 NSLMDYENSFATRLFSKK-----SCIVHR--MNKDAMPISLDDLTMYEOKGKPGGA 112
DB 2123 -KIESYLKKEGIDKLFEGKGLGNLSNIVYEESLNDNAIP--KDLNMI PKDLGS----- 2174
QY 113 PKDLMYSVNPTRVEDL 129
DB 2175 --KTLISLISPTVEVNNL 2189

RESULT 15

AG0017
phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) [imported] - Yersinia pestis (s
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG0017
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-539 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89001.1; PID:g15978243; GSPDB:GN00175
C:Genetics:
A:Gene: pckA
C:Superfamily: phosphoenolpyruvate carboxykinase (ATP)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 8.0%; Score 79.5; DB 2; Length 539;
Best Local Similarity 22.4%; Pred. No. 16;
Matches 45; Conservative 34; Mismatches 65; Indels 57; Gaps 11;

QY 1 MKLTMEV--GLGLAAPGPATVYVINGNDGNV-----DSSGQGSYSINGVHRVANID 52
DB 210 MKKGMSMKNYLLPLKGISMHGCSANV--GEKDVAFIFGLSGTGKTLTDPKRLIG-D 267
QY 53 NNNGWMSLMDYENS--FAATRLFSKKS--CIVHRMKNKAMPISLDDLTMYEOKGKPGGA 93
DB 268 DEHGMD-DGVEFEGCGYAKTIKLSSEAEPIYAHAKRDLLEVNVYVLADGYDPNDGS 326
QY 94 -----LDDLTMYEOKGKGP-----GAPPKDLMYSVNPTRVEDLNT 131
DB 327 KLTNTVSTPIYHIDIVKPVSKAGHATKVIPLTADAGVLPVPSRL--TANOTGYHFLSG 365
QY 132 FGKTIAGMCRGI-----PTYVA 148
DB 386 FPAKLAGTERGVTEPTPFSA 406

Thu Sep 5 11:23:30 2002

us-09-821-726-16.rpt

Page 6

Search completed: September 4, 2002, 16:47:39
Job time: 375 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:41 : Search time 124.34 Seconds

(without alignments)
256.000 Million cell updates/sec

Title: US-09-821-726-16

Perfect score: 993

Sequence: 1 MKLTFVVGILGLAAGFA.....TADILILKMSRCSTSVET 184

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	23	6	191 11	Q9D0T7
2	167.5	16.9	184	11	Q9C0S6
3	93	9.4	618	5	Q9V6Z9
4	91	9.2	577	5	Q961R5
5	89.5	9.0	292	5	Q25762
6	88.5	8.9	860	5	Q19852
7	88	8.9	2206	12	Q99F74
8	88	8.9	2206	12	Q99F74
9	86.5	8.7	658	3	Q99F75
10	86	8.7	531	2	Q93JF5
11	85	8.6	2206	12	Q99F75
12	84	8.5	319	8	Q34834
13	83.5	8.4	782	5	Q94431
14	83.5	8.4	782	5	Q94429
15	83.5	8.4	782	5	Q94414
16	83.5	8.4	782	5	Q25730

17	83.5	8.4	782	5	Q26007	Q26007 plasmodium
18	82.5	8.3	493	9	Q9JMM8	Q9JMM8 bacterioph
19	82	8.3	602	6	Q9GL34	Q9GL34 bos taurus
20	81	8.2	553	11	Q9OWR9	Q9OWR9 mus musculu
21	81	8.2	617	16	Q98QPI	Q98QPI mycoplasma
22	80.5	8.1	547	5	P910D6	P910D6 caenorhabdi
23	80.5	8.1	728	10	Q9SD92	Q9SD92 arabidopsis
24	80.5	8.1	782	5	Q25875	Q25875 plasmodium
25	80.5	8.1	782	5	Q9U430	Q9U430 plasmodium
26	80.5	8.1	1332	5	Q9BN17	Q9BN17 drosophila
27	80.5	8.1	2295	5	Q9TY98	Q9TY98 plasmodium
28	80	8.1	2009	5	Q9VXW0	Q9VXW0 drosophila
29	80	8.1	3194	16	Q9ZLM3	Q9ZLM3 helicobacte
30	79.5	8.0	494	2	Q05527	Q05527 comamonas a
31	79.5	8.0	1215	1	Q9UMR7	Q9UMR7 pyrococcus
32	79.5	8.0	1960	5	Q9UOK8	Q9UOK8 plasmodium
33	79.5	8.0	2432	12	Q91OP4	Q91OP4 aichi virus
34	79	8.0	186	5	Q01876	Q01876 caenorhabdi
35	79	8.0	338	4	Q13533	Q13533 homo sapien
36	78.5	7.9	501	3	Q9BID4	Q9BID4 anopheles g
37	78	7.9	319	3	Q96U67	Q96U67 neurospora
38	78	7.9	642	5	Q17169	Q17169 caenorhabdi
39	78	7.9	664	5	Q27435	Q27435 plasmodium
40	77.5	7.8	419	5	Q77316	Q77316 plasmodium
41	77.5	7.8	428	3	Q12646	Q12646 neocallimas
42	77.5	7.8	439	3	Q92401	Q92401 agaricus bi
43	77.5	7.8	458	10	Q9FVH2	Q9FVH2 arabidopsis
44	77.5	7.8	459	10	Q9M354	Q9M354 arabidopsis
45	77.5	7.8	782	5	Q26104	Q26104 plasmodium

ALIGNMENTS

RESULT 1
Q9D0T7 PRELIMINARY: PRT: 191 AA.
AC Q9D0T7: 01-JUN-2001 (TREMURel. 17, Created)
DT 01-JUN-2001 (TREMURel. 17, Last sequence update)
DE 01-JUN-2001 (TREMURel. 17, Last annotation update)
BT 1190003M12RIK PROTEIN.
GN 1190003M12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK004474; BAB23320.1;
DR MGI:1916138; 1190003M12RIK.

SEQUENCE 191 AA; 20772 MW; 76D7DBA4796AE8B4D CRC64;

Query Match 23.68; Score 234; DB 11; Length 191;

Best Local Similarity 31.14; Pred. No. 6.3e-15;

Matches 56; Conservative 40; Mismatches 66; Indels 18; Gaps 7;

QY 3 LTMFVGLGLLGAAPGFAYTVNINGNDG-NDVGS-GQSVSINGVHVANIDNNNGMDSW 60
 DB 21 VTPELV-----PALALT---NTSDSYPLDGSVGTOTIHVDALRGVLSIRDSVQSEW 69
 QY 61 NSLMDYENSFAATRLFSKSCIVHRMKNKAMPSTLQDI-DTWKQKQKGGAPPKDLMY 119
 DB 70 DGVMDYKNDLLAAKLFKSCACVLAAMPAPPSLIDITQALGKQASGHP-PTRGILTY 126
 QY 120 SYNPRVVDLNTFGPKINGMCRGIPITYA-EEIPGPNQPLYSKRCYTADILIRMSFCG 178
 DB 127 TVLPSRIKNAQYGVPIKDLCAVPTTFARQOKESTALTMDPDCSELQGLSTFGLSICG 186

RESULT 2

Q9CQ56 PRELIMINARY; PRT; 184 AA.

AC Q9CQ56; TISSUE-STOMACH, AND PANCREAS;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 1810036H07RIK PROTEIN.
 CN 1810036H07RIK
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE-STOMACH, AND PANCREAS;
 MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
 RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohisaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK008986; BAB26008.1;
 DR EMBL: AK007451; BAB25046.1;
 DR EMBL: AK007705; BAB25201.1;
 DR MGD: MGI:1913534; 1810036H07RIK.
 QY MD: MGI:1913534; 1810036H07RIK.
 QY SEQUENCE 184 AA; 20469 MW; 612A18FABE652230 CRC64;

Query Match 16.98; Score 167.5; DB 11; Length 184;
 Best Local Similarity 25.74; Pred. No. 1.7e-08;
 Matches 46; Conservative 46; Mismatches 76; Indels 11; Gaps 5;

QY 5 MFVVGILGLLAAPGFAYTVNINGNDG-GQSVSINGVHVANIDNNNGMDSWMSLW 64
 DB 8 LVVLSIFGTQSAEFTFPIFPKNG---GNIGETVITIDNQGNATLINHSGSCSSTIF 64
 QY 65 DYENSFAATRLFSKSCIVHRMKNKAMPSTLQDI-DTWKQKQKGGAPPKDLMYSNP- 123

DB 65 DYKRGITASRVLSRRACRYIKMDHKAIPALDLQGFIXEKQMAIDS-PEYTWRYNPL 123

QY 124 ---TRVEDLNTFGPKIACMCRGIPITYAEEIPGPNQPLYSKRCYTADILIRMSFCG 178
 DB 124 KSLITKYV-DWFLFGSPITRLCKHMPLEGEVATKPRE-VSTGCAKVGILGLTGVSTICG 180

RESULT 3

Q9V629 PRELIMINARY; PRT; 618 AA.

AC Q9V629; Drosophila melanogaster (Fruit fly).
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CG8547 PROTEIN.
 CN CG8547.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Planck C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Doonan K.J., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dublin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mitsuhashi N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relibert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shne B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003815; AAF58267.2;
 DR FlyBase: FBgn0033919; CG8547.
 DR InterPro: IPR001230; Prentylin.
 DR PROSITE: PS00294; PRENTYLIN;
 QY SEQUENCE 618 AA; 68023 MW; 7C82273A67F32C6C CRC64;

Query Match 9.48; Score 93; DB 5; Length 618;
 Best Local Similarity 21.74; Pred. No. 1.3;

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QY      12  GLAAGCAATVAINCNDGNV--DGGGQGSYSNGVHNANNIDNNNGWSNLMDENS 69
      1 : ||| : : : : : : : : : : : : : : : : : : : : : : : : :
Db      215  GILPAGCTKATTTVRRVRYTYEITPATGCSNTSTNRTN---TLNNSN---TLSSTYKHES 268
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      70  FAATRLFSKSKCIHV-----RANKDA-MPSLOLDLDMVFKPOK----- 105
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      269  HNSQNFNSOLSPRHPOPSHVPTVVNTYESYTLNRNSDRPVVNSQSYEIRHKETTR 328
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      106  -----CKGPGGAPP--KDLVSYSNPT-RVEDLTFGPKIAGMGRG---IPTYYA 148
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      329  GVSPPGRQLPLSGPAGTPRGNTVLYNIHTDHNVTNLEPPOORYPPRSPAHSENYYG 388
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      149  EEIIPGNPQ---LYSKKCYTD 167
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      389  PHSF-PLQPGVNRYYKKTETSEN 410
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      4
0961R5      PRELIMINARY:      PRT:      577 AA.
AC      0961R5;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      GH09466P.
GN      CG8547.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
      [1]
NN      SEQUENCE FROM N.A.
RP      STRAIN=Y, CN BW:SP.
RA      Stepleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA      Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA      Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA      Nuno J., Pacliel J., Paragas V., Park S., Phouanavong S., Wan K.,
RA      Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RL      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AY051417; AAK92841.1; -
SQ      SEQUENCE      577 AA;      63582 MW;      8581C85BD1D026A CRC64;

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Query Match          9.28; Score 91; DB 5; Length 577;
Best Local Similarity 20.78; Prod. No. 1.9;
Matches 34; Conservative 33; Mismatches 51; Indels 46; Gaps 8;

QY      12 GLAAPGFAATVNINGDGNV--DGSGOASSTINGCIVANVINIINNNDWDSNLSIMDIENS 69
       ||| ||| |::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
Db      215 GILPAPCTKVTTYRTYTIELPATGPGSNTSTINRTH--TLNNSN--TLLSITYKHHS 268
               ::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
QY      70 FAATLEFSKSCSIYH-----RMNKDA-MPSLODLDTVWEKQ----- 105
       ::||| |::||| |::||| |::||| |::||| |::||| |::||| |::|||
Db      269 HNSQNFQSOLSPVHPQPSHVPTVVYNTESESYFLNNSDRPVYSNSYELREHKETTR 328
               ||| ||| |::||| |::||| |::||| |::||| |::||| |::|||
QY      106 -----GGGPGAPP-KDLMYSVPY-RVEDLNTFFGR 135
              ||| ||| |::||| |::||| |::||| |::||| |::||| |::|||
Db      329 GVSPPQRQLPLGSGPAGTPPGNRVTYVNIHKTDHVNVTNELPPO 372
               ||| ||| |::||| |::||| |::||| |::||| |::||| |::|||

RESULT      5
ID           Q25762
AC           Q25762     PRELIMINARY; PRT; 292 AA.
DT           01-NOV-1996 (TREMBLrel. 01, Created)
DT           01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT           01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE           P82 (FRAGMENT).
GN           RAP-I..
OS           Plasmodium falciparum.
```

OC Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RX NCBI_Taxid=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=INDD (INDIAN ISOLATE D);
 RX MEDLINE=92244303; PubMed=1574089;
 RA Howard R.F.;
 RT "The sequence of the p82 rhoptry protein is highly conserved between
 RT two Plasmodium falciparum isolates.";
 RL Mol. Biochem. Parasitol. 51:327-330(1992).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=INDD (INDIAN ISOLATE D);
 RX MEDLINE=96379224; PubMed=8784775;
 RA Howard R.F.; Peterson C.;
 RT "Limited RAP-1 sequence diversity in field isolates of Plasmodium
 RT falciparum.";
 RL Mol. Biochem. Parasitol. 77:95-98(1996).
 DR EMBL; U41074; AAC47090.1; -;
 FT NON_TER 1
 FT 292 292
 SO SEQUENCE 292 AA; 32345 MW; A35C979C3FEC3019 CR664;

	Query Match	9.0%;	Score 89.5;	DB 5;	Length 292;
	Best Local Similarity	24.7%;	Pred. No. 1.1;		
	Matches	36;	Conservative	20;	Mismatches 63; Indels 27; Gaps
QY	26	NGDGE-NVDCSGOQSVSLNGVHNVANIDNNQWDSWNS--LMDYENSFAATRLFSKSC	81		
Db	12	INADGINTVNGDNNYKTI--INNDENFEDYVWYPIPNKKEFLNYSNEFSSEFLNKSS	69		
QY	82	IYHRMKNKDMPSTJODIDTIVYKQKCKGGGAPK-----DLMTSVMPTRY	126		
Db	70	V-----DDGNINILTDTSTNSNKSCK-KGHGRSRVNASASAAAILLEDDSKDMEKASPSVY	123		
QY	127	EDLNTGPKIAQMCRCGIPYYAEIIP	152		
Db	124	KTSTPSGTQTSGLKSSPSITKSSP	149		
RESULT	6				
ID	019852				
AC	019852:	PRELIMINARY;	PRT;	860	AA.
DT	01-NOV-1996	(TREMblrel. 01, Created)			
DT	01-OCT-2001	(TREMblrel. 18, Last sequence update)			
DT	01-DEC-2001	(TREMblrel. 19, Last annotation update)			
DE	HYPOTHEICAL_96.1_KDA PROTEIN.				
GN	F28B4.2.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID=6239;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN-BRISTOL N2;				
RC	MEDLINE=99069613; PubMed=9851916;				
RA	None;				
RT	"Genome sequencing of the nematode C. elegans: a platform for				
RT	investigating biology. The C. elegans Sequencing Consortium. ";				
RL	Science 282:2012-2018(1998).				
RL	[2]				
RR	SEQUENCE FROM N.A.				
RR	STRAIN-BRISTOL N2;				
RC	Leimbach D.;				
RT	"The sequence of C. elegans cosmid F28B4. ";				
RL	Submitted (JAN 1996) to the EMBL/Genbank/DBJ databases.				
RL	[3]				
RR	SEQUENCE FROM N.A.				
RR	STRAIN-BRISTOL N2;				
RC	Waterston R.;				
RA	Direct Submission. ";				
RT					

Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
EMBL: U42834; AAA83583.2; -
DR HSP; Q61193; 1RUF
DR InterPro: IPR00159; RA.
DR InterPro: IPR000651; RasGEFN.
DR InterPro: IPR01895; RasGRF_CDC25.
DR Pfam: PF00788; RA; 1.
DR Pfam: PF00617; RasGEF; 1.
DR Pfam: PF00618; RasGEFN; 1.
DR SMART: SM00314; RA; 1.
DR SMART: SM00147; RasGEF; 1.
DR SMART: SM00229; RasGEFN; 1.
DR PROSITE: PS00720; GDS_CDC25; 1.
DR Hypothetical protein.
KW SEQUENCE 860 AA; 96122 MW; 16088524FBC65CA5 CRC64;

Query Match 8.9%; Score 88.5; DB 5; Length 860;
Best Local Similarity 25.0%; Pred. No. 5.4;
Matches 27; Conservative 15; Mismatches 61; Indels 5; Gaps 2;

OY 29 DGNVSGSQGSVINGVNHVANIDNNNGDSVNSLMDYENFPAATRLFSKKSCTIVHNMK 88
ID 099FJ4 PRELIMINARY; PRT; 2206 AA.
AC 099FJ4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE POLYPROTEIN.
OS Porcine teschovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Teschovirus.
OX NCBI_TaxID=118140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VIR 3764/86;
RX MEDLINE-21105197; PubMed-11160660;
RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
Stelzner A., Prager D., Wurm R.;
RT "Porcine Teschoviruses Comprise at Least Eleven Distinct Serotypes:
Molecular and Evolutionary Aspects.";
RT J. Virol. 75:1620-1631(2001).
RL EMBL: AF296112; AAK12406.1; -
DR HSP; Q88590; 1TWF.
DR HSP; Q88590; 1TWF.
DR InterPro: IPR004004; Calic_i.pol_hel.
DR InterPro: IPR001676; Rhv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR001205; RNA_pol_P3D.
DR Pfam: PF00073; rhv; 2.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
DR PRINTS: PR00918; CALICYRUSNS.
SQ SEQUENCE 2206 AA; 247376 MW; 76FDA9A4A1ADA08E CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;
Best Local Similarity 24.1%; Pred. No. 20;
Matches 52; Conservative 18; Mismatches 66; Indels 80; Gaps 11;

OY 4 TMFVVLGLGLAAGFAVTVNING-----NDGNVSGSQGSVINGVNHVANIDNNNGMD- 58
ID 059779 PRELIMINARY; PRT; 658 AA.
AC 059779;
DB 275 TRFHGGCLGVFAIRPEFVSFKLOGIPLTYDGNKDG-----NVSNI-----WDK 317

OY 59 -----SWNSLMDYENS-----FAATRLFSKKSCTIVH-----RMN 87
ID 099FJ3
AC 099FJ3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE POLYPROTEIN.
OS Porcine teschovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Teschovirus.
OX NCBI_TaxID=118140;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VIR 2500/99;
RX MEDLINE-21105197; PubMed-11160660;
RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
Stelzner A., Prager D., Wurm R.;
RT "Porcine Teschoviruses Comprise at Least Eleven Distinct Serotypes:
Molecular and Evolutionary Aspects.";
RT J. Virol. 75:1620-1631(2001).
RL EMBL: AF296113; AAK12407.1; -
DR HSP; Q88590; 1TWF.
DR HSP; Q88590; 1TWF.
DR InterPro: IPR004004; Calic_i.pol_hel.
DR InterPro: IPR001676; Rhv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR001205; RNA_pol_P3D.
DR Pfam: PF00073; rhv; 2.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
DR PRINTS: PR00918; CALICYRUSNS.
SQ SEQUENCE 2206 AA; 247391 MW; 24C81E3E20C37405 CRC64;

Query Match 8.9%; Score 88; DB 12; Length 2206;
Best Local Similarity 24.1%; Pred. No. 20;
Matches 52; Conservative 20; Mismatches 64; Indels 80; Gaps 12;

OY 4 TMFVVLGLGLAAGFAVTVNING-----NDGNVSGSQGSVINGVNHVANIDNNNGMD- 58
ID 059779 PRELIMINARY; PRT; 658 AA.
AC 059779;
DB 275 TRFHGGCLGVFAIRPEFVSFKLOGIPLTYDGNKDG-----NVSNI-----WDK 317
OY 59 -----LMDYENSFAAT-----RLFSKKSCTIVH-----RMN 87
ID 059779
AC 059779;
DB 318 FTAMHNPFAEMFAGAWYSHAYDITDKHMYKPKLEHGIGISPSL-----CFPHOLINPRTN 373
OY 88 KDPMSLQDLD-----TWVEQKKGKGGAPPKDLMSVNPTRVEDINT 131
ID 059779
AC 059779;
DB 374 SSATLCLPVDGCPITDVTVHCPMAIVVVLRELVALGCPSPVDINVSAPC---DVEY 430
OY 132 FGPRTAGMCRG--IPYVAEIPGPNOPLSKKCYTA 166
ID 059779
AC 059779;
DB 431 HGLRQDSMYGPIPKF---DIDASKALFSSTQPYTA 463

Query Match 9
Best Local Similarity 24.1%; Pred. No. 20;
Matches 52; Conservative 18; Mismatches 66; Indels 80; Gaps 11;

DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE HYPOTHELICAL 69.7 KDA ASN/THR-RICH PROTEIN C320.02C IN CHROMOSOME
 DE III.
 CN SPCC320.02C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 NC NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Medler H., Wambutt R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 468-658 FROM N.A.
 RC STRAIN=972;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL022245; CAA18304.1; -
 DR EMBL; AL031764; CAA21105.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 658 AA; 69695 MW; 63082230B6488AC5 CRC64;

Query Match 8.7%; Score 86.5; DB 3; Length 658;
 Best Local Similarity 25.4%; Pred. No. 6.1;
 Matches 36; Conservative 26; Mismatches 53; Indels 27; Gaps 7;

QY 1 MKLTFVVGILGLAAGF---AYTVNINGDGNVDSGQSVSINGVHVV---ANI-- 51
 DB 321 METTINIVGNDSTSPSONFKSGKTFVSNANSSNSN-DGSSSKSIDGVSFVNAFKQLVND 379
 QY 52 ---DNNNGWDSNLMWYENSEFAT-RLFSKKSIVHRMKNKDAPSLQDDLTWYKCKGK 107
 DB 380 NSSNNSSGNTDSTTIGAAVFAAGFFSOHSCDLASGMSKSAOEGONGFLSWSE--- 436
 QY 108 GPGGAPPKDLM---YSVNPTR 125
 DB 437 -----AKNLKNTKNTYSANOSQ 452

RESULT 10
 Q93JF5 PRELIMINARY; PRT; 531 AA.
 ID Q93JF5;
 AC Q93JF5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHELICAL 58.7 KDA PROTEIN.
 CN STRAC16H6.07.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Collins M.R., Harris D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapalpe D., Eichner A., Cullum J.,
 Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL MOL. Microbiol. 21:77-96(1996).
 DR EMBL; AL596162; CAC44586.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 531 AA; 58656 MW; 714F1033D5C29B3F CRC64;

Query Match 8.7%; Score 86; DB 2; Length 531;
 Best Local Similarity 28.4%; Pred. No. 5.2;
 Matches 27; Conservative 12; Mismatches 34; Indels 22; Gaps 4;

QY 96 DLDTMVKEKGKGGGAPKDLWYVN--PTREVDL-----NTEGPKTAGMCRGTPYV 147
 DB 92 DVALVLRGKGGKGGAPDALAQVNDPRYAASSLLAVALSSVSSAMRGVCKSRPERA 151
 QY 148 AEEIP-----GPN--OPLYSKKCYTADI 168
 DB 152 AESLPLRVEIPALPARGGPDLVRLPEPLGWTVDV 186

RESULT 11
 Q99FJ5 PRELIMINARY; PRT; 2206 AA.
 ID Q99FJ5;
 AC Q99FJ5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE POLYPROTEIN.
 OS Porcine teschovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Teschovirus.
 NC NCB1_TaxID=118140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VIR 918-19/85;
 RX MEDLINE=21105197; PubMed=11160660;
 RA Zell R., Dauber M., Krumholz A., Henke A., Birch-Hirschfeld E.,
 Stelzner A., Prager D., Wurm R.;
 RT "Porcine Teschoviruses Comprise at Least Eleven Distinct Serotypes:
 RT Molecular and Evolutionary Aspects."
 RL J. Virol. 75:1620-1631(2001).
 DR EMBL; AF296111; AAK12405.1; -
 DR HSSP; O88590; 1TME.
 DR MEROPS; C03.UPC; -
 DR InterPro: IPR004004; Calici_pol_hel.
 DR InterPro: IPR001676; Rnv.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR Pfam: PF00073; Rnv; 2.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00910; RNA_helicase; 1.
 DR PRINTS: PR00918; RALCVTRUSNS.
 SQ SEQUENCE 2206 AA; 247295 MW; 113CC439CB2C774F CRC64;

Query Match 8.6%; Score 85; DB 12; Length 2206;
 Best Local Similarity 23.6%; Pred. No. 38;
 Matches 51; Conservative 21; Mismatches 64; Indels 80; Gaps 12;

QY 4 TMFVVGILGLAAGFAYTVNING---NDGNVDSGQSVSINGVHVVANIDNNNGMD- 58
 DB 275 TRFHGGCLGVFAIPFVSYSKLOGIPLTYDGNKGD-----VNSNI-----WDR 317
 QY 59 ---SWNS-----LMDYENSF-----AATRLPSKKGCIYH-----RAN 87
 DB 318 FTTWHNPDMFCAMWYSHAYDDKHKWYKLEQYGGISPSLIF---CFPHOLINPRTN 373
 QY 88 KDAMPSLQDL-----TMVKEKGKGGGAPKDLWYVNPTREVDLNT 131
 DB 374 SSATLCPLPFDVCGPLTDVTVHCPMAIVVVVRLTLVALGCTPSVDINVSVAFC---DYEV 430
 QY 132 FGPRIAGMCRG-IPTVVAEETPGNOLYSKKCYTA 166

Db 431 HGLRODSMTGCPKPF--DIDASKALFSTQPYTA 463

RESULT 12

034834 PRELIMINARY; PRT; 319 AA.

AC 034834: PRELIMINARY; PRT; 319 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTON ORF.
 OS Kluyveromyces lactic (Yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K8;
 RX MEDLINE=92035081; PubMed=1657415;
 RA Hardy C.M., Clark-Walker G.D.;
 RT "Nucleotide sequence of the COX1 gene in Kluyveromyces lactic
 mitochondria DNA: Evidence for recent horizontal transfer of a group
 II intron."
 RL Curr. Genet. 20:99-114(1991).
 DR EMBL: X57546; CAA0768.1; -
 KW Mitochondrion.
 SQ SEQUENCE 319 AA; 37564 MW; 4706288776D11F85 CRC64;

Query Match 8.5%; Score 84; DB 8; Length 319;
 Best Local Similarity 26.9%; Pred. No. 4.3;
 Matches 29; Conservative 20; Mismatches 39; Indels 20; Gaps 4;

QY 24 NINGDGNVDSGQGSVSINGVHNVANIDNNNGWDSNLSMDYEN--SFAATRLFSKKS 80
 DB 23 NHHNNNNNNPFGQSPVIGNMTAGMKNKYNNSNNSNNNNNNYKLTLYGTNLS--- 79
 QY 81 CIYHRMKNKAMPISLQDLPVMEKQKGGPGAPKPKDLMSVNPTRPD 128
 DB 80 ---NLMKNKYNTMM-IKYMK-----IPNNIMTMINCILTD 113

RESULT 13

090431 PRELIMINARY; PRT; 782 AA.

AC 090431: PRELIMINARY; PRT; 782 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
 GN RAPI.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saul A.;
 RT "Efficacy of vaccines containing Rhoptry-Associated proteins RAPI and
 RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF205282; AAF23403.1; -
 FT NON TER 782
 SQ SEQUENCE 782 AA; 90066 MW; B344948D5806F7DC CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;
 Best Local Similarity 24.0%; Pred. No. 15;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;

QY 26 NGNDG-NVDGSGQGSVSINGVHNVANIDNNNGWDSNLSMDYEN--SFAATRLFSKKS 81
 DB 11 NHHNNNNNNPFGQSPVIGNMTAGMKNKYNNSNNSNNNNNNYKLTLYGTNLS--- 79

Db 18 NVADGINVGNDDNYKTI--INDDFNEDDYNWTPINKKEFLNSYEDKSSSEFLNKSS 75

QY 82 IVHGMNNDAMPISLQDLPVMEKQKGGPGAPK-----DLMTSVNPTRV 126
 DB 76 V-----DDGNINLTDITSNKSCK-KGGRSRYRSASAAALIEEDSKDMEFKASPSV 129

QY 127 EDLTFGPKIAGMCRGIPYVAEIP 152
 DB 130 KTSFSGTQTSGLKSSSPSTKSSP 155

RESULT 14

090429 PRELIMINARY; PRT; 782 AA.

AC 090429: PRELIMINARY; PRT; 782 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RHOPTRY-ASSOCIATED PROTEIN 1.
 GN RAPI.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVO;
 RA Saul A.;
 RT "Efficacy of vaccines containing Rhoptry-Associated proteins RAPI and
 RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF205284; AAF23405.1; -
 KW Mitochondrion.
 SQ SEQUENCE 782 AA; 90041 MW; 27F2EA9BC930434E CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;
 Best Local Similarity 24.0%; Pred. No. 15;
 Matches 35; Conservative 21; Mismatches 63; Indels 27; Gaps 6;

QY 26 NGNDG-NVDGSGQGSVSINGVHNVANIDNNNGWDSNLSMDYEN--SFAATRLFSKKS 81
 DB 18 NVADGINVGNDDNYKTI--INDDFNEDDYNWTPINKKEFLNSYEDKSSSEFLNKSS 75
 QY 82 IVHGMNNDAMPISLQDLPVMEKQKGGPGAPK-----DLMTSVNPTRV 126
 DB 76 V-----DDGNINLTDITSNKSCK-KGGRSRYRSASAAALIEEDSKDMEFKASPSV 129

QY 127 EDLTFGPKIAGMCRGIPYVAEIP 152
 DB 130 KTSFSGTQTSGLKSSSPSTKSSP 155

RESULT 15

090414 PRELIMINARY; PRT; 782 AA.

AC 090414: PRELIMINARY; PRT; 782 AA.
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RHOPTRY-ASSOCIATED PROTEIN-1.
 GN RAPI.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCI/HN;
 RA Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
 RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF206631; AAF15365.1; -
 KW Mitochondrion.
 SQ SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;

Query Match 8.4%; Score 83.5; DB 5; Length 782;

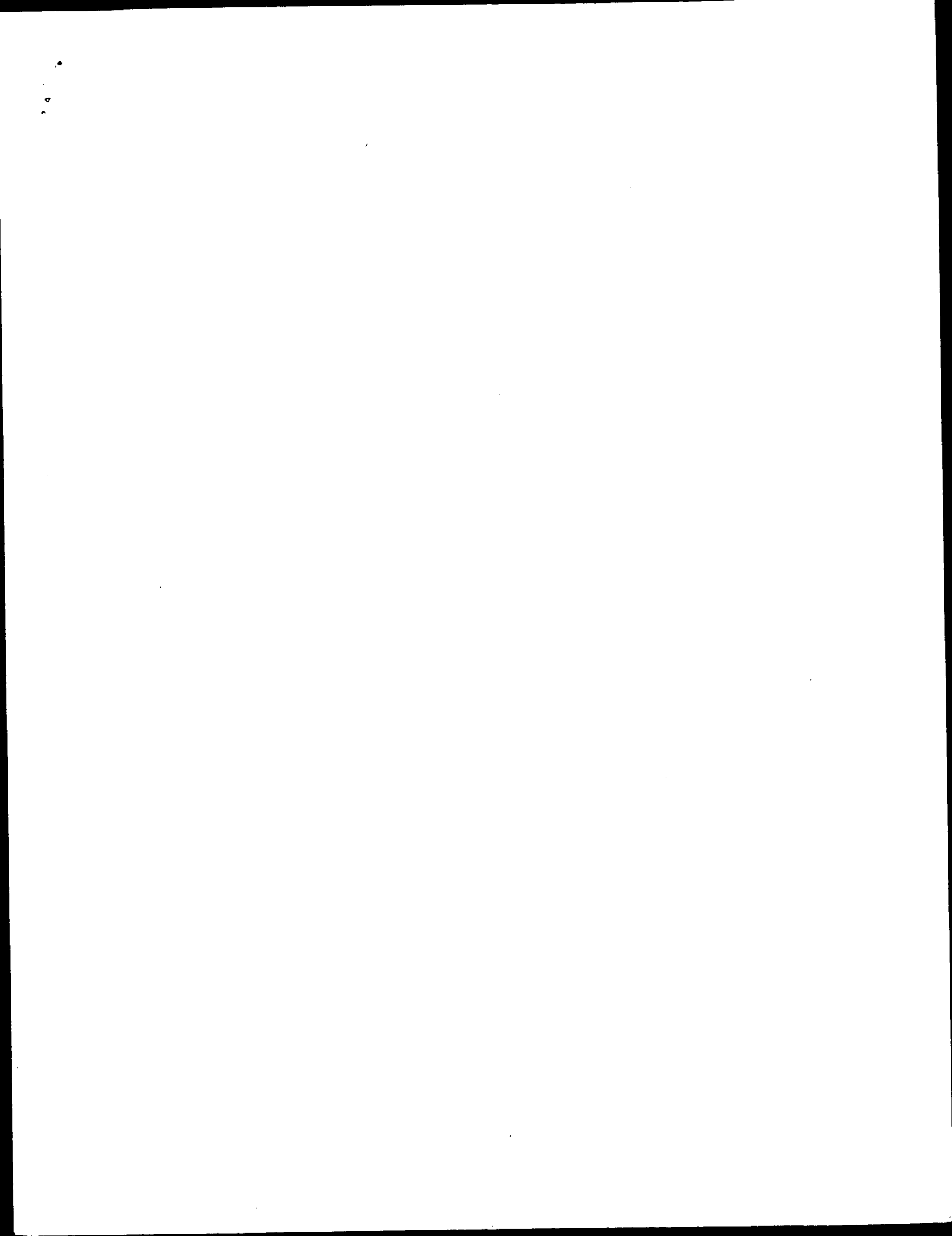
Thu Sep 5 11:23:31 2002

us-09-821-726-16.rspt

Page 7

[illegible]

Search completed: September 4, 2002, 17:01:44
Job time: 1165 sec



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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:10 ; Search time 57.74 Seconds

(Without alignments)
78.260 Million cell updates/sec

Title: US-09-821-726-13

Perfect score: 994

Sequence: 1 MKRTVFAGLGVFLAPALA.....YTSVLMIVDISFGDTVEN 185

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BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents-AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	80.5	8.1	652	4	US-08-559-896B-2
2	77.5	7.8	428	3	US-09-118-319-5
3	77.5	7.8	430	2	US-08-945-848-8
4	74	7.4	606	4	US-09-187-124-2
5	73.5	7.4	533	1	US-08-445-586-10
6	73	7.3	1507	3	US-08-929-329-5
7	72	7.2	334	1	US-08-241-465B-19
8	72	7.2	380	2	US-08-227-108-16
9	72	7.2	380	1	US-09-073-674-16
10	72	7.2	432	3	US-09-118-319-2
11	71.5	7.2	533	1	US-08-484-493-13
12	71.5	7.2	533	1	US-08-484-494-13
13	71.5	7.2	533	1	US-08-345-212-13
14	71.5	7.2	533	2	US-08-249-003-13
15	71.5	7.2	533	4	US-08-236-311-4
16	71	7.1	434	3	US-08-457-918-4
17	71	7.1	434	1	US-08-227-108-18
18	71	7.1	434	3	US-08-227-108-18
19	70.5	7.1	379	2	US-08-073-674-18
20	70.5	7.1	379	1	US-08-073-674-18
21	70.5	7.1	1181	1	US-08-316-397B-4
22	70.5	7.1	1181	2	US-09-034-306-4
23	70.5	7.1	1181	4	US-09-259-437-4
24	70.5	7.1	1181	5	PCT-US93-09782-4
25	70.5	7.1	1220	3	US-08-930-996A-2
26	70.5	7.1	418	2	US-08-873-479-44
27	70	7.0			Sequence 44, Appl

28	70	7.0	467	4	US-09-002-361-3	Sequence 3, Appl
29	70	7.0	496	4	US-09-002-361-2	Sequence 2, Appl
30	70	7.0	855	1	US-08-344-536-2	Sequence 2, Appl
31	70	7.0	855	3	US-08-920-562-2	Sequence 2, Appl
32	70	7.0	2391	2	US-08-446-855A-2	Sequence 2, Appl
33	70	7.0	2391	4	US-09-150-741-2	Sequence 2, Appl
34	69.5	7.0	1240	3	US-08-930-996A-4	Sequence 4, Appl
35	69	6.9	238	4	US-09-216-295-12	Sequence 12, Appl
36	69	6.9	259	4	US-09-041-889-28	Sequence 28, Appl
37	69	6.9	323	3	US-09-041-889-28	Sequence 29, Appl
38	69	6.9	361	1	US-08-415-751-3	Sequence 4, Appl
39	69	6.9	377	3	US-09-041-889-29	Sequence 4, Appl
40	68.5	6.9	211	4	US-08-856-253-4	Sequence 6, Appl
41	68.5	6.9	459	3	US-09-118-319-6	Sequence 2, Appl
42	68.5	6.9	459	4	US-09-286-691-2	Sequence 2, Appl
43	68.5	6.9	459	4	US-08-687-147-2	Sequence 6, Appl
44	68.5	6.9	512	4	US-08-856-253-6	Sequence 4, Appl
45	68.5	6.9	1003	1	US-08-571-758-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-559-896B-2
Sequence 2, Application US/0859896B
Patent No. 6310046
GENERAL INFORMATION:
APPLICANT: Patrick E. Duffy
APPLICANT: Christian F. Ockenhouse
TITLE OF INVENTION: SEQUESTIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: USA MRC - MCMR-JA
CITY: FORT DETRICK, FREDERICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,896B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-559-896B-2

Query Match
Best Local Similarity 8.1%; Score 80.5; DB 4; Length 652;
Matches 38; Conservative 23; Mismatches 44; Indels 55; Gaps 9;
QY 21 NYN-----DVNDNNNAGSGQGV-SVNNEN-----VANVDNNNGGDSWNS 62
DB 404 NYNVFIIDNNDSNNNNNNNNNDVNNNNKFTNNNNYNNVEVELVRRLLDKG-AKIED 462

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OY      63  IMYGN-----GFAATLLEFKCTCIYHAKKE-----YMSJSDLAALKEK 104
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Db      463  IIDFENKEIKKOKNNVNSIYNLFMSKVGKDNPJIOHKKEENDVYKRNQ----IIQD 518
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OY      105  KLOGKGGGPPPKGLMYSVNPK-----VDDLSKFG 135
          |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      519  NIKKKG-----QKDNTEMLDNKKETITIDIKANVDIDKNG 553
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RESULT 2
US-09-118-319-5
Sequence 5, Application US/09118319

```

1  APPLICANT: Li, Xin-liang
2  APPLICANT: Chen, Huizhong
3  APPLICANT: Jüנגedahl, Lars G.
4  TITLE OF INVENTION: Ornithomycase Cellulase Celp Protein and Coding Sequences
5  FILE REFERENCE: 33-98sequence listing
6  CURRENT APPLICATION NUMBER: US/09/118,319
7  CURRENT FILING DATE: 1998-07-17
8  NUMBER OF SEQ ID NOS: 9
9  SOFTWARE: PatentIn Ver. 2.0
10 SEQ ID NO 5
11 LENGTH: 428
12 TYPE: prt
13 ORGANISM: Neocallimastix patriciarum
14
15 US-09-118-319-5

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Query Match	7.88;	Score 77.5;	DB 3;	Length 428;
Best Local Similarity	22.78;	Pred. No. 1.2;		
Matches	37;	Mismatches	66;	Indels 39; Gaps 5
		Conservative	21;	

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QY      17  PALANNIDVDDNNAGSGGOVSYNNEINAVANDNNNGMGMSWMSIDYNGEAAATRL  76
      QY      58  PGAPSPNNASNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  109
      Db      77  QAKTCTVHHAKKEVWPSIQ--SLDAVYEKKLQG-----KPGQGP  114
      QY      110 DNOIVANPKFIEVWSSSLPRLSYDLQCKAKVKNVPTAVLWMDGATGEVADHLKAAGSK  163
      Db      115 PPKGLMYSV-----NPNK-----VDSLKFEKGNIAANNCRGIPY  148
      QY      170 TVYFIMIMIPTRDCNANASAGAGAGLANTYKGYNDIARTIRST  212
      Db

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RESULT 3
US-08-945-848-8
; Sequence 8, Application US/08945848
; Patent No. 5968772

APPLICANT: MATSUHITO, Aizo
TITLE OF INVENTION: PEARL PROTEIN(MACREIN) AND PROCESS FOR
TITLE OF INVENTION: THE SAME
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,848
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19036/34324
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-945-848-8

Query Match	7.8%	Score 77.5;	DB 2;	Length 430;
Best Local Similarity	24.3%	Pred. No. 1.2;		
Matches	42;	Conservative	18;	Mismatches 51;
				Gaps 8

QY 21 NYNIDVDDNNAG-----SQQQSVSYNNEHNVANVDNNNGMSPMSIMDWIGGFAA 7
Db 242 NGNNSTYNGNGNNGNNGNNGNGYNGDNGNGDNGNGNGDNGNGDNGNGNGGNGNGENGN 301
QY 74 --RLPQKTCYTHKKMKREMPMSIQSLDALYKEKKLGKGPGGPEPKGLMTSYNPKAYDDL 13
Db 302 NGENGKHGCRKKKKK-----HLSRI-----LECAVRNDKVAEF 33
QY 132 SKFGKNIAMNCRGIPYMAEMQKQSL-----FFYSGT-----CYTTSVLMTV 174
Db 336 KKGGE-----EGIDVHLTPPEMALPPLLYRHHYTYEGSLTTPC-TESLVMV 382

RESULT 4
US-09-187-124-2
Sequence 2, Application US/09187124A

? Patent No. 6255563
 ? GENERAL INFORMATION
 ? APPLICANT: Emmemann, Michael
 ? APPLICANT: Kossmann, Jens
 ? TITLE OF INVENTION: NUCLEIC ACID MOLECULES CODING FOR DEBRANCHING ENZYMES
 ? TITLE OF INVENTION: FROM POTATO
 ? FILE REFERENCE: GPR8
 ? CURRENT APPLICATION NUMBER: US/09/187,124A
 ? CURRENT FILING DATE: 1998-11-05
 ? EARLIER APPLICATION NUMBER: PCT/EP97/02292
 ? EARLIER FILING DATE: 1997-05-06
 ? EARLIER APPLICATION NUMBER: DE 196 18 125.9
 ? EARLIER FILING DATE: 1996-05-06
 ? NUMBER OF SEQ ID NOS: 2
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 2
 ? LENGTH: 606
 ? TYPE: prt
 ? ORGANISM: Solanum tuberosum

Query Match	7.43;	Score 74;	DB 4;	Length 606;
Best Local Similarity	35.03;	Pred. No. 5.1;		
Matches 14;	Conservative 10;	Mismatches 16;	Indels 0;	Gaps 0.

QY 40 VSANNENHNVANDNNNGWDSWNSIMDYCGNFAATRFQKK 79
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Db 369 VTYNNKHNLANGEDNKDGENHNHNSWNCGECEGFASIFVKK 408

RESULT 5
US-08-445-586-10
; Sequence 10, Application US/08445586
; Patent No. 5627050
; GENERAL INFORMATION:

```

APPLICANT: Takeshita, Sunao
APPLICANT: Ito, Toshimi
APPLICANT: Otawara-Hamamoto, Yoko
APPLICANT: Amano, Egon
TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,586
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,887
FILING DATE: 26-AUG-1993
APPLICATION NUMBER: JP 230030/92
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 324034/92
FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Foreman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 02481.1322-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-445-586-10

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Query Match
Best Local Similarity 7.4%; Score 73.5; DB 1; Length 533;
Matches 42; Conservative 20; Mismatches 48; Indels 47; Gaps 11:
QY 43 NNEHNVAVND-----NNGMD-----SMNSIMD---YNGCFATRLFOKKTCTIVHKMKK 88
DB 291 NNTVYIFSTDMGGQTLAGGNNWPLRGKKW-SLMEGGYGVGFVAPSLRLKQGV---KNR 345
QY 89 EVMPSIOGLDALVY-----EKKLOG-----KGGGPPPK-GIMSVNPNKYVDLSK 133
DB 346 ELIHSMQLPLTVLARGHTNGTKPLIDFDMKTKISEGSPRIELHLHIDNFDVDS-SP 404
QY 134 FGNKIANNCRGIPYMAEEMQEASLFFYSGTCYTTSV 170
DB 405 CPRN-----SMAPAKDSSLPETYS--AFNTSV 429

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```

RESULT 6
US-08-929-329-5
Sequence 5, Application US/08929329
Patent No. 6120770
GENERAL INFORMATION:
APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Kappe, Stefan

```

```

TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESS: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYDROTHERMAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium yoelii
US-08-929-329-5

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Query Match
Best Local Similarity 7.3%; Score 73; DB 3; Length 1507;
Matches 46; Conservative 23; Mismatches 71; Indels 74; Gaps 12:
QY 19 LANYNDIVND-----NNNA-----GSGQOVSYSVNNHNVN-----NVDNNGMD----- 58
DB 527 LKNTNMDSENSFTSFHNTVAPTHYBGNKSKFTGVNKKRENTYGTODINLNANNYINOPKN 586
QY 59 -----SMNSIMDYNGGFAATRLFOKKTCTIVHKMKKEVPSIOSL 97
DB 587 KPNPQAEYMDRFDIEKNHIYIDMKODGKRGSG---KL--RYNTIISH-----ETADTOSL 636
QY 98 -----DALKEKKLQCKGGPPKGLMYSV-NPNKYVDLSKFGKNIANNCRG--IPTM 149
DB 637 LITDKDIDICPNHYSGRAGSCPNYKGSIVVKTPEISNGNHNLSNLFNIRGTGYLNTM 696
QY 150 AEEM-----OEASLFFYSGTCYTTSVLWITVDISFC 179
DB 697 KSNVELPYEKSGLAMHNG-----DLVSC 719

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RESULT 7
US-08-241-465B-19
Sequence 19, Application US/08241465B
Patent No. 5719125
GENERAL INFORMATION:
APPLICANT: Fujio SUZUKI
APPLICANT: Yuji HIRAKI
APPLICANT: Kazuhito TAKAHASHI
APPLICANT: Junko SUZUKI
APPLICANT: Atsuko KOHARA
APPLICANT: Akiko MORI

```

APPLICANT: EI YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-1 PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-465B-19

Query Match 7.2%; Score 72; DB 1; Length 334;
Best Local Similarity 20.3%; Pred. No. 3.7; 74; Indels 14; Gaps 4;
Matches 29; Conservative 26; Mismatches 74; Indels 14; Gaps 4;
QY 21 NYNDVNDNNAGSGQ-SVSNNENHNAVNDNNMGDSNIMWYNGFAATRLPQK 79
DB 76 HTYMSIN-----GRLDGSMEIDAGNNLETFKMGSAEFAIVNDFONGITGIRPAGE 129
QY 80 TCIYHMKKEWPSIOSLDALVKEKTLQK-GPGGPPKGLMYSVNPKNKVDLSKFGKNI 138
DB 130 KCIYKQVKARIPVGAATKOSISKLEKIMPKYEENSLIWAIVDPYKXNSFLSKV 189
QY 139 ANMCRGI-----PTYMAEEMOE 155
DB 190 LELCGDLPIFWLKPYPKEIORE 212

RESULT 8
US-08-241-465B-20
Sequence 20 Application US/08241465B
Patent No. 5719125
GENERAL INFORMATION:
APPLICANT: Fujio SUZUKI
APPLICANT: YUJI HIRAKI
APPLICANT: Kazuhito TAKAHASHI
APPLICANT: Junko SUZUKI
APPLICANT: Jun KONDO
APPLICANT: Atsuko KOHARA
APPLICANT: AKIKO MORI
APPLICANT: EI YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-1 PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-241-465B-20

Query Match 7.2%; Score 72; DB 1; Length 334;
Best Local Similarity 20.3%; Pred. No. 3.7; 74; Indels 14; Gaps 4;
Matches 29; Conservative 26; Mismatches 74; Indels 14; Gaps 4;
QY 21 NYNDVNDNNAGSGQ-SVSNNENHNAVNDNNMGDSNIMWYNGFAATRLPQK 79
DB 76 HTYMSIN-----GRLDGSMEIDAGNNLETFKMGSAEFAIVNDFONGITGIRPAGE 129
QY 80 TCIYHMKKEWPSIOSLDALVKEKTLQK-GPGGPPKGLMYSVNPKNKVDLSKFGKNI 138
DB 130 KCIYKQVKARIPVGAATKOSISKLEKIMPKYEENSLIWAIVDPYKXNSFLSKV 189
QY 139 ANMCRGI-----PTYMAEEMOE 155
DB 190 LELCGDLPIFWLKPYPKEIORE 212

RESULT 9
US-08-227-108-16
Sequence 16 Application US/08227108
Patent No. 5807726
GENERAL INFORMATION:
APPLICANT: Blanchard, Claire
APPLICANT: Benicourt, Claude
APPLICANT: Julien, Jean-Louis
TITLE OF INVENTION: Recombinant Dog Gastric Lipase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,108
FILING DATE: 03-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fannuccl, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 7620-033

MOLECULE TYPE: protein
5-09-073-674-16

TITLE OF INVENTION:	GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION:	IDURONATE 2-SULFATASE

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-493-13

Query Match 7.2%; Score 71.5; DB 1; Length 533;
Best Local Similarity 26.8%; Pred. No. 8.4; Indels 47; Gaps 11;
Matches 42; Conservative 20; Mismatches

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DB 291 NNIVFIFSTDNQGOTLAGNNMPLRGKW-SLMEGVGVGVFVASPLLKQGV---KNR 345
QY 89 EVMSIQLDALVK-----EKKLOG-----KPGGPPPK-GIMSVNPNKYDDLSK 133
DB 346 ELIHSDWLPFLVTLARGHTNGTKPLDGFVWKTISEGSPPRIELHNDPFDVS-SP 404
QY 134 FGNIANMCRGIPITYAAEEMQEASLFYSGTCYTSV 170
DB 405 CPRN-----SMAPAKDSSLPETYS--AFNTISV 429

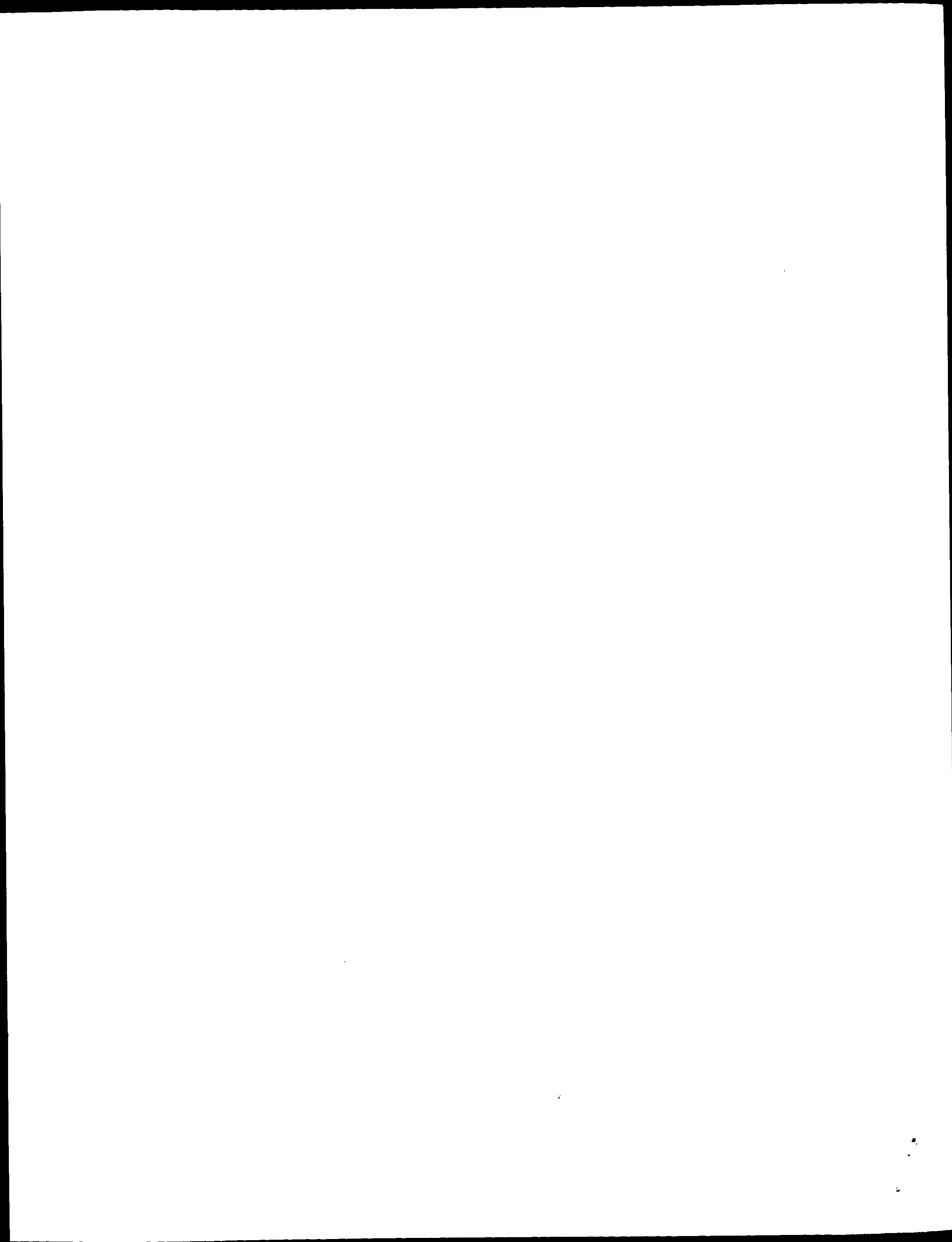
RESULT 13
US-08-484-494-13
Sequence 13, Application US/08484494
Patent No. 5798239
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,494
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-494-13

Query Match 7.2%; Score 71.5; DB 1; Length 533;
Best Local Similarity 26.8%; Pred. No. 8.4; Indels 47; Gaps 11;
Matches 42; Conservative 20; Mismatches

QY 43 NNEHNANVND-----NNGMD-----YNGFAATRLFOKKTCTIVHKKK 88
DB 291 NNIVFIFSTDNQGOTLAGNNMPLRGKW-SLMEGVGVGVFVASPLLKQGV---KNR 345
QY 89 EVMSIQLDALVK-----EKKLOG-----KPGGPPPK-GIMSVNPNKYDDLSK 133
DB 346 ELIHSDWLPFLVTLARGHTNGTKPLDGFVWKTISEGSPPRIELHNDPFDVS-SP 404
QY 134 FGNIANMCRGIPITYAAEEMQEASLFYSGTCYTSV 170
DB 405 CPRN-----SMAPAKDSSLPETYS--AFNTISV 429

RESULT 14
US-08-345-212-13
Sequence 13, Application US/08345212
Patent No. 5932211
GENERAL INFORMATION:
APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielicki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530



RESULT 12
B69823
conserved hypothetical protein yhcN - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C/Accession: B69823
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, J.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzini, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Iech, J.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:08 ; Search time 57.74 Seconds
(without alignments)
8.038 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90

Sequence: 1 KKEYMPSIQSLDALVKEKK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pap:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pap:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	44.4	1964	2	US-08-790-912-3
2	40	44.4	2052	4	US-08-790-912-2
3	37.5	41.7	2548	4	US-09-172-422-1
4	37	41.1	24	2	US-08-491-527A-12
5	37	41.1	476	3	US-08-704-711A-21
6	37	41.1	476	4	US-08-448-489-14
7	37	41.1	498	1	US-08-470-202-59
8	37	41.1	498	1	US-08-470-202-60
9	37	41.1	498	1	US-08-471-770-59
10	37	41.1	498	1	US-08-471-770-60
11	37	41.1	498	2	US-08-468-059-59
12	37	41.1	498	2	US-08-468-059-60
13	37	41.1	498	4	US-09-109-916-59
14	37	41.1	498	4	US-09-109-916-60
15	37	41.1	568	2	US-08-835-170-4
16	37	41.1	568	4	US-09-359-257-4
17	37	41.1	588	2	US-08-835-170-2
18	37	41.1	588	4	US-09-359-257-2
19	37	41.1	1045	2	US-08-553-436A-6
20	37	41.1	1525	4	US-09-396-651B-1
21	37	41.1	1536	1	US-08-038-862-2
22	37	41.1	1536	1	US-08-302-832-2
23	37	41.1	1536	2	US-08-530-198-2
24	37	41.1	1536	2	US-08-469-880-2
25	37	41.1	1536	2	US-08-728-470-2
26	37	41.1	1536	2	US-08-617-697-2
27	37	41.1	1536	4	US-08-719-641-2

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Sequence 3, Appli
Sequence 3, Appli
Sequence 46, Appli
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Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-790-912-3
; Sequence 3, Application US/08790912
; Patent No. 5976542
; GENERAL INFORMATION:
; APPLICANT: Weiser, Jeffrey N.
; APPLICANT: Plaut, Andrew G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,912
; FILING DATE: 29-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,939
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary, Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 7600-4UI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1964 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-912-3

Query Match 44.4%; Score 40; DB 2; Length 1964;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KEVMPISQSLD 12
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Db 1230 KEVLPQLKLD 1240

RESULT 2
US-08-790-912-2
; Sequence 2, Application US/08790912
; Patent No. 5976542
; GENERAL INFORMATION:
; APPLICANT: Weiser, Jeffrey N.
; APPLICANT: Plaut, Andrew G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
; OF STREPTOCOCCUS PNEUMONIAE INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,912
; FILING DATE: 29-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,939
; FILING DATE: 23-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leary, Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 7600-401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 567-2020
; TELEFAX: (215) 567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2052 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-790-912-2

Query Match 44.4%; Score 40; DB 2; Length 2052;
Best Local Similarity 63.6%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KEVMPISQSLD 12
|||:|:|:|
Db 1303 KEVLPQLKLD 1313

RESULT 3
US-09-172-422-1
; Sequence 1, Application US/09172422A
; Patent No. 6300485
; GENERAL INFORMATION:
; APPLICANT: Adams, Arwen E.
; APPLICANT: Chiu, Choi Ying
; APPLICANT: Duhl, David
; APPLICANT: Gorman, Susan W.
; APPLICANT: Leng, Song
; APPLICANT: Sheffield, Val
; APPLICANT: Welch, Juliet

; TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
; TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYPEPTIDES,
; FILE REFERENCE: 200130.442
; CURRENT APPLICATION NUMBER: US/09/172,422A
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2548
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-172-422-1

Query Match 41.7%; Score 37.5; DB 4; Length 2548;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 1 KKEVMPISI-QSLDALVKKK 19
|||:|:|:|:|:|
Db 1509 EKEMEQIRQQTDLKERRK 1528

RESULT 4
US-08-491-527A-12
; Sequence 12, Application US/08491527A
; Patent No. 5824483
; GENERAL INFORMATION:
; APPLICANT: Houston, Michael E.
; APPLICANT: Hodges, Robert S.
; TITLE OF INVENTION: Conformationally-Restricted Combinatorial
; TITLE OF INVENTION: Library Composition and Method
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,527A
; FILING DATE: 16-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,199
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/245,507
; FILING DATE: 18-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 7900-0008.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: LPS epitope library peptide, Fig. 5A

US-08-491-527A-12

Query Match 41.1%; Score 37; DB 2; Length 24;
Best Local Similarity 47.4%; Pred. No. 5.1;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVREKK 19
| | | : | : | | |
DB 6 KKEHFLVQKIHLEKEIK 24

RESULT 5

US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-21

Query Match 41.1%; Score 37; DB 3; Length 476;
Best Local Similarity 56.2%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 6 PSIQSLDALV--KEKK 19
| | | : | | | | |
DB 382 PTIRKIDAAVSDKEKK 397

RESULT 6

US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match 41.1%; Score 37; DB 4; Length 476;
Best Local Similarity 56.2%; Pred. No. 1.6e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 6 PSIQSLDALV--KEKK 19
| | | : | | | | |
DB 382 PTIRKIDAAVSDKEKK 397

RESULT 7

US-08-470-202-59
; Sequence 59, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8

; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-470-202-59

Query Match 41.1%; Score 37; DB 1; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 QKQVSPSAPPMEAEVKEQE 473

RESULT 8
US-08-470-202-60
; Sequence 60, Application US/08470202
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4

; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael J. Blake
; REGISTRATION NUMBER: 37,096
; REFERENCE/DOCKET NUMBER: 05495-0001-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-470-202-60

Query Match 41.1%; Score 37; DB 1; Length 498;
Best Local Similarity 36.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEKK 19
Db 455 QKQVSPSAPPMEAEVKEQE 473

RESULT 9
US-08-471-770-59
; Sequence 59, Application US/08471770
; Patent No. 5770427
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht v.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,770
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/132,653
; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 33 646.5
; FILING DATE: 06-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 35 718.7
; FILING DATE: 22-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 44 541.8
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 18 186.4
; FILING DATE: 01-JUN-1993

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:39 ; Search time 124.34 Seconds
(without alignments)
257.392 Million cell updates/sec

Title: US-09-821-726-13

Perfect score: 994

Sequence: 1 MKFTIVFAGLGVFLAPALA.....YTTSLVIVDISFGDIVEN 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query		Match	Length	DB ID	Description
		Match	Length				
1	245	24.6	191	11	Q9D0T7		Q9D0T7 mus musculus
2	195	19.6	184	11	Q9C0S6		Q9C0S6 mus musculus
3	98	9.9	568	5	Q9N138		Q9N138 pinctada ma
4	97	9.8	588	5	Q964F6		Q964F6 plasmodium
5	97	9.8	1208	5	Q97101		Q97101 dictyosteli
6	96.5	9.7	1844	5	Q97287		Q97287 plasmodium
7	95.5	9.6	1318	5	Q95PH4		Q95PH4 dictyosteli
8	93	9.4	764	5	Q96234		Q96234 plasmodium
9	91.5	9.2	596	5	Q964F7		Q964F7 plasmodium
10	91.5	9.2	600	5	Q964F5		Q964F5 plasmodium
11	91.5	9.2	600	5	Q95NL3		Q95NL3 plasmodium
12	90	9.1	604	5	Q964F8		Q964F8 plasmodium
13	90	9.1	1245	5	Q96195		Q96195 plasmodium
14	89	9.0	608	5	Q97331		Q97331 plasmodium
15	88.5	8.9	186	5	O01876		O01876 caenorhabdi
16	88	8.9	660	5	O00885		O00885 dictyosteli

SUMMARIES

ALIGNMENTS

RESULT 1
Q9D0T7
ID Q9D0T7 PRELIMINARY; PRT; 191 AA.
AC Q9D0T7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1190003M12RIK PROTEIN.
GN 1190003M12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;

Q9u573 dictyosteli
Q77328 plasmodium
Q77363 plasmodium
Q9nu7 plasmodium
Q25770 plasmodium
Q25770 plasmodium
Q23847 dictyosteli
Q9tx75 plasmodium
Q9bnn0 plasmodium
Q9vxd5 drosophila
Q96253 plasmodium
Q96422 plasmodium
Q96133 plasmodium
O06304 mycobacteri
Q97239 plasmodium
Q9u0j3 plasmodium
Q9u0h8 plasmodium
Q9u0k8 plasmodium
Q97384 plasmodium
Q97306 plasmodium
O15784 dictyosteli
Q9p12 dictyosteli
Q96x44 saccharomyc
Q25774 plasmodium
Q9u0k4 plasmodium
Q9ict2 chimpanzee
Q23853 dictyosteli
Q9p5j0 neurospora
Q9xzs0 dictyosteli

SEQUENCE 191 AA; 20772 MW; 76D7DB4796AEB4D CRC64;

Query Match 24.6%; Score 245; DB 11; Length 191;
Best Local Similarity 31.8%; Pred. No. 6.9e-16;
Matches 56; Conservative 37; Mismatches 71; Indels 12; Gaps 5;

Qy 10 LLGVFLAPALANYIDVNDNNAGS--GQOSVSVNHNHNVANNVNDNNGWDSWNSIWDYCN 68
Db 20 LVTYVLPALALTN--TSDSYPLDGSVGTOTIHVDALRGVVSIRDNSVQSEMDGVMDYKN 77

Qy 69 GFAATRLFOKTCIVHKMKVMPSTQSDALVKEKLGKQPGG--PPKGLMYSVNEN 126
Db 78 DLLAAKLFKMACVLAKMDFAPFSLDITQAL-----GKQASGYPYPPRGITVTLVLS 131

Qy 127 KVDLSLFRGNIAKMGCIPTVMAEEMOE--ASLFFYSGTCYTTSVLWIVDISFCGD 181
Db 132 RIKNLAQGVPIKOLCRAPVTYFARQKEGTALTMDDSCSELQLLSFMGLSCIG 187

RESULT 2
Q9CQS6 PRELIMINARY; PRT; 184 AA.

AC Q9CQS6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 1810036H07RIK PROTEIN.
GN 1810036H07RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=STOMACH, AND PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamliya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR ENBL; AK008986; BAB26008.1; -;
DR ENBL; AK007451; BAB25046.1; -;
DR ENBL; AK007705; BAB25201.1; -;
DR MGD; MGI:1913534; 1810036H07RIK.
SQ SEQUENCE 184 AA; 20469 MW; 612A18FABE652230 CRC64;

Query Match 19.6%; Score 195; DB 11; Length 184;
Best Local Similarity 27.1%; Pred. No. 4.4e-11;
Matches 51; Conservative 43; Mismatches 78; Indels 16; Gaps 5;

Qy 1 MKFTIVFAGLGVFLAPALANYIDVNDNNAGSQQOSVSVNHNHNVANNVNDNNGWDSW 60
Db 1 MKPLVAFVLVLSIRGIGSQAEIEFNIEFVPSKNGNIGQETVIDNQQTATINHSGCCS 60

Qy 61 NSIWDYNGNFAATRLFOKTCIVHKMKVMPSTQSDALVKEKLGKQPGGPPKGLM 120

Db 61 TTFIDYKHGYTASRVLSRRACYVIKMDHKAIPALDKLQRELYEKQTMN---AIDSPYTW 117
Qy 121 YSNVP-----NKVDDLSKFGKNIANMCRGIPTY---MAEEMOEASLFFYSGTCYTTSVLW 172
Db 118 VRYNPLKSLITKV-DWFLFGSPIROLCKHMPLEGEVATKPKYS-----TCACAKVGLG 172
Qy 173 IVDISFCG 180
Db 173 ILGVSIQG 180

RESULT 3
Q9NL38 PRELIMINARY; PRT; 568 AA.

AC Q9NL38;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE N66 MATRIX PROTEIN.
GN Pinctada maxima.
OS Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pterioidea;
OC Pterioidea; Pteriidae; Pinctada.
OX NCBI_TaxID=104660;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE LAYER;
RX MEDLINE=20160475; PubMed=10694502;
RA Kono M., Hayashi N., Samata T.;
RT "Molecular mechanism of the nacreous layer formation in Pinctada maxima.";
RL Biochem. Biophys. Res. Commun. 269:213-218(2000).
DR ENBL; AB032613; BAA90540.1; -;
DR HSSP; P23589; IDMY.
DR InterPro; IPR001148; Carb_anhydriase.
DR InterPro; IPR002952; Eggshell.
DR Pfam; PF00194; carb_anhydriase; 1.
DR PRINIS; PR01228; EGGSHLL.
DR PRODOM; PD000865; Carb_anhydriase; 2.
KW Matrix protein.
SQ SEQUENCE 568 AA; 62377 MW; 4AD9242A96EB642F CRC64;

Query Match 9.9%; Score 98; DB 5; Length 568;
Best Local Similarity 24.8%; Pred. No. 0.41;
Matches 41; Conservative 20; Mismatches 62; Indels 42; Gaps 7;

Qy 27 NDDNNAGSQOSVSVNHNHNVANNVNDNNGWDSWNS-----IWDYGN--GFAATR 74
Db 381 NGNNNGNGSNGNGNGNGNGNGNGNGNGNGSDGLRRWDLANVRMHAER 440

Qy 75 LFQKTCIVHKMKVMPSTQSDALVKEKLGKQPGGPPKGLMYSVNPNKVDLSKF 134
Db 441 YHFGSGCIVKAKR-----LSRILECAVHKVREKRG--EEKGLDVIDITPMV----- 489

Qy 135 GKNTANMCRGIPTVMAEEMOEASLFFYSGTCYT-----TSVLWIVD 175
Db 490 -----LP-----PMKYRHYTYEGSLTTPPCNETVLWVVE 519

RESULT 4
Q964F6 PRELIMINARY; PRT; 588 AA.

AC Q964F6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
GN MEROZOITE SURFACE PROTEIN 8.
DE MSP8.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]

RESULT 15

	Query Match	8.9%;	Score 88.5;	DB 5;	Length 186;
	Best Local Similarity	24.0%;	Pred. No. 0.87;		
	Matches 36;	Conservative 20;	Mismatches 51;	Indels 43;	Gaps
Qy	21	NYNIDVDDNNAGSGQSVSNNHHVANVDNNGW---	DSWNISWDYNGGFAATRLFQ	77	
		: :	: : :	:	:
Db	28	NNWSGGNNAGSGGSWGNGNANNNNNNGSNNNGWNNNDWSSNYNGGSNAANEPMK	87		
		: :	: : :	:	:
Qy	78	KKTCTIV-----HKMK----	KEYMPSI-QSLDALVKEKKLGKGPGGPPPKGLMSYVNPNKV	128	
		: :	: : :	:	:
Db	88	TKQTAYAGDSDSNKNKWTKNQVEDMFKKSIDDRGDETQLF-----	126		
		: :	: : :	:	:
Qy	129	DDLSEFGKNIANMCRGIPTYMAEEEMQEASL	158		
		: :	: : :	:	:
Db	127	DDFKKIDKN-----YKTSVPQESL	146		
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Search completed: September 4, 2002, 17:01:41
Job time: 1162 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:33 ; Search time 75.48 Seconds
(without alignments)
24.188 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90

Sequence: 1 KEVMPSTQSLDALVKEKK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	47	52.2	2895	2	H85362	hypothetical prote
2	45	50.0	430	2	C64554	ATP-dependent nucl
3	45	50.0	431	2	C71954	hypothetical prote
4	44.5	49.4	1676	2	E71410	probable centromer
5	44	48.9	1336	2	T23310	hypothetical prote
6	43	47.8	283	2	T47174	hypothetical prote
7	43	47.8	633	2	S62737	DNA topoisomerase
8	43	47.8	734	2	E72271	5-methyltetrahydro
9	43	47.8	4869	2	S66572	ryanodine receptor
10	42.5	47.2	463	2	B81725	fumarate hydratase
11	42	46.7	199	2	I49343	probable isomerase
12	42	46.7	203	2	C55552	2-hydroxychromene-
13	42	46.7	339	2	B97755	hypothetical prote
14	42	46.7	574	2	T41207	hypothetical prote
15	41	45.6	130	2	AC2477	hypothetical prote
16	41	45.6	238	2	S70195	hypothetical prote
17	41	45.6	292	2	D42284	kfiA protein - Esc
18	41	45.6	340	2	D71688	spaz2 protein - Sh
19	41	45.6	361	2	T00437	hypothetical prote
20	41	45.6	434	2	J00182	probable protein d
21	41	45.6	464	2	D95043	monodehydroascorba
22	41	45.6	464	2	F97913	hypothetical prote
23	41	45.6	753	2	B71472	conserved hypotet
24	40.5	45.0	451	2	D69356	probable primosoma
25	40.5	45.0	1225	2	A49464	serine hydroxymeth
26	40	44.4	107	2	H84839	chromosome segrega
27	40	44.4	156	2	G97150	late embryogenesis
28	40	44.4	162	2	I64239	hypothetical prote
29	40	44.4	173	2	T19290	ribosomal protein
						hypothetical prote

30	40	44.4	331	2	G83939	myo-inositol catab
31	40	44.4	399	2	E64180	lipid-A-disacchari
32	40	44.4	414	2	G64091	cell division prot
33	40	44.4	434	2	T47545	monodehydroascorba
34	40	44.4	465	2	D81312	hypothetical prote
35	40	44.4	482	2	E89629	spore germination
36	40	44.4	524	1	S60406	hypothetical prote
37	40	44.4	548	1	A26511	amds protein - Eme
38	40	44.4	663	2	B70460	excinuclease ABC C
39	40	44.4	863	2	T51002	hypothetical prote
40	40	44.4	987	2	G86201	hypothetical prote
41	40	44.4	1013	2	T48422	hypothetical prote
42	40	44.4	1815	2	B95942	conserved hypotet
43	40	44.4	1963	2	B98002	IgA-specific metal
44	40	44.4	3488	2	T34418	hypothetical prote
45	39.5	43.9	179	2	H83741	hypothetical prote

ALIGNMENTS

RESULT 1

H85362

hypothetical protein AT4g30990 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C:Accession: H85362

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488

A:Accession: H85362

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2895 <STO>

A:Cross-References: GB:NC_001268; NID:g2720001; PIDN:CAB79817.1; GSPDB:GN00140

C:Genetics:

A:Gene: AT4g30990

A:Map position: 4

Query Match

Best Local Similarity 52.2%; Score 47; DB 2; Length 2895;

Matches 7; Conservative 38.9%; Pred. No. 78;

Mismatches 8; Indels 3; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19

Db ::::|||||:::|:

Db 57 EEMLPVSQSLIIIMQKE 74

RESULT 2

C64554

ATP-dependent nuclease - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: C64554

R:Tomb, J.F.; White, O.; Kervilange, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467

A:Accession: C64554

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-430 <TOM>

A:Cross-References: GB:AE000511; NID:g2313363; PIDN:AAD07339.1; PID:g231

Query Match

Best Local Similarity 50.0%; Score 45; DB 2; Length 430;

Matches 8; Conservative 42.1%; Pred. No. 21;

Mismatches 6; Indels 5; Gaps 0;

```

QY 1 KKEVMPISQSLDALVKEK 19
|:|:| | | | | | | | | |
Db 313 KEEMLPPIQKLEQATKREQ 331

RESULT 3
C71954
hypothetical protein jhp0260 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: C71954
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: C71954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-431 <ARN>
A:Cross-references: GB:AE001463; GB:AE001439; NID:94154775; PIDN:RAD05839.1; PID:9415478
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0260

Query Match 50.0%; Score 45; DB 2; Length 431;
Best Local Similarity 42.1%; Pred. No. 21;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEK 19
|:|:| | | | | | | | | |
Db 314 KEEMLPPIQKLEQATKREQ 332

RESULT 4
E71410
probable centromere protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C:Accession: E71410
R:Byvan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A:Reference number: A71400; MUID:98121113
A:Accession: E71410
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1676 <BEV>
A:Cross-references: GB:Z97337; NID:g2244829; PID:e326823; PID:g2244833
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 49.4%; Score 44.5; DB 2; Length 1676;
Best Local Similarity 55.6%; Pred. No. 1.le+02;
Matches 10; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 KEVMPISQSLDALVKEK 18
|:|:| | | | | | | | | |
Db 1356 KEINPSIKTIEQAFVKEK 1373

RESULT 5
T23310
hypothetical protein K04D7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23310
R:Wild, A.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19725
A:Accession: T23310
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1336 <WIL>
A:Cross-references: EMBL:Z69664; PIDN:CAA93515.1; GSPDB:GN00022; CESP:K04D7.5
A:Experimental source: clone K04D7
C:Genetics:
A:Gene: CESP:K04D7.5
A:Map position: 4
A:Introns: 28/2; 116/3; 153/3; 270/1; 351/3; 579/3; 699/3; 1002/3; 1024/3; 1080/3; 11
Query Match 48.9%; Score 44; DB 2; Length 1336;
Best Local Similarity 57.1%; Pred. No. le+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDAL 14
|:|:| | | | | | | | | |
Db 759 EKELMPSTSSIDSL 772

RESULT 6
T47174
hypothetical protein DKFp762I166.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47174
R:Blöcker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24376
A:Accession: T47174
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-283 <AAA>
A:Cross-references: EMBL:AL162072
A:Experimental source: adult melanoma (Mewo cell line); clone DKFp762I166
C:Genetics:
A:Note: DKFp762I166.1
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 47.8%; Score 43; DB 2; Length 283;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEK 18
|:|:| | | | | | | | | |
Db 248 EEVQMELRALRALVKEQ 264

RESULT 7
S62737
DNA topoisomerase I - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S62737; A72400
R:Bouthier de la Tour, C.; Kaltoum, H.; Portemer, C.; Confalonieri, F.; Hubert, R.; D
Biochim. Biophys. Acta 1264, 279-283, 1995
A:Title: Cloning and sequencing of the gene coding for topoisomerase I from the exte
A:Reference number: S62737; MUID:96138548
A:Accession: S62737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-633 <BOU>
A:Cross-references: EMBL:U27841; NID:9881493; PIDN:AAA68949.1; PID:g881494
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic

```

2-hydroxychromene-2-carboxylate isomerase - *Pseudomonas putida* plasmid NAH7

C:Species: Pseudomonas putida
C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 29-Sep-1999
C:Accession: C55552

R:Eaton, R.W.
J. Bacteriol. 176, 7757-7762, 1994
A:Title: Organization and evolution of naphthalene catabolic pathways: sequence of the pNAH7 plasmid.

A:Reference number: A55552; PMID:95095951

A:Accession: C55552

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-203 <EAT>

A:Cross-references: GB:U09057; NID:g483790; PIDN:AAA66358.1; PID:g483793

C:Genetics:

A:Gene: nahd

A:Genome: plasmid

A:Start codon: GTG

C:Superfamily: 2-hydroxychromene-2-carboxylate isomerase

Query Match 46.7%; Score 42; DB 2; Length 203;
Best Local Similarity 53.3%; Pred. No. 29;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 VMPISQSLDALVKEK 18

Db 118 IAPDLESPLAVSEK 132

RESULT 13

B97755 hypothetical protein RC0442 [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001

C:Accession: B97755

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; PMID:21442074; PMID:11557893

A:Accession: B97755

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-339 <KUR>

A:Cross-references: GB:AE006914; PIDN:AAL02980.1; PID:g15619513; GSPDB:GN00173

C:Genetics:

A:Gene: RC0442

C:Superfamily: yceG protein

Query Match 46.7%; Score 42; DB 2; Length 339;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 PSIOSLDALVKEK 19

Db 276 PSLKSLAVVKS 289

RESULT 14

T41207

hypothetical protein SPCC1902.02 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T41207

R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21928

A:Accession: T41207

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-574 <SEE>

A:Cross-references: EMBL:AL049521; PIDN:CAB40004.1; GSPDB:GN00068; SPDB:SPCC1902.02

A:Experimental source: strain 972h-; cosmid c1902

C:Genetics:
A:Gene: SPCC663.16c; SPDB:SPCC1902.02

A:Map position: 3

A:Introns: 14/1; 68/1

Query Match 46.7%; Score 42; DB 2; Length 574;
Best Local Similarity 40.0%; Pred. No. 89;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 EVMPSIOSLDALVKE 17

Db 90 KILPSVYNLDTAIKE 104

RESULT 15

AC2477 hypothetical protein all5371 [imported] - Anabaena sp. (strain PCC 7120)

C:Species: Anabaena sp.

A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002

C:Accession: AC2477

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.;

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; PMID:21595285; PMID:11759840

A:Accession: AC2477

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA877070.1; PID:g17134510; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all5371

Query Match 45.6%; Score 41; DB 2; Length 130;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKE 17

Db 52 KEVMASPGELDPLVRE 67

Search completed: September 4, 2002, 16:47:35

Job time: 371 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:37 ; Search time 124.34 Seconds
(without alignments)
26.435 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90

Sequence: 1 KKEYMPSIQSLDALVKEKK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL_19.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	54.4	592	5 Q9VZW4	Q9VZW4 drosophila
2	47	52.2	2895	10 O65551	O65551 arabidopsis
3	46	51.1	388	16 Q92P38	Q92P38 rhizobium m
4	45	50.0	430	16 O25052	O25052 helicobacte
5	45	50.0	431	16 Q92MG0	Q92MG0 helicobacte
6	45	50.0	1712	5 Q9VS99	Q9VS99 drosophila
7	45	50.0	1716	5 Q961N2	Q961N2 drosophila
8	45	50.0	1912	5 Q9NGV1	Q9NGV1 drosophila
9	45	50.0	5081	13 O13054	O13054 makaira nig
10	44.5	49.4	1676	10 O23332	O23332 arabidopsis
11	44	48.9	1336	5 Q21216	Q21216 caenorhabdi
12	43	47.8	156	10 Q9LJV3	Q9LJV3 arabidopsis
13	43	47.8	283	4 Q9NSK3	Q9NSK3 homo sapien
14	43	47.8	489	4 Q9BR76	Q9BR76 homo sapien
15	43	47.8	4869	13 Q90985	Q90985 gallus gall
16	42.5	47.2	299	3 Q9UVK3	Q9UVK3 candida alb

ALIGNMENTS

RESULT 1

Q9VZW4	Q9VZW4	PRELIMINARY;	PRT;	592 AA.
ID	Q9VZW4;			
AC	Q9VZW4;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	CG2077 PROTEIN.			
GN	CG2077.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY.			
RX	MEDLINE=20196006; PubMed=10731132;			
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wap K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
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RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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Rajasekharan V., Rasmussen K.A., Nixon K., Nusskern D.R., Reese M.G.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*";
Science 287:2185-2195(2000).
EMBL; AF003476; AAF47701.1; -.
FlyBase; FBgn0035386; CG2077.
InterPro; IPR001454; Hydrolase.
Pfam; PF00702; Hydrolase; 2.
SEQUENCE 592 AA; 65213 MW; 56DE69C300F978E7 CRC64;

Query Match 54.4%; Score 49; DB 5; Length 592;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KKEVMPISQSLDALVLEKK 19
| : : | : : | : |||
Db 93 KNEILSSVQTAKFMKEK 111

RESULT 2
O6551 PRELIMINARY; PRT; 2895 AA.

ID O6551;
AC O6551;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 326.6 KDA PROTEIN.
GN F6118_100 OR ATAG30990.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptocytia; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Benes V., Rechmann S., Borkova D., Ansoerge W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL022198; CAAL18194.1; -.
DR EMBL; AL161578; CAB79817.1; -.
DR InterPro; IPR000408; RCC1.
DR PROSITE; PS00626; RCC1_2; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 2895 AA; 326599 MW; EF4A600A4378A01E CRC64;

Query Match 52.2%; Score 47; DB 10; Length 2895;
Best Local Similarity 38.9%; Pred. No. 1.4e+02;
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

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RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RL pylori.";
DR Nature 388:539-547(1997).
DR EMBL: AE000546; AAD07339.1; -.
DR TIGR: HF0275; -.
DR InterPro: IPR002885; PPR.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 430 AA; 49684 MW; E702669D4297A52C CRC64;

Query Match 50.0%; Score 45; DB 16; Length 430;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KKEVMPISQSLDALVKEKK 19
Db 313 KEEMLP1QKLEQATKERQ 331
|:::| | | |:::|

RESULT 5
Q92MG0 PRELIMINARY; PRT; 431 AA.
AC Q92MG0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE.
GN JHP0260.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RA "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
DR EMBL: AE001463; AAD05839.1; -.
DR InterPro: IPR002885; PPR.
KW Complete proteome.
SQ SEQUENCE 431 AA; 49895 MW; E4095C519A52DAC CRC64;

Query Match 50.0%; Score 45; DB 16; Length 431;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KKEVMPISQSLDALVKEKK 19
Db 314 KEEMLP1QKLEQATKERQ 332
|:::| | | |:::|

RESULT 6
Q9VS99 PRELIMINARY; PRT; 1712 AA.
AC Q9VS99;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE SP2523 PROTEIN.
GN SP2523 OR CG7493.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;

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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003558; AAF50528.2; -.
DR FLYBase: FBgn0035808; SP2523.
SQ SEQUENCE 1712 AA; 187520 MW; 35D189F958AAE030 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1712;
Best Local Similarity 45.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 8; Mismatches 1; Indels 2; Gaps 1;

Qy 1 KKEVMPISQSLDALVKEKK 18
Db 1450 RTEVVPSSQVESIEALLKQK 1469
|:::| |:::| |:::|

RESULT 7
Q961N2 PRELIMINARY; PRT; 1716 AA.
ID Q961N2
AC Q961N2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GH14650P.
GN SP2523.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;

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RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051490; AAK92914.1; -
SQ SEQUENCE 1716 AA; 187955 MW; 63ACE8D1339E5396 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1716;
Best Local Similarity 45.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 8; Mismatches 1; Indels 2; Gaps 1;

QY 1 KKEVMP--IQSLDALVKEK 18
: ||:| :|:|:|:|:|
Db 1454 RTEVVPSSQVESIEALLKQK 1473

RESULT 8
Q9NGV1 PRELIMINARY; PRT; 1912 AA.
AC Q9NGV1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE SP2523.
GN SP2523 OR CG7493.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOPLASMIC RETICULUM;
RA Serano T.L., Pendleton J.D., Rubin G.M.;
RT "A reverse genetic screen for genes involved in Drosophila
RT development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF239611; AAF63503.1; -
DR FlyBase; FBgn0035808; SP2523.
SQ SEQUENCE 1912 AA; 209847 MW; 5B124A6961B58C71 CRC64;

Query Match 50.0%; Score 45; DB 5; Length 1912;
Best Local Similarity 45.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 8; Mismatches 1; Indels 2; Gaps 1;

QY 1 KKEVMP--IQSLDALVKEK 18
: ||:| :|:|:|:|:|
Db 1650 RTEVVPSSQVESIEALLKQK 1669

RESULT 9
O13054 PRELIMINARY; PRT; 5081 AA.
AC O13054;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RYANODINE RECEPTOR RYR1 ISOFORM.
GN RYR1.
OS Makaira nigricans (Blue marlin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Xiphiidae; Makaira.
OX NCBI_TaxID=13604;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA Franck J.P.C., Keen J.E., Londraville R.L., Morrisette J.,

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RA Beamsley M., Block B.A.;
RT "Cloning and characterization of fiber type-specific ryanodine
RT receptor isoforms in skeletal muscles of fish (Makaira nigricans).";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97329; AAB58117.1; -
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001682; Channel_pore_Ca_Na.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR003608; MIR.
DR InterPro; IPR001215; Ryanodn_receptor.
DR InterPro; IPR000699; RYDR_ITPR.
DR InterPro; IPR003032; RYR.
DR InterPro; IPR003877; SPRY.
DR InterPro; IPR003878; SPRY_domain.
DR Pfam; PF00520; ion_trans; 1.
DR Pfam; PF02815; MIR; 4.
DR Pfam; PF01365; RYDR_ITPR; 2.
DR Pfam; PF02026; RYR; 4.
DR Pfam; PF00622; SPRY; 3.
DR PRINTS; PR00795; RYANODINER.
DR SMART; SM00472; MIR; 4.
DR SMART; SM00449; SPRY; 3.
KW Receptor.
SQ SEQUENCE 5081 AA; 576220 MW; 5A3D7E253CFEC09B CRC64;

Query Match 50.0%; Score 45; DB 13; Length 5081;
Best Local Similarity 56.2%; Pred. No. 5.2e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKE 17
:|:|:|:|:|:|
Db 3277 QELCPDIPELDALLKE 3292

RESULT 10
O23332 PRELIMINARY; PRT; 1676 AA.
AC O23332;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CENTROMERE PROTEIN HOMOLOG.
GN AT4G14760.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98121113; PubMed-9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.,
RA Wedler E., Wambutt R., Weitzenecker T., Pohl T.M., Terryn N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
RA Silvey M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
RA Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansoorge W., Cooke R., Berger C.,
RA Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
RA Schueller C., Chalwatzis N.;
RT "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT Arabidopsis thaliana."
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97337; CAB10255.1; -

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DR EMBL; ALJ161539; CAB78518.1; -;
SQ SEQUENCE 1676 AA; 192957 MW; FEC783B8A2A047E0 CRC64;

Query Match 49.4%; Score 44.5; DB 10; Length 1676;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 KEVMPISQSLD-ALVKEK 18
||: |||:::| ||||
Db 1356 KEINPSIKTIQAPVKEK 1373

RESULT 11

Q21216 Q21216 PRELIMINARY; PRT; 1336 AA.
AC Q21216;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE K04D7.5 PROTEIN.
GN K04D7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wild A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RS [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RT Science 282:2012-2018(1998).
DR EMBL; Z69664; CAA93515.1; -;
DR InterPro; IPR001552; Acyl-CoA-dh.
DR PROSITE; PS00073; ACYL-CoA-DH_2; UNKNOWN_1.
SQ SEQUENCE 1336 AA; 152551 MW; 07057CE0B4A3F51B CRC64;

Query Match 48.9%; Score 44; DB 5; Length 1336;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDAL 14
: ||: ||| | | | | |
Db 759 EKELMPSTSSIDSL 772

RESULT 12

O9LJV3 O9LJV3 PRELIMINARY; PRT; 156 AA.
AC O9LJV3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GB|AAC69115.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;

RX MEDLINE=203363099; PubMed=10907853;
RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety P1,
TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000389; BAB01424.1; -;
SQ SEQUENCE 156 AA; 17854 MW; FCPEC18EF009588E CRC64;

Query Match 47.8%; Score 43; DB 10; Length 156;
Best Local Similarity 47.4%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KKEVMPISQSLDALVKEK 19
| || |:::| | || | |
Db 88 KSEVAVELEALQAMVKEK 106

RESULT 13

Q9NSK3 Q9NSK3 PRELIMINARY; PRT; 283 AA.
AC Q9NSK3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE HYPOTHETICAL 31.4 KDA PROTEIN (FRAGMENT).
GN DKFZP7621166.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MELANOMA (MEWO CELL LINE);
RA Bloecher H., Boeher M., Brandt P., Mewes H.W., Weill B., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL162072; CAB82408.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 283 AA; 31436 MW; 3E33782A2086E9EE CRC64;

Query Match 47.8%; Score 43; DB 4; Length 283;
Best Local Similarity 52.9%; Pred. No. 56;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEK 18
: ||| |:::| | || | |
Db 248 EEVMOELRALVKEQ 264

RESULT 14

O9BR76 O9BR76 PRELIMINARY; PRT; 489 AA.
AC O9BR76;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO CORONIN, ACTIN BINDING PROTEIN 1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA, CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; BC006449; AAH06449.1; -;
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:03 ; Search time 158.52 Seconds
(without alignments)
7.708 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	91.7	185	20	AAW99667 Human secreted pro
2	55	91.7	185	21	AAW99667 Human PRO1005 prot
3	55	91.7	185	21	AAW99667 Human signal pepti
4	55	91.7	185	21	AAW99667 Membrane-bound pro
5	55	91.7	185	22	AAW99667 Human PRO1005 (UNQ
6	55	91.7	185	22	AAW99667 Human PRO1005 prot
7	55	91.7	186	21	AAW99667 Human secreted pro
8	55	91.7	194	19	AAW99667 Cancer associated
9	55	91.7	194	20	AAW99667 Human ovarian tumo
10	41	68.3	971	22	ABW63836 Drosophila melanog
11	39	65.0	55	21	AAG22477 Arabidopsis thalia

12	39	65.0	55	21	AAG50024 Arabidopsis thalia
13	39	65.0	107	21	AAG22475 Arabidopsis thalia
14	39	65.0	107	21	AAG50022 Arabidopsis thalia
15	39	65.0	131	22	AAW25898 Human protein sequ
16	38	63.3	86	18	AAW20389 H. pylori secreted
17	38	63.3	87	18	AAW20389 H. pylori secreted
18	38	63.3	126	22	AAW20941 Human polypeptide
19	37	61.7	141	22	AAW20941 Human polypeptide
20	37	61.7	141	22	ABG15727 Novel human diago
21	36	60.0	173	20	ABG15727 Drosophila melanog
22	36	60.0	278	22	ABG15727 Feline B7-1S prote
23	36	60.0	292	21	ABG15727 Novel human diago
24	36	60.0	292	21	ABG15727 Feline CD80 (B7-1)
25	36	60.0	292	21	ABG15727 Feline CD80 (B7-1)
26	36	60.0	292	21	ABG15727 Cat CD80 (B7-1)-TA
27	36	60.0	464	22	ABG15727 Cat CD80 (B7-1)-SY
28	35	58.3	66	20	AAW48396 Drosophila melanog
29	35	58.3	128	22	ABG19787 Human prostate can
30	35	58.3	143	22	ABG25406 Novel human diago
31	35	58.3	147	22	ABG25406 Novel human diago
32	35	58.3	152	22	ABG25394 Novel human diago
33	35	58.3	154	21	AAW09759 Arabidopsis thalia
34	35	58.3	161	22	ABW60927 Drosophila melanog
35	35	58.3	170	22	ABG15075 Novel human diago
36	35	58.3	173	21	AAW35515 C. albicans caplin
37	35	58.3	173	21	AAW35515 N-terminal RNA tri
38	35	58.3	174	21	AAW09758 Arabidopsis thalia
39	35	58.3	235	20	AAW41077 Canine B7-1S prote
40	35	58.3	304	20	AAW41075 Canine B7-1 protei
41	35	58.3	336	13	AAW25116 Non-A, Non-B Hepat
42	35	58.3	385	22	ABG00660 Novel human diago
43	35	58.3	390	22	ABG01405 Novel human diago
44	35	58.3	492	22	ABG11879 Novel human diago
45	35	58.3	581	22	ABG24148 Novel human diago

ALIGNMENTS

RESULT 1

AAW99667 ID AAW99667 standard; Protein; 185 AA.
AC AAW99667;

DT 07-JUN-1999 (first entry)

XX Human secreted protein clone ej90_5 protein.

XX Human; secreted protein; nutritional; cytokine; cell proliferation;
XX differentiation; immune stimulating; vaccine; haematopoiesis regulation;
XX tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
XX anti-inflammatory; cadherin; tumour invasion suppressor;
XX tumour inhibition; gene therapy.

XX Homo sapiens.

XX WO9907840-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16318.

XX 04-AUG-1998; 98US-0130189.

XX 06-AUG-1997; 97US-0906708.

XX (GEM) GENETICS INST INC.

XX Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

XX Merberg D, Racie LA, Steining RJ, Treacy M;

XX WPI; 1999-167419/14.

XX N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
PS Claim 34; Page 98-99; 107pp; English.
XX
CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
SQ Sequence 185 AA;

Query Match 91.7%; Score 55; DB 20; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
| | | | | | | | | |
Db 78 kktctvkhmkk 88

RESULT 2
ID AAB24067 standard; Protein; 185 AA.
XX
AC AAB24067;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1005 protein sequence SEQ ID NO:34.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotrophic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; gliad disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
XX WO200053755-A2.
XX
PD 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99WO-US05028.
XX
PR 02-JUN-1999; 99WO-US12252.
XX
PR 23-JUN-1999; 99US-0141037.
XX
PR 07-JUL-1999; 99US-0143048.
XX
PR 26-JUL-1999; 99US-0145698.
XX
PR 30-NOV-1999; 99WO-US28313.
XX
PR 20-DEC-1999; 99WO-US30911.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX

DR WPI; 2000-572270/53.
XX N-PSDB; AAC58377.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
PS Claim 61; Fig 22; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, cell
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC carcinomas, sarcomas, glioblastomas, other disorders such as neuronal,
CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC gliad, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoele disorders, and inflammatory.
CC CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 185 AA;

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
| | | | | | | | | |
Db 78 kktctvkhmkk 88

RESULT 3
ID AAY87272 standard; Protein; 185 AA.
XX
AC AAY87272;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
XX
KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neurotrophic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
OS Homo sapiens.
XX
XX WO200000610-A2.
XX
PD 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1999; 98US-0090762.
XX

PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang WT, Gorgone CA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR N-PSDB; AA298157.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
PS Claim 1; Page 193-194; 327pp; English.
XX
CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins Hspp-1 to Hspp-134. Hspps have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can
CC be used in gene therapy. Hspps can be used to treat or prevent disorders
CC associated with decreased activity or function of Hspp. Antagonists of
CC Hspp are used to treat or prevent disorders associated with increased
CC activity or function of Hspp. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). Hspp
CC nucleic acids can be used for the recombinant production of Hspp, for
CC detecting Hspp in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. Hspp are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, Hspp-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of Hspp
CC from natural sources.
XX
SQ Sequence 185 AA;

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Preq. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
| | | | | | | |
Db 78 kktctivhkmk 88

RESULT 4
AAY66686
ID AAY66686 standard; protein; 185 AA.
XX
AC AAY66686;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PR01005.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
KW
XX Homo sapiens.
OS
XX WO9963088-A2.
PN
XX

PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088455.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.

PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091513.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 11-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098025.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
PR (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
PI
PI
a XX

DR WPI; 2000-072883/06.
DR N-PSDB; AAZ65023.
XX
XX Membrane-bound proteins and related nucleotide sequences -
PT
XX
XX claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 185 AA;
SQ

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
Db 78 kktctvHKMKK 88

RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
AC AAB65209;
XX
XX 02-APR-2001 (first entry)
XX Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
DE
XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
XX WO2000073454-A1.
PN
XX
PD 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US08439.
PF
XX
XX 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR	18-FEB-2000; 2000WO-US04341.
PR	22-FEB-2000; 2000WO-US04414.
PR	24-FEB-2000; 2000WO-US04914.
PR	24-FEB-2000; 2000WO-US05004.
PR	02-MAR-2000; 2000WO-US05841.
PR	15-MAR-2000; 2000WO-US06884.
PR	20-MAR-2000; 2000WO-US07377.
XX	(GETH) GENENTECH INC.
PA	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX	Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI	Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI	Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI	Zhang Z;
XX	
DR	WPI; 2001-032160/04.
DR	N-PSDB; AAF44169.
XX	
XX	PRO polynucleotides used to produce polypeptides used to target
PT	bioactive molecules such as toxins, radiolabels or antibodies, to
PT	specific cells, to cause targeted cell death -
XX	
PS	Claim 12; Fig 139; 935pp; English.
XX	
CC	The present invention describes human secreted and transmembrane PRO
CC	proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC	can be used for targeted delivery of bioactive molecules, such as
CC	toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC	sequences, and their fragments, can be used as hybridisation probes, in
CC	chromosomal and gene mapping, and in the generation of anti-sense RNA
CC	and DNA. They may also be used to produce transgenic animals which are
CC	used to develop and screen therapeutically useful reagents. The PRO
CC	nucleotide and protein sequence can be used for tissue typing and in
CC	treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC	AAAF44270 to AAFA44470 represent PCR primers and hybridisation probes used
CC	in the isolation of human PRO sequences. AAFA44087 to AAFA44269 and
CC	AAAB65134 to AAAB65300 represent human PRO polynucleotide and protein
CC	sequences given in the exemplification of the present invention..
XX	
SQ	Sequence 185 AA;
	Query Match 91.7%; Score 55; DB 22; Length 185;
	Best Local Similarity 90.9%; Pred. No. 0.12;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 KKTCTVHKMKK 11
Db	78 kktctivhkmmk 88
RESULT	6
AAAB50957	ID
XX	AAAB50957 standard; Protein; 185 AA.
AC	AAAB50957;
XX	
DT	21-MAR-2001 (first entry)
XX	
DE	Human PRO1005 protein.
XX	
KW	Human; PRO; cytostatic; neutropic; neuroprotective; respiratory general;
KW	antiflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW	PRO agonist; cancer; inflammatory disorder; immunological disorder..
OS	Homo sapiens.
XX	
PD	WO200073348-A2.
XX	
PD	07-DEC-2000.
XX	
PF	30-MAY-2000; 2000WO-US14941.

KW nootropic; antibacterial; virucide; fungicide; fungicide; ophthalmological; human;
 KW vulnery; gene therapy; infection; secreted protein.

OS Homo sapiens.

PN WO200061623-A1.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-US08979.

XX 09-APR-1999; 99US-0128693.

PR 26-APR-1999; 99US-0130991.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;

XX WPI; 2000-647418/52.

XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -

XX Claim 11; Page 598; 716pp; English.

XX Sequences AAB39321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.

XX Sequence 186 AA;

Query Match 91.7%; Score 55; DB 21; Length 186;

Best Local Similarity 90.9%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMK 11

|||||||

Db 78 kktctvkhmk 88

RESULT 8

AAW69974

ID AAW69974 standard; Protein; 194 AA.

XX AAW69974;

XX 16-NOV-1998 (first entry)

XX Cancer associated protein.

XX Cancer; PCR; Northern blotting; ribonuclease protection assay;

XX diagnosis; metastatic cancer.

XX Synthetic.

XX

PN WO9837187-A1.

XX 27-AUG-1998.

XX 18-FEB-1998; 98WO-JP00667.

XX 21-FEB-1997; 97JP-0052508.

XX (TAKI) TAKARA SHUZO CO LTD.

XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;

XX WPI; 1998-467552/40.

XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences

XX Claim 14; Page 64-65; 92pp; Japanese.

XX The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.

XX Sequence 194 AA;

Query Match 91.7%; Score 55; DB 19; Length 194;

Best Local Similarity 90.9%; Pred. No. 0.13;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMK 11

|||||||

Db 87 kktctvkhmk 97

RESULT 9

AAW76591

ID AAW76591 standard; Protein; 194 AA.

XX AAW76591;

XX 10-APR-2000 (first entry)

XX Human ovarian tumor EST fragment encoded protein 87.

XX Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.

XX Homo sapiens.

XX DE19817557-A1.

XX 21-OCT-1999.

XX 09-APR-1998; 98DE-1017557.

XX 09-APR-1998; 98DE-1017557.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX

DR WPI; 1999-591920/51.
 DR N-PSDB; AAZ77487.
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents.
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-Z77572.
 XX
 SQ Sequence 194 AA;

Query Match 91.7%; Score 55; DB 20; Length 194;
 Best Local Similarity 90.9%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKK 11
 |||||
 Db 87 kktctvhhmmk 97

RESULT 10
 ABB63836
 ID ABB63836 standard; Protein; 971 AA.
 AC ABB63836;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 18300.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07939.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX
 PS Disclosure; SEQ ID NO 18300; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 971 AA;

Query Match 68.3%; Score 41; DB 22; Length 971;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMKK 11
 |||||
 Db 942 kttcavhmkq 952

RESULT 11
 AAG22477
 ID AAG22477 standard; Protein; 55 AA.
 XX
 AC AAG22477;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 25420.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 XX
 PN EPI033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
 PR 05-MAY-1999; 99US-0132484.
 PR 06-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 11-MAY-1999; 99US-0132863.
 PR 14-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.

PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	14-JUN-1999;	99US-0138847.
PR	16-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	17-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	24-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	23-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	22-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0156559.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.

PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.0%; Score 39; DB 21; Length 55;

Best Local Similarity 70.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 10

Db 7 kkcctfhkqk 16

RESULT 12

AAG50024

ID AAG50024 standard; Protein; 55 AA.

XX AC AAG50024;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 63347.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 28-APR-1999; 99US-0130891.

XX PR 30-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 04-MAY-1999; 99US-0132407.

XX PR 05-MAY-1999; 99US-0132484.

XX PR 06-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 07-MAY-1999; 99US-0132487.

XX PR 11-MAY-1999; 99US-0132863.

XX PR 14-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 18-MAY-1999; 99US-0134370.

XX PR 19-MAY-1999; 99US-0134768.

XX PR 20-MAY-1999; 99US-0134941.

XX PR 21-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139452.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
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PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
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PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match

Best local Similarity 65.0%; Score 39; DB 21; Length 55;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	KKTCIVHKMK	10
Db	7	kkccifhkqk	16

RESULT 13

AAG22475

ID AAG22475 standard; Protein; 107 AA.

XX AC AAG22475;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 25418.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

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PR 29-MAR-1999; 99US-0126785.

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PR 30-AUG-1999; 99US-0151303.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 29-SEP-1999; 99US-0156596.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

65.0%; Score 39; DB 21; Length 107;

Best Local Similarity 70.0%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 10
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Db 59 kkecfhkqk 68

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ID AAG50022 standard; Protein; 107 AA.

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AC AAG50022;

XX
DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 63345.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 65.0%; Score 39; DB 21; Length 107;
 Best Local Similarity 70.0%; Pred No. 31;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 10
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 Db 59 kkcctfkhkqk 68

RESULT 15

AAH25898
 ID AAH25898 standard; Protein; 131 AA.
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 AC AAH25898;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:1413.
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 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnery; antulcer; osteopathic; eczema;
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200153455-A2.
 XX
 PD 26-JUL-2001.
 XX
 XX 22-DEC-2000; 2000WO-US35017.
 XX
 PF 23-DEC-1999; 99US-0471275.
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI: 2001-457603/49.
 DR N-PSDB; AAH99839.
 XX
 PT Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
 XX
 PS Claim 20; Page 287; 1217pp: English.
 XX
 CC AAH99166 to AAH99904 encode the human proteins given in AAH25225 to
 CC AAH25963. The proteins can have activities based on the tissues and
 CC cells they are expressed in, such as: antinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
 CC antulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
 CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 CC encoding them can be used in gene therapy, antisense therapy and vaccine
 CC production. The proteins and polynucleotides are useful for screening for
 CC agonists or antagonists of a protein and for the treatment and diagnosis
 CC of disorders associated with the activity of a protein e.g. inflammation,
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 CC neurological disorders.
 XX
 XX Sequence 131 AA;

Query Match 65.0%; Score 39; DB 22; Length 131;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 10
: : : : :
Db 84 eetcfihkik 93

Search completed: September 4, 2002, 16:45:03
Job time: 379 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:07 ; Search time 57.74 Seconds
(without alignments)
4.653 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTICIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	58.3	173	3	US-09-188-579-87
2	35	58.3	173	4	US-09-315-444-87
3	34	56.7	516	3	US-08-948-564-12
4	33	55.0	399	2	US-08-742-621-3
5	33	55.0	399	2	US-08-750-134A-11
6	33	55.0	399	4	US-09-363-745-11
7	33	55.0	410	4	US-09-106-075A-88
8	33	55.0	479	4	US-09-004-838-41
9	33	55.0	483	4	US-09-004-838-117
10	33	55.0	768	1	US-08-454-455-4
11	33	55.0	1140	2	US-08-657-641-7
12	33	55.0	1140	5	PCT-US94-07233-7
13	33	55.0	1366	4	US-09-004-838-22
14	33	55.0	1890	4	US-09-004-838-88
15	32	53.3	27	4	US-09-345-468-21
16	32	53.3	50	4	US-09-052-089A-15
17	32	53.3	292	4	US-09-345-468-18
18	32	53.3	313	4	US-09-345-468-16
19	32	53.3	381	2	US-08-867-057-1
20	32	53.3	381	2	US-08-867-057-3
21	32	53.3	381	2	US-09-128-369-1
22	32	53.3	381	2	US-09-128-369-3
23	32	53.3	419	4	US-09-011-197-4
24	32	53.3	826	1	US-07-638-431-2
25	32	53.3	826	5	PCT-US92-00018-2
26	31.5	52.5	457	1	US-08-416-478A-8
27	31.5	52.5	457	2	US-08-474-988B-8

ALIGNMENTS

RESULT 1

US-09-188-579-87
; Sequence 87, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase
; OTHER INFORMATION: domain of the capping enzyme.
US-09-188-579-87

Query Match 58.3%; Score 35; DB 3; Length 173;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CIVHKMK 10
||| |||

Db 82 CIVHKMK 88
||| |||

RESULT 2

US-09-315-444-87
; Sequence 87, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 87
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of N-terminal RNA triphosphatase
; OTHER INFORMATION: domain of the capping enzyme.
US-09-315-444-87

US-09-315-444-87

Query Match 58.3%; Score 35; DB 4; Length 173;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CIVHKMK 10
II IIII
DB 82 CIYHKMK 88

RESULT 3

US-08-948-564-12
; Sequence 12, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Siminsky, Balazs
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; METHODS OF PRODUCING Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512th Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-948-564-12

Query Match 56.7%; Score 34; DB 3; Length 516;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTClVH 7
II IIII
DB 126 KKLClVH 132

RESULT 4

US-08-742-621-3
; Sequence 3, Application US/08742621
; Patent No. 5856129
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: COLEMAN, ROGER
; TITLE OF INVENTION: NOVEL HUMAN PURINOCEPTOR
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,621
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0147 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 166438
US-08-742-621-3

Query Match 55.0%; Score 33; DB 2; Length 399;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8
III: II
DB 215 KTCIVHK 221

RESULT 5

US-08-750-134A-11
; Sequence 11, Application US/08750134A
; Patent No. 5985603
; GENERAL INFORMATION:
; APPLICANT: VALERA, SOLEDAD
; APPLICANT: BUELL, GARY
; TITLE OF INVENTION: P2X RECEPTORS (PURINOCEPTOR FAMILY)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,134A
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:

NAME: CRAWFORD, ARTHUR C.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1430-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4006
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-750-134A-11

Query Match 55.0%; Score 33; DB 2; Length 399;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8
 |||: ||
 Db 215 KTCLEPHK 221

RESULT 6

US-09-363-745-11
 Sequence 11, Application US/09363745
 Patent No. 6194162

GENERAL INFORMATION:
 APPLICANT: VALERA, SOLEDAD
 APPLICANT: BUELL, GARY
 TITLE OF INVENTION: P2x RECEPTORS (PURINOCEPTOR FAMILY)
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/363,745
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/750,134
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAWFORD, ARTHUR C.
 REGISTRATION NUMBER: 25,327
 REFERENCE/DOCKET NUMBER: 1430-116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4006
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 399 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-363-745-11

Query Match 55.0%; Score 33; DB 4; Length 399;
 Best Local Similarity 71.4%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHK 8

Db 215 KTCLEPHK 221
 |||: ||

RESULT 7

US-09-106-075A-88
 Sequence 88, Application US/09106075A
 Patent No. 6316250

GENERAL INFORMATION:
 APPLICANT: Hjelle MD, Brian
 APPLICANT: Jenison, Steve
 TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
 TITLE OF INVENTION: the HARDS Virus.
 FILE REFERENCE: 10312-8UL, Hjelle et al. (210312.0009)
 CURRENT APPLICATION NUMBER: US/09/106,075A
 CURRENT FILING DATE: 1998-06-29
 PRIOR APPLICATION NUMBER: 08/210,762
 PRIOR FILING DATE: 1994-03-22
 PRIOR APPLICATION NUMBER: 08/141,035
 PRIOR FILING DATE: 1993-10-26
 PRIOR APPLICATION NUMBER: 08/120,096
 PRIOR FILING DATE: 1993-09-13
 PRIOR APPLICATION NUMBER: 08/111,519
 PRIOR FILING DATE: 1993-08-25
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 88
 LENGTH: 410
 TYPE: PRT

ORGANISM: Four Corners hantavirus
 US-09-106-075A-88

Query Match 55.0%; Score 33; DB 4; Length 410;
 Best Local Similarity 55.6%; Pred. No. 3.1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMK 11
 |||: |||:
 Db 376 TCVNKKVOK 384

RESULT 8

US-09-004-838-41
 Sequence 41, Application US/09004838
 Patent No. 6350933

GENERAL INFORMATION:
 APPLICANT: Michelmore, Richard W.
 APPLICANT: Shen, Kathy
 APPLICANT: Meyers, Blake
 TITLE OF INVENTION: Procedures and Materials for
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/004,838
 FILING DATE: 09-JAN-1998
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/781,734
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:

```

; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 479 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..479
; OTHER INFORMATION: /note= "RLG2A protein"
US-09-004-838-41

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Query Match 55.0%; Score 33; DB 4; Length 479;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY 2 KTCIVHKMK 11
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Db 2 KTTMHRLKK 11

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RESULT 9
US-09-004-838-117
; Sequence 117, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Micheltore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; FEATURE:
; NAME/KEY: -
; LOCATION: 1..483
; OTHER INFORMATION: /note= "RG2N deduced sequence"
US-09-004-838-117

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Query Match 55.0%; Score 33; DB 4; Length 483;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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```

QY 2 KTCIVHKMK 11
|| :||:|
Db 3 KTTMHRLKK 12

```

```

RESULT 10
US-08-454-455-4
; Sequence 4, Application US/08454455
; Patent No. 5635601
; GENERAL INFORMATION:
; APPLICANT: Moyle, Matthew
; APPLICANT: McLean, John W.
; TITLE OF INVENTION: NOVEL BETA INTEGRIN SUBUNIT
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,455
; FILING DATE: 30-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193989
; FILING DATE: 09-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004142
; FILING DATE: 13-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670607
; FILING DATE: 14-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0699C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-454-455-4

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Query Match 55.0%; Score 33; DB 1; Length 768;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 4 CIVHKMK 10
|:||||
Db 531 CLCHKMK 537

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RESULT 11
US-08-657-641-7
; Sequence 7, Application US/08657641
; Patent No. 5945277
; GENERAL INFORMATION:
; APPLICANT: Nichol, Stuart T.
; APPLICANT: Spiropoulos, Christina F.
; APPLICANT: Ksiazek, Thomas G.
; APPLICANT: Rollin, Pierre E.
; TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: REAGENTS FOR DETECTION AND PREVENTION OF INFECTION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Candler Building
; STREET: 127 Peachtree Street, NE
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,641
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,591
; FILING DATE: 07-OCT-1993
; APPLICATION NUMBER: US 1414,074
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perryman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414,089
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hantavirus
; STRAIN: New
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M Segment
; UNITS: 1140 AA
US-08-657-641-7

Query Match 55.0%; Score 33; DB 2; Length 1140;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11
||:|:|:|
Db 408 TCLVKNVQK 416

RESULT 12
PCT-US94-07233-7
; Sequence 7, Application PC/TUS9407233

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS AND REAGENTS FOR DETECT
; NUMBER OF SEQUENCES: 12
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07233
; FILING DATE: 24-JUN-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,724
; FILING DATE: 24-JUN-1993
; APPLICATION NUMBER: US 08/591,133
; FILING DATE: 07-OCT-1993
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hantavirus
; STRAIN: New
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: M Segment
; UNITS: 1140 AA
PCT-US94-07233-7

Query Match 55.0%; Score 33; DB 5; Length 1140;
Best Local Similarity 55.6%; Pred. No. 7.4e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11
||:|:|:|
Db 408 TCLVKNVQK 416

RESULT 13
US-09-004-838-22
; Sequence 22, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734

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; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY:
; LOCATION: 1..1366
; OTHER INFORMATION: /note= "RLG2A amino acids"
US-09-004-838-22

Query Match 55.0%; Score 33; DB 4; Length 1366;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
Db 185 KTTMHRLKK 194

RESULT 14
US-09-004-838-88
; Sequence 88, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1890 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY:
; LOCATION: 1..1890
; OTHER INFORMATION: /note= "RG2A deduced sequence"
US-09-004-838-88

Query Match 55.0%; Score 33; DB 4; Length 1890;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
Db 185 KTTMHRLKK 194

RESULT 15
US-09-345-468-21
; Sequence 21, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevial, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-21

Query Match 53.3%; Score 32; DB 4; Length 27;
Best Local Similarity 40.0%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTICIVHKMK 10
Db 6 RKKCLQHRMR 15

Search completed: September 4, 2002, 16:46:08
Job time: 329 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:20 ; Search time 704.77 Seconds
(without alignments)
5.494 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
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12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
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19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
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24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	60	100.0	11	22	US-09-821-726-4
2	60	100.0	42	22	US-09-821-726-6
3	60	100.0	185	22	US-09-821-726-13
4	56	93.3	185	22	US-09-821-726-18
5	55	91.7	150	13	US-08-906-708-24
6	55	91.7	182	20	US-09-684-524-212
7	55	91.7	182	24	US-10-050-704-212

8	55	91.7	185	1	PCT-US98-16318-18	Sequence 18, Appl
9	55	91.7	185	15	US-09-130-189-18	Sequence 18, Appl
10	55	91.7	185	20	US-09-684-524-105	Sequence 105, App
11	55	91.7	185	21	US-09-709-238-211	Sequence 211, App
12	55	91.7	185	21	US-09-746-783-146	Sequence 146, App
13	55	91.7	185	23	US-09-941-992-211	Sequence 211, App
14	55	91.7	185	23	US-09-989-279-211	Sequence 211, App
15	55	91.7	185	23	US-09-989-293A-211	Sequence 211, App
16	55	91.7	185	23	US-09-989-721-211	Sequence 211, App
17	55	91.7	185	23	US-09-989-722-211	Sequence 211, App
18	55	91.7	185	23	US-09-989-723-211	Sequence 211, App
19	55	91.7	185	23	US-09-989-724-211	Sequence 211, App
20	55	91.7	185	23	US-09-989-725-211	Sequence 211, App
21	55	91.7	185	23	US-09-989-726-211	Sequence 211, App
22	55	91.7	185	23	US-09-989-727-211	Sequence 211, App
23	55	91.7	185	23	US-09-989-728-211	Sequence 211, App
24	55	91.7	185	23	US-09-989-729A-211	Sequence 211, App
25	55	91.7	185	23	US-09-989-730-211	Sequence 211, App
26	55	91.7	185	23	US-09-989-731-211	Sequence 211, App
27	55	91.7	185	23	US-09-989-732-211	Sequence 211, App
28	55	91.7	185	23	US-09-989-734-211	Sequence 211, App
29	55	91.7	185	23	US-09-989-735-211	Sequence 211, App
30	55	91.7	185	23	US-09-989-862-211	Sequence 211, App
31	55	91.7	185	23	US-09-990-427-211	Sequence 211, App
32	55	91.7	185	23	US-09-990-436-211	Sequence 211, App
33	55	91.7	185	23	US-09-990-437-211	Sequence 211, App
34	55	91.7	185	23	US-09-990-438-211	Sequence 211, App
35	55	91.7	185	23	US-09-990-439-211	Sequence 211, App
36	55	91.7	185	23	US-09-990-440-211	Sequence 211, App
37	55	91.7	185	23	US-09-990-441-211	Sequence 211, App
38	55	91.7	185	23	US-09-990-442-211	Sequence 211, App
39	55	91.7	185	23	US-09-990-443-211	Sequence 211, App
40	55	91.7	185	23	US-09-990-444-211	Sequence 211, App
41	55	91.7	185	23	US-09-990-456-211	Sequence 211, App
42	55	91.7	185	23	US-09-990-562-211	Sequence 211, App
43	55	91.7	185	23	US-09-990-711-211	Sequence 211, App
44	55	91.7	185	23	US-09-990-726-211	Sequence 211, App
45	55	91.7	185	23	US-09-991-073-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-4
; Sequence 4, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-4

Query Match 100.0%; Score 60; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKTCTIVHKMKK 11
Db 1 KKTCTIVHKMKK 11

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RESULT 2
US-09-821-726-6
; Sequence 6, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-6

Query Match          100.0%; Score 60; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
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Db 1 KKTCTIVHKMKK 11

RESULT 3
US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match          100.0%; Score 60; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
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Db 78 KKTCTIVHKMKK 88

RESULT 4
US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match          93.3%; Score 56; DB 22; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.095;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
   |||||
Db 78 KKTCTIVHKMKK 88

RESULT 5
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-906-708-24

Query Match          91.7%; Score 55; DB 13; Length 150;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
   |||||
Db 78 KKTCTIVHKMKK 88

RESULT 6
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US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match 91.7%; Score 55; DB 20; Length 182;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 7
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 91.7%; Score 55; DB 24; Length 182;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 8
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.

; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 91.7%; Score 55; DB 1; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 9
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 91.7%; Score 55; DB 15; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 10
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1

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; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match          91.7%; Score 55; DB 20; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
Db 78 KKTCTVHKMK 88

RESULT 11
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
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; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKTCTVHKMK 11
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Db 78 KKTCTVHKMK 88

RESULT 12

US-09-746-783-146
; Sequence 146, Application US/09746783
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.
; Howes, Steven H.
; Fechtel, Kim

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

NUMBER OF SEQUENCES: 231

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/746,783

FILING DATE: 21-Dec-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Milasincic, Debra J.

REGISTRATION NUMBER: 46,931

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-09-746-783-146

Query Match 91.7%; Score 55; DB 21; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 78 KKTCTVHKMK 88
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RESULT 13

US-09-941-992-211
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC1
; CURRENT APPLICATION NUMBER: US/09/941,992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 91.7%; Score 55; DB 23; Length 185;
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Db 78 KKTCTVHKMK 88

RESULT 14

US-09-989-279-211

; Sequence 211, Application US/09989279

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090431
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match 91.7%; Score 55; DB 23; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
|||||||
Db 78 KKTCTVHKMK 88

RESULT 15
US-09-989-293A-211
; Sequence 211, Application US/0989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090445

Thu Sep 5 11:23:39 2002

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 91.7%; Score 55; DB 23; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 KKTCTVHKMK 11
Db 78 KKTCTVHKMK 88

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:04:23 ; Search time 166.13 Seconds
(without alignments)
16.284 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 76338 seqs, 245939087 residues

Total number of hits satisfying chosen parameters: 76338

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	91.7	185	5	US-09-991-150-211
2	55	91.7	185	5	US-09-720-533-49
3	55	91.7	185	6	US-10-119-480-148
4	55	91.7	185	6	US-10-216-159A-148
5	55	91.7	185	6	US-10-216-162-148
6	55	91.7	185	6	US-10-216-163-148
7	55	91.7	185	6	US-10-216-164-148
8	55	91.7	185	6	US-10-216-165-148
9	55	91.7	185	6	US-10-216-166-148
10	55	91.7	185	6	US-10-216-167-148
11	55	91.7	185	6	US-10-216-168-148
12	55	91.7	185	6	US-10-216-160-148
13	55	91.7	185	6	US-10-218-849-148
14	55	91.7	185	6	US-10-218-930-148
15	55	91.7	185	6	US-10-219-003-148
16	55	91.7	185	6	US-10-218-612-148
17	55	91.7	185	6	US-10-218-956-148
18	55	91.7	185	6	US-10-219-010-148
19	55	91.7	185	6	US-10-218-765-148
20	55	91.7	185	6	US-10-218-784-148
21	55	91.7	185	6	US-10-219-061-148
22	55	91.7	185	6	US-10-219-062-148
23	55	91.7	185	6	US-10-219-063-148
24	55	91.7	185	6	US-10-219-064-148
25	55	91.7	185	6	US-10-219-065-148
26	55	91.7	185	6	US-10-219-066-148

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27 55 91.7 185 6 US-10-219-070-148 Sequence 148, App
28 55 91.7 185 6 US-10-219-071-148 Sequence 148, App
29 55 91.7 185 6 US-10-219-072-148 Sequence 148, App
30 55 91.7 185 6 US-10-219-073-148 Sequence 148, App
31 55 91.7 185 6 US-10-219-074-148 Sequence 148, App
32 55 91.7 185 6 US-10-219-075-148 Sequence 148, App
33 55 91.7 185 6 US-10-219-076-148 Sequence 148, App
34 55 91.7 185 6 US-10-219-077-148 Sequence 148, App
35 55 91.7 185 6 US-10-219-078-148 Sequence 148, App
36 55 91.7 185 6 US-10-219-079-148 Sequence 148, App
37 55 91.7 185 6 US-10-219-080-148 Sequence 148, App
38 55 91.7 185 6 US-10-219-081-148 Sequence 148, App
39 55 91.7 185 6 US-10-219-082-148 Sequence 148, App
40 55 91.7 185 6 US-10-219-083-148 Sequence 148, App
41 55 91.7 185 6 US-10-219-084-148 Sequence 148, App
42 55 91.7 185 6 US-10-219-085-148 Sequence 148, App
43 55 91.7 185 6 US-10-219-086-148 Sequence 148, App
44 55 91.7 185 6 US-10-219-087-148 Sequence 148, App
45 55 91.7 185 6 US-10-219-088-148 Sequence 148, App

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ALIGNMENTS

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RESULT 1
US-09-991-150-211
; Sequence 211, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: Acids Encoding the Same
; FILE REFERENCE: P2730P1C48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 211
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-211

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Query Match 91.7%; Score 55; DB 5; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KKTCTIVHKMKK 11
Db 78 KKTCTIVHKMKK 88

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RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 91.7%; Score 55; DB 5; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||
Db 78 KKTCTVHKMKK 88

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||
Db 78 KKTCTVHKMKK 88

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11
|||||
Db 78 KKTCTVHKMKK 88

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC2
CURRENT APPLICATION NUMBER: US/10/216.162
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-162-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 6
US-10-216-163-148
Sequence 148, Application US/10216163
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC3
CURRENT APPLICATION NUMBER: US/10/216.163

CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
Db 78 KKTCTIVHKMK 88

RESULT 7
US-10-216-164-148
Sequence 148, Application US/10216164
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC5
CURRENT APPLICATION NUMBER: US/10/216.164
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-164-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
 |||||
 Db 78 KKTCTIVHKMK 88

RESULT 8
 US-10-216-165-148
 ; Sequence 148, Application US/10216165
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3530PIC7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-165-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
 |||||
 Db 78 KKTCTIVHKMK 88

RESULT 9
 US-10-216-166-148
 ; Sequence 148, Application US/10216166
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3530PIC9
 ; CURRENT APPLICATION NUMBER: US/10/216,166
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-166-148

Query Match 91.7%; Score 55; DB 6; Length 185;
 Best Local Similarity 90.9%; Pred. No. 0.075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
 |||||
 Db 78 KKTCTIVHKMK 88

RESULT 10
 US-10-216-167-148
 ; Sequence 148, Application US/10216167
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMK 88

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMK 88

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; Remaining Prior Application data removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMK 88

RESULT 13

US-10-218-849-148

; Sequence 148, Application US/10218849

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3530PIC11

; CURRENT APPLICATION NUMBER: US/10/218,849

; CURRENT FILING DATE: 2002-08-12

; -Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 148

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-218-849-148

Query Match 91.7%; Score 55; DB 6; Length 185;

Best Local Similarity 90.9%; Pred. No. 0.075;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11

| | | | | | | | | |

Db 78 KKTCTVHKMKK 88

RESULT 14

US-10-218-930-148

; Sequence 148, Application US/10218930

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3530PIC13

; CURRENT APPLICATION NUMBER: US/10/218,930

; CURRENT FILING DATE: 2002-08-12

; -Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 148

; LENGTH: 185

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-218-930-148

Query Match 91.7%; Score 55; DB 6; Length 185;

Best Local Similarity 90.9%; Pred. No. 0.075;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKMKK 11

| | | | | | | | | |

Db 78 KKTCTVHKMKK 88

RESULT 15

US-10-219-003-148

; Sequence 148, Application US/10219003

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3530PIC12

; CURRENT APPLICATION NUMBER: US/10/219,003

; CURRENT FILING DATE: 2002-08-12

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/081819

; PRIOR FILING DATE: 1998-04-15

; PRIOR APPLICATION NUMBER: 60/081955

; PRIOR FILING DATE: 1998-04-15

; PRIOR APPLICATION NUMBER: 60/082804

; PRIOR FILING DATE: 1998-04-22

; PRIOR APPLICATION NUMBER: 60/084441

; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/085323

; PRIOR FILING DATE: 1998-05-13

; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/086392

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/089532

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089538

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089905

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/090472

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090557

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: 60/090691

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/090695

; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 91.7%; Score 55; DB 6; Length 185;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
| | | | | | | | | |
Db 78 KKTCTIVHKMKK 88

Search completed: September 4, 2002, 17:04:23

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:31 ; Search time 75.48 Seconds
(without alignments)
14.003 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PTR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	65.0	320	T28379	ORF MSV218 hypothe
2	38	63.3	82	D64699	hypotheical prote
3	38	63.3	86	G71819	hypotheical prote
4	38	63.3	245	H97025	phospholipase C re
5	38	63.3	553	T19894	hypotheical prote
6	37	61.7	389	D96738	hypotheical prote
7	36	60.0	222	T26213	hypotheical prote
8	36	60.0	266	D71675	hypotheical prote
9	36	60.0	399	AC1601	hypotheical prote
10	36	60.0	598	F69792	hypotheical prote
11	36	60.0	671	T10755	hypotheical prote
12	36	60.0	935	T19011	kinasin-related pr
13	36	60.0	2484	T26216	hypotheical prote
14	36	60.0	2607	T26215	hypotheical prote
15	35	58.3	150	F59108	hypotheical prote
16	35	58.3	207	T05289	hypotheical prote
17	35	58.3	247	T40461	hypotheical prote
18	35	58.3	283	G96810	unknown protein T1
19	35	58.3	324	G84610	hypotheical prote
20	35	58.3	327	F84610	hypotheical prote
21	35	58.3	329	A55221	debranase inhibito
22	35	58.3	350	T34557	hypotheical prote
23	35	58.3	389	T23516	hypotheical prote
24	35	58.3	585	T18885	hypotheical prote
25	35	58.3	636	G96717	hypotheical prote
26	35	58.3	738	D86345	hypotheical prote
27	35	58.3	1326	B56395	secretory phosphol
28	35	58.3	1465	A56395	secretory phosphol
29	34	56.7	104	T39020	hypotheical prote

30	34	56.7	133	2	S28187	interleukin-4 - pi
31	34	56.7	162	2	PN0533	ribonuclease (EC 3
32	34	56.7	223	2	AB1541	ABC transporters,
33	34	56.7	257	2	A25394	SURF-2 protein - m
34	34	56.7	300	2	A81418	pseudouridylylate sy
35	34	56.7	303	2	S44455	transcription fact
36	34	56.7	329	2	T04244	hypotheical prote
37	34	56.7	361	2	T26610	hypotheical prote
38	34	56.7	373	2	D87790	protein B0207.7 [1
39	34	56.7	406	2	D69878	pantothenate metab
40	34	56.7	452	2	S78481	retinoic acid rece
41	34	56.7	457	2	S39713	probable aldehyde
42	34	56.7	458	2	S06123	retinoic acid rece
43	34	56.7	516	2	T05940	cytochrome P450 83
44	34	56.7	525	2	T47409	hypotheical prote
45	34	56.7	595	2	T49384	related to NR1 pr

ALIGNMENTS

RESULT 1

T28379
ORF MSV218 hypotheical protein - Melanoplus sanguinipes entomopoxvirus
C:Species: Melanoplus sanguinipes entomopoxvirus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T28379
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A:Reference number: 220484; MUID:99102612
A:Accession: T28379
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-320 <AFO>
A:Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97747.1; PID:g4049787
C:Genetics:
A:Note: MSV218

Query Match 65.0%; Score 39; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHK 8
DB 26 KKVCIHKK 33

RESULT 2

D64699
hypotheical protein HPI436 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: D64699
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKee
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467
A:Accession: D64699
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-82 <TOM>
A:Cross-references: GB:AE000644; GB:AE000511; NID:g2314609; PIDN:AAD08488.1; PID:g231

Query Match 63.3%; Score 38; DB 2; Length 82;
Best Local Similarity 54.5%; Pred. No. 7;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
: | : | : | : |
Db 66 QKACLLHKDKK 76

RESULT 3

hypothetical protein jhp1329 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
R:Accession: G71819
C:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: G71819
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <ARN>
A:Cross-references: GB:AE001556; GB:AE001439; NID:g4155938; PIDN:AAD06905.1; PID:g415593
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1329

Query Match 63.3%; Score 38; DB 2; Length 86;
Best Local Similarity 54.5%; Pred. No. 7.3;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11
: | : | : | : |
Db 70 QKACLLHKDKK 80

RESULT 4

phospholipase C related protein [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
R:Accession: H97025
C:Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78995.1; PID:gl5023929; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1019

Query Match 63.3%; Score 38; DB 2; Length 245;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTIVHK 8
: | : | : | : |
Db 29 KTTCTIIHK 36

RESULT 5

hypothetical protein C41G7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:Accession: T19894
R:Steward, C.

submitted to the EMBL Data Library, October 1996
A:Reference number: Z19192
A:Accession: T19894
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-553 <WIL>
A:Cross-references: EMBL:Z81048; PIDN:CAB02840.1; GSPDB:GN00019; CESP:C41G7.3
A:Experimental source: clone C41G7
C:Genetics:
A:Gene: CESP:C41G7.3
A:Map position: 1
A:Introns: 25/1; 81/2; 106/3; 157/1; 179/3; 245/3; 368/1; 389/3; 423/3; 517/3

Query Match 63.3%; Score 38; DB 2; Length 553;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11
: | : | : | : |
Db 235 KTCVVERIKQ 244

RESULT 6

D96738
hypothetical protein F14023.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Accession: D96738
C:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D96738
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <STO>
A:Cross-references: GB:AE005173; NID:g7239515; PIDN:AAF43241.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14023.1
A:Map position: 1

Query Match 61.7%; Score 37; DB 2; Length 389;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 10
: | : | : | : |
Db 234 KVTCLSHKFK 243

RESULT 7

T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R:Accession: T26213
R:Ainscough, R.

submitted to the EMBL Data Library, August 1996
A:Reference number: Z20173
A:Accession: T26213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-222 <WIL>
A:Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3b

A:Map position: 5

A:Introns: 27/1; 77/2; 201/2

Query Match 60.0%; Score 36; DB 2; Length 222;

Best Local Similarity 66.7%; Pred. No. 37;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMK 11

||| :||

Db 122 TCJANKLKK 130

RESULT 8

D71675

hypothetical protein RP689 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C:Accession: D71675

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499

A:Accession: D71675

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-266 <AND>

A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAAI5136.1; PID:e134297

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: RP689

Query Match 60.0%; Score 36; DB 2; Length 266;

Best Local Similarity 64.3%; Pred. No. 43;

Matches 9; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 KKTCTCIVHKMK 10

|||||

Db 135 KKTCLDFIVHKMK 148

RESULT 9

AC1601

hypothetical protein lin1348 [imported] - Listeria innocua (strain Cl1p11262)

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC1601

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species

A:Reference number: AB1077; MUID:21337279; PMID:11679669

A:Accession: AC1601

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-399 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96579.1; PID:gl6413821; GSPDB:GN00178

A:Experimental source: strain Cl1p11262

C:Genetics:

A:Gene: lin1348

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 399;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTCIVHKMK 11

|||||

Db 374 KKTSLLEFKK 384

RESULT 10

F69792

hypothetical protein yeeB - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000

C:Accession: F69792

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A:Reference number: A69580; MUID:98044033

A:Accession: F69792

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-598 <GUN>

A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12497.1; PID:e11826

A:Experimental source: strain 168

C:Genetics:

A:Gene: yeeB

C:Superfamily: Bacillus subtilis hypothetical protein yeeB

Query Match 60.0%; Score 36; DB 2; Length 598;

Best Local Similarity 66.7%; Pred. No. 85;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KTCIVHKMK 10

|||||

Db 466 KTCIKHKK 474

RESULT 11

T10755

kinesin-related protein 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 29-Sep-1999

C:Accession: T10755

R:Sperry, A.O.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z17121

A:Accession: T10755

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-671 <SPE>

A:Cross-references: EMBL:U44979; NID:g2772515; PID:g2772516

A:Experimental source: strain Sprague-Dawley, testes

C:Genetics:

A:Gene: KRP2

C:Superfamily: kinesin-related protein KIF2; kinesin motor domain homology

F:205-542/Domain: kinesin motor domain homology <KMT>

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 671;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTCIVHKMK 11

Db 136 RKSCIVKEMEK 146
:|:|:|:|:|:|

RESULT 12

T19011

hypothetical protein C06C6.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19011

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19059

A:Accession: T19011

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-935 <WIL>

A:Cross-references: EMBL:Z93374; PTDN:CAB07557.1; GSPDB:GN00023; CESP:C06C6.7

A:Experimental source: clone C06C6

C:Genetics:

A:Gene: CESP:C06C6.7

A:Map position: 5

A:Introns: 28/1; 55/1; 80/1; 801/2; 865/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 935;

Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMKK 11

:|:|:|:|:|:|

Db 825 QSCIVHKLKR 834

RESULT 13

T26216

hypothetical protein W06A7.3c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26216

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26216

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2484 <WIL>

A:Cross-references: EMBL:Z78066; PTDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3c

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 2484;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11

:|:|:|:|:|:|

Db 2384 TCANKLKK 2392

RESULT 14

T26215

hypothetical protein W06A7.3a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26215

R:Ainscough, R.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z20173

A:Accession: T26215
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2607 <WIL>

A:Cross-references: EMBL:Z78066; PTDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A:Experimental source: clone W06A7

C:Genetics:

A:Gene: CESP:W06A7.3a

A:Map position: 5

A:Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match

Best Local Similarity 60.0%; Score 36; DB 2; Length 2607;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCIVHKMKK 11

:|:|:|:|:|:|

Db 2507 TCANKLKK 2515

RESULT 15

F59108

hypothetical protein pX01-143 - Bacillus anthracis virulence plasmid pX01

C:Species: Bacillus anthracis

C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000

C:Accession: F59108

R:Okimaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koeh

J. Bacteriol. 181, 6509-6515, 1999

A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harb

A:Reference number: A59091; MUID:99445483

A:Accession: F59108

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-150 <OKI>

A:Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32446.1; PID:g4894358

A:Experimental source: strain Sterne

C:Genetics:

A:Gene: pX01-143

A:Genome: plasmid

Query Match

Best Local Similarity 58.3%; Score 35; DB 2; Length 150;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMKK 11

:|:|:|:|:|:|

Db 77 KGACMLHKKK 87

Search completed: September 4, 2002, 16:47:33

Job time: 369 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:05 : Search time 34.18 Seconds
(without alignments)
12.461 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTIVHKMK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	55	91.7	1 CLIP_HUMAN	Q9ns71 homo sapien
2	48	80.0	1 CLIP_MOUSE	Q9cr36 mus musculus
3	36	60.0	1 Y689_RICPR	Q9zcn4 rickettsia
4	36	60.0	1 KRP2_RAT	Q62909 rattus norv
5	36	60.0	1 MCAK_CRIGR	P70096 cricetus
6	35	58.3	1 YCXA_EUGGR	P31561 euglena gra
7	35	58.3	1 MCE1_CABEL	Q17607 caenorhabdi
8	34	56.7	1 YTD_SCHPO	Q14218 schizosacch
9	34	56.7	1 IL4_PIG	Q04745 sus scrofa
10	34	56.7	1 SUR2_MOUSE	P09926 mus musculus
11	34	56.7	1 TFH3_HUMAN	Q13889 homo sapien
12	34	56.7	1 DHA2_BACSU	P39616 bacillus su
13	34	56.7	1 RRA_NOTVI	P18514 notophthalm
14	34	56.7	1 ALB2_SALSA	Q03156 salmo salar
15	34	56.7	1 KPCL_HUMAN	P24723 homo sapien
16	34	56.7	1 KPCL_MOUSE	P23298 mus musculus
17	34	56.7	1 KPCL_RAT	Q64617 rattus norv
18	34	56.7	1 KPCE_RABIT	P10830 oryctolagus
19	34	56.7	1 KPCE_HUMAN	Q02156 homo sapien
20	34	56.7	1 KPCE_MOUSE	P16054 mus musculus
21	34	56.7	1 KPCE_RAT	P09216 rattus norv
22	34	56.7	1 KPCE2_APLCA	P16975 aplysia cal
23	34	56.7	1 KPCE2_MYCPG	P47326 mycoplasma
24	33	55.0	1 TRBG_ECOLI	P41072 escherichia
25	33	55.0	1 ALL1_LEPUS	P80384 lepidoglyph
26	33	55.0	1 YE12_HAEIN	P45197 haemophilus
27	33	55.0	1 Y599_METJA	Q58016 methanococc
28	33	55.0	1 IOD2_FUNHE	P79747 fundulus he
29	33	55.0	1 CHEB_THEMA	Q9wyn9 thermotoga
30	33	55.0	1 CHEB_RHIME	Q52883 rhizobium m
31	33	55.0	1 CHEB_AGR75	Q05128 agrobacteri
32	33	55.0	1 P2X1_HUMAN	P51575 homo sapien
33	33	55.0	1 C71F_ARATH	P58046 arabidopsis

34	33	55.0	603	1	UVRC_CHLPN	Q9z6w6 chlamydia p
35	33	55.0	768	1	ITB8_RABIT	P26013 oryctolagus
36	33	55.0	844	1	MCEL_VACCC	P20979 vaccinia vi
37	33	55.0	844	1	MCEL_VACCV	P04298 vaccinia vi
38	33	55.0	844	1	MCEL_VARV	P33057 variola vir
39	32	53.3	90	1	VGE_BPPHX	P03639 bacterioph
40	32	53.3	91	1	RACC_ECOLI	P15033 escherichia
41	32	53.3	141	1	ALL2_TYRPU	O02380 tyrophagus
42	32	53.3	343	1	TRA_CORDI	P35879 corynebacte
43	32	53.3	400	1	TRA3_RHIME	P80011 rhizobium m
44	32	53.3	400	1	Y4PO_RHISN	P55620 rhizobium s
45	32	53.3	438	1	YZ32_METJA	Q60289 methanococc

ALIGNMENTS

```

RESULT 1
CLIP_HUMAN
ID CLIP_HUMAN STANDARD; PRT; 199 AA.
AC Q9NS71;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein.
GN CALL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stomach;
RX MEDLINE=20296773; PubMed=10835488;
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT "Isolation of two novel genes, down-regulated in gastric cancer.";
RL Jpn. J. Cancer Res. 91:459-463(2000).
CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC detected in cancer tissue or gastric cancer cell lines.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-----
CC EMBL; AB039886; BAA92433.1; -.
DR MIN; 606402; -.
SQ SEQUENCE 199 AA; 21999 MW; C0998B8B9A1338D7A CRC64;

```

Query Match 91.7%; Score 55; DB 1; Length 199;
Best Local Similarity 90.9%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KKTCTIVHKMK 11
| | | | | | | |
Db 92 KKTCTIVHKMK 102

```

RESULT 2
CLIP_MOUSE
ID CLIP_MOUSE STANDARD; PRT; 184 AA.
AC Q9CR36; Q9D7K7; Q9CTZ5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE CALL protein homolog.
GN CALL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 CC -----
 DR EMBL; AK008990; BAB26010.1; -;
 DR EMBL; AK008622; BAB25784.1; -;
 DR EMBL; AK008641; BAB25801.1; -;
 DR EMBL; AK008647; BAB25803.1; -;
 DR EMBL; AK008722; BAB25856.1; -;
 DR EMBL; AK008745; BAB25872.1; -;
 DR EMBL; AK008933; BAB25975.1; -;
 DR EMBL; AK008956; BAB25988.1; -;
 DR EMBL; AK009145; BAB26103.1; -;
 DR EMBL; AK019050; BAB31525.1; -;
 FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;
 Query Match 80.0%; Score 48; DB 1; Length 184;
 Best Local Similarity 72.7%; Pred. NO. 0.06;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKTICIVHKMK 11
 DB 78 KKSCIVHRMKN 88
 RESULT 3
 Y689_RICPR STANDARD; PRT; 266 AA.
 ID Y689_RICPR
 AC Q9ZCN4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein RP689.
 GN RP689.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsia;
 OX NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MADRID E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -!- SIMILARITY: STRONG, TO R.PROWAZEKII RP688. SOME TO H.INFLUENZAE
 CC LICD.
 CC -----
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 CC -----
 DR EMBL; AJ235272; CAAL5126.1; -;
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 13 33 POTENTIAL.
 SQ SEQUENCE 266 AA; 31400 MW; 0624B3F66EDE9FE5 CRC64;
 Query Match 60.0%; Score 36; DB 1; Length 266;
 Best Local Similarity 64.3%; Pred. NO. 13;
 Matches 9; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
 QY 1 KKTCT---IVHKMK 10
 DB 135 KKTCLDIFIVHKMK 148
 RESULT 4
 KRP2_RAT STANDARD; PRT; 671 AA.
 ID KRP2_RAT
 AC Q62909;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Kinesin-related protein 2.
 GN KRP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=96228687; PubMed=8688559;
 RA Sperry A.O., Zhao L.-P.;
 RT "Kinesin-related proteins in the mammalian testes: candidate motors
 RT for meiosis and morphogenesis.";
 RL Mol. Biol. Cell 7:289-305(1996).
 RN [2]
 RP REVISIONS.
 RA Sperry A.O.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MOTOR PROTEIN, ACTIVE IN MEIOSIS.
 CC -!- TISSUE SPECIFICITY: TESTIS. LOCALIZED TO THE TESTIS.
 CC CELLS OF THE SEMINIFEROUS EPITHELIA IN THE TESTIS.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAK/KIF2
 CC SUBFAMILY.
 CC -----
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DR EMBL; U44979; AAC53528.1; -.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 2.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil; Meiosis.
FT DOMAIN 1 198 GLOBULAR (POTENTIAL).
FT DOMAIN 199 540 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 541 671 COILED COIL (POTENTIAL).
FT NP_BIND 294 301 ATP (POTENTIAL).
SQ SEQUENCE 671 AA; 75661 MW; F2B54598C78D8DE CRC64;

Query Match 60.0%; Score 36; DB 1; Length 671;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTICIVHKMK 11
   :|:|:|:|:|
Db 136 RKSCIVKEMEK 146

RESULT 5
MCAC_CRIGR
ID MCAC_CRIGR STANDARD; PRT; 718 AA.
AC P70096;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Mitotic centromere-associated kinesin (MCAC) (Kinesin-like protein 6).
GN KNSL6.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95122643; PubMed=7822426;
RA Wordeman L., Mitchison T.J.;
RT "Identification and partial characterization of mitotic centromere-
associated kinesin, a kinesin-related protein that associates with
centromeres during mitosis."
RL J. Cell Biol. 128:95-105(1995).
RN [2]
RP REVISIONS.
RA Wordeman L.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRESENT THROUGHOUT THE CELL CYCLE. ASSOCIATES WITH
CENTROMERES AT EARLY PROPHASE, AND REMAINS ASSOCIATED WITH THE
CENTROMERE UNTIL AFTER TELOPHASE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. MCAC/KIF2
SUBFAMILY.
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CC
DR EMBL; U11790; AAB17358.2; -.
DR HSSP; P17119; 3KAR.
DR InterPro; IPR001752; kinesin.
DR Pfam; PF00225; kinesin; 2.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.

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DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil;
Nuclear protein.
FT DOMAIN 1 246 GLOBULAR (POTENTIAL).
FT DOMAIN 247 612 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 613 651 COILED COIL (POTENTIAL).
FT DOMAIN 689 716 COILED COIL (POTENTIAL).
FT NP_BIND 342 349 ATP (POTENTIAL).
FT DOMAIN 409 412 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 718 AA; 80918 MW; 16ABD8BC66AD11B2 CRC64;

Query Match 60.0%; Score 36; DB 1; Length 718;
Best Local Similarity 54.5%; Pred. No. 33;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTICIVHKMK 11
   :|:|:|:|:|
Db 184 RKSCIVKEMEK 194

RESULT 6
YCXA_EUGGR
ID YCXA_EUGGR STANDARD; PRT; 350 AA.
AC P31561;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 40.9 kDa protein in 16S rRNA 3'region (ORF350).
OS Euglena gracilis.
OC Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z.
RX MEDLINE=93347989; PubMed=8346031;
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
RA Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA."
RL Nucleic Acids Res. 21:3537-3544(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z.
RA Schlunegger B., Stutz E.;
RT "The Euglena gracilis chloroplast genome: structural features of a
DNA region possibly carrying the single origin of DNA replication."
RL Curr. Genet. 8:629-634(1984).
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CC
DR EMBL; Z11874; -. NOT_ANNOTATED_CDS.
DR EMBL; X70810; CAA50140.1; -.
DR PIR; S34557; S34557.
DR PIR; S36933; S36933.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 350 AA; 40861 MW; 1ACA7EC540FF51 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 350;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTICIVHKMK 9
   :|:|:|:|:|
Db 342 KKKCLLHKI 350

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RESULT 7
MCEL_CABEL
ID MCEL_CABEL STANDARD; PRT; 573 AA.
AC Q17607; 002558;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE mRNA capping enzyme [Includes: Polynucleotide 5'-triphosphatase
DE (EC 3.1.3.33) (mRNA 5'-triphosphatase) (TPase); mRNA
DE guanylyltransferase (EC 2.7.7.50) (GTP--RNA guanylyltransferase)
DE (Gtase)].
DE CEL-1 OR C03D6.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RL Burton J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[3]
RN CHARACTERIZATION, AND MUTAGENESIS OF CYS-124.
RP MEDLINE-97344078; PubMed-9200605;
RX Takagi T., Moore C.R., Diehn F., Buratowski S.;
RT "An RNA 5'-triphosphatase related to the protein tyrosine
RT phosphatases.";
RL Cell 89:867-873(1997).
CC -!- FUNCTION: BIFUNCTIONAL mRNA CAPPING ENZYME EXHIBITING RNA 5'-
CC TRIPHOSPHATASE ACTIVITY IN THE N-TERMINAL PART AND MRNA
CC GUANYLYLTRANSFERASE ACTIVITY IN THE C-TERMINAL PART. CATALYZES THE
CC FIRST TWO STEPS OF CAP FORMATION: BY REMOVING THE GAMMA-PHOSPHATE
CC FROM THE 5'-TRIPHOSPHATE END OF NASCENT MRNA TO YIELD A
CC DIPOSPHATE END, AND BY TRANSFERRING THE GMP MOIETY OF GTP TO THE
CC 5'-DIPOSPHATE TERMINUS.
CC -!- CATALYTIC ACTIVITY: 5'-phosphopolynucleotide + H(2)O =
CC polynucleotide + phosphate.
CC -!- CATALYTIC ACTIVITY: GTP + (5')ppp-mRNA = diphosphate +
CC G(5')ppp-mRNA.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- INDUCTION: INHIBITED BY MAGNESIUM.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE NON-RECEPTOR
CC CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE EUKARYOTIC
CC GTASE FAMILY.
CC
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CC
CC EMBL; AF003925; AAB61344.1; -.
CC DR EMBL; 275525; CAA99765.1; ALT_INIT.
CC DR WormPep; C03D6.3; CE15578.
CC DR InterPro; IPR000340; DS_phosphatase.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR InterPro; IPR001339; mRNA_cap_enzyme.
CC DR Pfam; PF01331; mRNA_cap_enzyme; 1.
CC DR SMART; SM00012; PTPC_DSPC; 1.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
CC DR mRNA processing; mRNA capping; Transferase; Nucleotidyltransferase;
CC Hydrolase; Multifunctional enzyme; Nuclear protein.
CC KW

```

```

FT DOMAIN 1 212 TPASE.
FT DOMAIN 229 573 GTASE.
FT ACT_SITE 124 124 RNA 5'-TRIPHOSPHATASE.
FT ACT_SITE 299 299 GUANYLYLATION SITE (BY SIMILARITY).
FT MUTAGEN 124 124 C->S: LOSS OF ACTIVITY.
FT MUTAGEN 124 124 C->A: LOSS OF ACTIVITY.
SQ SEQUENCE 573 AA; 66336 MW; F50ACA59F1815F47 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 573;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CIVHKMK 10
DB 82 CIVHKMK 88
II IIII

RESULT 8
YDTD_SCHPO
ID YDTD_SCHPO STANDARD; PRT; 104 AA.
AC Q14218;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 11.7 kDa protein C6B12.13 in chromosome I.
GN SPAC6B12.13.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YFR003C.
CC
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CC
CC EMBL; Z98531; CAB11073.1; -.
CC DR Hypothetical protein.
CC KW
FT DOMAIN 78 97 SER-RICH.
SQ SEQUENCE 104 AA; 11659 MW; E4753ACFB8302D00 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 104;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKTCTIVHKMK 11
DB 64 KVCCTIFHKQK 74
II IIII

RESULT 9
IL4_PIG
ID IL4_PIG STANDARD; PRT; 133 AA.
AC Q04745; Q29054;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-4 precursor (IL-4) (B-cell stimulatory factor 1) (BSF-1)
DE (Lymphocyte stimulatory factor 1).
GN IL4.
OS Sus scrofa (Pig).

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CC -----
 DR EMBL; Z30093; CAA82909.1; -
 DR TRANSFAC; T02188; -
 DR MIM; 601750; -
 KW Transcription regulation; DNA repair; Nuclear protein; Zinc-finger.
 FT ZNFING 268 285 C4-TYPE.
 SQ SEQUENCE 303 AA; 33893 MW; BIDD95EE876D3F9E CRC64;

Query Match 56.7%; Score 34; DB 1; Length 303;
 Best Local Similarity 45.5%; Pred. No. 35;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
 | | : | | |
 Db 139 KALCYIHRMKN 149

RESULT 12
 ID DHA2_BACSU STANDARD; PRT; 457 AA.
 AC P39616;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable aldehyde dehydrogenase YMDH (EC 1.2.1.3).
 GN YMDH OR IPA-58R.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020337; PubMed=7934828;
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
 RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
 RA Rapoport G., Danchin A.;
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97
 kb region from 325 degrees to 333 degrees.";
 RL Mol. Microbiol. 10:371-384(1993).
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.

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CC EMBL; X73124; CAA51614.1; -
 DR EMBL; Z99123; CAB15822.1; -
 DR PIR; S39713; S39713.
 DR HSSP; P11883; IAD3.
 DR Subtilist; BG10604; ywdH.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR Pfam; PF00171; algedh; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; Complete proteome.
 FT ACT_SITE 211 211 BY SIMILARITY.
 FT ACT_SITE 245 245 BY SIMILARITY.
 SQ SEQUENCE 457 AA; 50765 MW; C238D9FD07DFB92A CRC64;

Query Match 56.7%; Score 34; DB 1; Length 457;
 Best Local Similarity 75.0%; Pred. No. 51;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTVHK 8
 | | | | | |
 Db 215 KSPCTVHK 222

RESULT 13
 ID RRA_NOTVI STANDARD; PRT; 458 AA.
 AC P18514; Q91155;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Retinoic acid receptor alpha (RAR-alpha).
 GN RARA OR NR1B1.
 OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Notophthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
 RX MEDLINE=90015190; PubMed=2552324;
 RA Ragsdale C.W. Jr., Petkovich M., Gates P.B., Chambon P., Brookes J.P.;
 RT "Identification of a novel retinoic acid receptor in regenerative
 RT tissues of the newt."
 RL Nature 341:654-657(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
 RX MEDLINE=93087213; PubMed=1333589;
 RA Ragsdale C.W., Gates P.B., Brookes J.P.;
 RT "Identification and expression pattern of a second isoform of the newt
 RT alpha retinoic acid receptor."
 RL Nucleic Acids Res. 20:5851-5851(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR RETINOIC ACID. THIS METABOLITE
 CC HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINOIC ACID IS
 CC A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
 CC CELLS FUNCTIONS BY DIRECTLY REGULATING GENE EXPRESSION.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
 CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR1 SUBFAMILY.

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CC EMBL; X17585; CAA35602.1; -
 DR EMBL; Z14254; CAA78621.1; -
 DR PIR; S06123; S06123.
 DR HSSP; P10826; 1HRA.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Steroidhormone_receptor.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLT; 1.
 DR SMART; SM00399; znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Multigene family; Alternative splicing.
 FT DOMAIN 1 86 MODULATING.
 FT DNA_BIND 87 152 NUCLEAR RECEPTOR-TYPE.

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FT ZN_FING 87 107 C4-TYPE.
FT ZN_FING 123 147 C4-TYPE.
FT ZN_FING 153 199 HINGE..
FT ZN_FING 200 419 LIGAND-BINDING.
FT VARSPLIC 1 59 MASNGSGCPSSGGHMGYPVPHYAFFPPHMLGGLSPGSLA
FT GIPHPLPYSAYSTPSPAT -> MYDSVEVSSPSPVIMIDFY
FT SONRACLMDKGLGHPVPGSPFIRNPHWSSSSHS (IN
FT ISOFORM ALPHA-2).
FT SEQUENCE 458 AA; 50637 MW; B4370822FBAADB54 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 458;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 KTCIVHKMK 11
DB 127 KTCIINKVTR 136
|||||:|:|

RESULT 14
ALB2_SALSA STANDARD; PRT; 608 AA.
ID ALB2_SALSA STANDARD; PRT; 608 AA.
AC Q03156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Serum albumin 2 precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93013056; PubMed=1398147;
RA Byrnes L., Gannon F.;
RT "Sequence analysis of a second cDNA encoding Atlantic salmon (Salmo
RT salar) serum albumin."
RL Gene 120:319-320(1992).
CC
CC -!- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: PLASMA.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE ALB/AF/AFVDB FAMILY.
CC
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CC
CC EMBL; X60776; CAA43187.1; ..
DR PIR; A46757; ABONS2.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; transport_prot; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 2.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal.
FT SIGNAL 1 14 POTENTIAL.
FT PROPEP 15 18
FT CHAIN 19 608 SERUM ALBUMIN 2.
FT REPEAT 22 194 1.
FT REPEAT 215 390 2.
FT REPEAT 411 591 3.

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FT DISULFID 26 72 POTENTIAL.
FT DISULFID 71 80 BY SIMILARITY.
FT DISULFID 93 108 BY SIMILARITY.
FT DISULFID 107 118 BY SIMILARITY.
FT DISULFID 142 187 BY SIMILARITY.
FT DISULFID 186 195 BY SIMILARITY.
FT DISULFID 218 264 BY SIMILARITY.
FT DISULFID 263 271 BY SIMILARITY.
FT DISULFID 283 299 BY SIMILARITY.
FT DISULFID 298 309 BY SIMILARITY.
FT DISULFID 336 381 BY SIMILARITY.
FT DISULFID 380 389 BY SIMILARITY.
FT DISULFID 414 460 BY SIMILARITY.
FT DISULFID 459 471 BY SIMILARITY.
FT DISULFID 484 500 BY SIMILARITY.
FT DISULFID 499 510 BY SIMILARITY.
FT DISULFID 537 582 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT CARBOHYD 501 501 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 608 AA; 67058 MW; C168DD349F4E16C5 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 608;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTICIVHK 8
DB 215 KSLCIVHK 222
|||||

RESULT 15
KPCL_HUMAN STANDARD; PRT; 682 AA.
ID KPCL_HUMAN STANDARD; PRT; 682 AA.
AC P24723;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.1-) (PKC-eta) (PKC-L).
GN PKCH OR PKCL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=91094824; PubMed=1986216;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RT "Isolation and characterization of PKC-L, a new member of the protein
RT kinase C-related gene family specifically expressed in lung, skin,
RT and heart."
RL Mol. Cell. Biol. 11:126-133(1991).
RN [2]
RP REVISIONS.
RX MEDLINE=92186874; PubMed=1545821;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RL Mol. Cell. Biol. 12:1404-1404(1992).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG TISSUE, LESS IN HEART
CC AND SKIN TISSUE.
CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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DR EMBL; M55284; AAA60100.1; -.
 DR PIR; A39666; A39666.
 DR HSSP; P28867; IPTQ.
 DR MIM; 605437; -.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000719; Euk_kinase.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Repeat; ATP-binding; Transferase;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
 FT DOMAIN 12 112 C2 DOMAIN.
 FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 245 294 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 354 613 PROTEIN KINASE.
 FT NP_BIND 360 368 ATP (BY SIMILARITY).
 FT BINDING 383 383 ATP (BY SIMILARITY).
 FT ACT_SITE 478 478 BY SIMILARITY.
 SQ SEQUENCE 682 AA; 77563 MW; 13D4EAB01F3B5AB8 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 682;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCIVHK 8

Db 206 TCVVK 211

Search completed: September 4, 2002, 17:05:06
 Job time: 1132 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:35 ; Search time 124.34 seconds
(without alignments)
15.304 Million cell updates/sec

Title: US-09-821-726-4
Perfect score: 60
Sequence: 1 KKTCTVHKMK 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	42	70.0	478	5 Q9U4M7	Q9U4M7 leishmania
2	41	68.3	971	5 Q9V6Y6	Q9V6Y6 drosophila
3	41	68.3	1261	5 Q95TJ2	Q95TJ2 drosophila
4	40	66.7	1138	12 Q55345	Q55345 hu39694 vir
5	40	66.7	1386	8 Q9XMS2	Q9XMS2 tetrahymena
6	39	65.0	320	12 Q9VVM4	Q9VVM4 melanoplus
7	38	63.3	82	16 Q25977	Q25977 helicobacte
8	38	63.3	86	16 Q9ZJ10	Q9ZJ10 helicobacte
9	38	63.3	245	16 Q97KA0	Q97KA0 clostridium
10	38	63.3	553	5 Q93367	Q93367 caenorhabdi
11	37	61.7	389	10 Q9M9T0	Q9M9T0 arabidopsis
12	37	61.7	610	5 Q9VC31	Q9VC31 drosophila
13	37	61.7	655	10 Q9C9I9	Q9C9I9 arabidopsis
14	37	61.7	1247	5 Q9GV23	Q9GV23 sarcophaga
15	36	60.0	173	6 Q95L17	Q95L17 felis silve
16	36	60.0	174	6 Q9GMZ9	Q9GMZ9 felis silve

17	36	60.0	198	16 Q992P2	Q992P2 streptococc
18	36	60.0	222	5 Q23188	Q23188 caenorhabdi
19	36	60.0	292	6 Q9GMZ8	Q9GMZ8 felis silve
20	36	60.0	292	6 Q02758	Q02758 felis silve
21	36	60.0	378	10 Q9MAD5	Q9MAD5 arabidopsis
22	36	60.0	399	16 Q92C43	Q92C43 listeria in
23	36	60.0	464	5 Q9V8D8	Q9V8D8 drosophila
24	36	60.0	598	16 Q34469	Q34469 bacillus su
25	36	60.0	721	11 Q922S8	Q922S8 mus musculu
26	36	60.0	762	10 Q943W8	Q943W8 cryza sativ
27	36	60.0	935	5 Q62033	Q62033 caenorhabdi
28	36	60.0	2484	5 Q9U347	Q9U347 caenorhabdi
29	36	60.0	2607	5 Q23187	Q23187 caenorhabdi
30	36	60.0	3901	5 Q9N533	Q9N533 caenorhabdi
31	35	58.3	143	5 Q965E2	Q965E2 psoroptes o
32	35	58.3	150	2 Q9X398	Q9X398 bacillus an
33	35	58.3	161	5 Q9VSU5	Q9VSU5 drosophila
34	35	58.3	207	10 Q65691	Q65691 arabidopsis
35	35	58.3	235	6 Q9TQ88	Q9TQ88 canis fami
36	35	58.3	235	6 Q9N0T0	Q9N0T0 canis fami
37	35	58.3	247	3 Q94357	Q94357 schizosacch
38	35	58.3	283	10 Q9C9R7	Q9C9R7 arabidopsis
39	35	58.3	304	6 Q9TQX1	Q9TQX1 canis fami
40	35	58.3	324	10 Q9SID9	Q9SID9 arabidopsis
41	35	58.3	327	10 Q9SIE0	Q9SIE0 arabidopsis
42	35	58.3	330	2 Q55228	Q55228 streptococc
43	35	58.3	334	12 Q06314	Q06314 hepatitis c
44	35	58.3	346	5 Q9U262	Q9U262 caenorhabdi
45	35	58.3	389	5 Q44147	Q44147 caenorhabdi

ALIGNMENTS

RESULT 1
Q9U4M7 ID Q9U4M7 PRELIMINARY; PRT; 478 AA.
AC Q9U4M7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 7138.4.
GN 7138.4.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Ravel C., Dubessay P., Blaineau C., Lignon M.-F., Bastien P.,
RA Dedet J.-P., Pages M.;
RT "Leishmania major chromosome 5 complete sequence."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF163772; AAF14644.1; -;
SQ SEQUENCE 478 AA; 55256 MW; 768A24D0C62A7CB7 CRC64;

Query Match 70.0%; Score 42; DB 5; Length 478;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKTCTVHKMK 10
|| || || || ||
Db 264 KQCTIHHMK 273

RESULT 2
Q9V6Y6 ID Q9V6Y6 PRELIMINARY; PRT; 971 AA.
AC Q9V6Y6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

GN ORF1386.
 OS Tetrahymena pyriformis.
 OG Mitochondrion.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 OX NCBI_TaxID=5908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20181866; PubMed=10715208;
 RA Edqvist J., Burger G., Gray M.W.;
 RT "Expression of mitochondrial protein-coding genes in Tetrahymena
 pyriformis.";
 RL J. Mol. Biol. 297:381-393(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20181865; PubMed=10715207;
 RA Burger G., Zhu Y., Littlejohn T.G., Greenwood S.J., Schnare M.N.,
 RA Lang B.F., Gray M.W.;
 RT "Complete sequence of the mitochondrial genome of Tetrahymena
 pyriformis and comparison with Paramecium aurelia mitochondrial DNA.";
 RL J. Mol. Biol. 297:365-380(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Burger G.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF160864; AAD41942.1; -;
 KW Mitochondrion.
 SQ SEQUENCE .1386 AA; 171837 MW; 310DBA7FECB6913A CRC64;

Query Match 66.7%; Score 40; DB 8; Length 1386;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHKM 9
 ||||| II;
 Db 382 KKTCTINHL 390

RESULT 6

Q9YVM4 PRELIMINARY; PRT; 320 AA.
 AC Q9YVM4
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE ORF MSV218 HYPOTHETICAL PROTEIN.
 GN MSV218.
 OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 OX NCBI_TaxID=83191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RX MEDLINE=99102612; PubMed=9847359;
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
 RL J. Virol. 73:533-552(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RA Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF063866; AAC97747.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 320 AA; 38982 MW; FCFBE193C5BA5F13 CRC64;

Query Match 65.0%; Score 39; DB 12; Length 320;
 Best Local Similarity 75.0%; Pred. No. 8.3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKTCTVHK 8
 ||||| II;
 Db 26 KKVCIHKK 33
 RESULT 7
 O25977 PRELIMINARY; PRT; 82 AA.
 AC O25977
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 9.6 KDA PROTEIN.
 GN HP1436.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori.";
 RL Nature 388:539-547(1997).
 DR EMBL: AE000644; AAD08488.1; -;
 DR TIGR: HP1436; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 82 AA; 9599 MW; 7AF6FBAF6B6B15 CRC64;

Query Match 63.3%; Score 38; DB 16; Length 82;
 Best Local Similarity 54.5%; Pred. No. 3.9;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKTCTVHKMK 11
 :|:|:| II;
 Db 66 QKACLLHKDKK 76

RESULT 8

Q9ZJ10 PRELIMINARY; PRT; 86 AA.
 AC Q9ZJ10
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE PUTATIVE.
 GN JHP1329.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.W., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).

RT "Genome sequence of the nematode C.elegans: A platform for
 RL investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: Z81048; CAB02840.1; -.
 DR InterPro: IPR004087; KH.
 DR InterPro: IPR004307; TSP0_MBR.
 DR Pfam: PF03073; TSP0_MBR; 1.
 DR SMART: SM00322; KH; 2.
 SQ SEQUENCE 553 AA; 61142 MW; EC1EC7AF77088735 CRC64;

Query Match 63.3%; Score 38; DB 5; Length 553;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 0; Gaps 0;

QY 2 KTCIVHKMKK 11
 Db 235 KTCVVEKIKQ 244

RESULT 11

Q9M910 PRELIMINARY; PRT; 389 AA.

AC Q9M910: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE F14023.1 PROTEIN (FRAGMENT).
 GN F14023.1.

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;
 RA Liu S., Yu G., Lee J., Sakano H., Jhaveri A., Lenz C., Toriumi M.,
 RA Chin C., Chiu J., Choi E., Gonzalez A., Hwang B., Koo T., Li J.,
 RA Liu A., Pham P., Vaysberg M., Altafi H., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Nguyen M., Palm C., Shinn P., Tambunga G., Davis R., Ecker J.,
 RA Federspiel N., Theologis A.;
 RT "The sequence of BAC F14023 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Theologis A.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AC012654; AAF43241.1; -.

DR HSP; P24941; IAO1.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR002290; Ser_thr_pkinase.

DR Pfam: PF00069; pkinase; 1.

DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Serine/threonine-protein kinase; Transferase.

FT NON_TER 1

SQ SEQUENCE 389 AA; 43323 MW; 6810824405569B89 CRC64;

Query Match 61.7%; Score 37; DB 10; Length 389;
 Best Local Similarity 70.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTCIVHKMK 10

Db 234 KVTCSHKFK 243

RESULT 12

DR EMBL: AE001556; AAD06905.1; -.
 KW Complete proteome.
 SQ SEQUENCE 86 AA; 10034 MW; 41E8E9AA37BE084A CRC64;

Query Match 63.3%; Score 38; DB 16; Length 86;
 Best Local Similarity 54.5%; Pred. No. 4;
 Matches 6; Conservative 3; Mismatches 0; Gaps 0;

QY 1 KTCIVHKMKK 11
 Db 70 QKACLLHKDKK 80

RESULT 9

ID Q97KA0 PRELIMINARY; PRT; 245 AA.

AC Q97KA0: 01-OCT-2001 (TREMBlrel. 18, Created)

DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)

DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)

DE PHOSPHOLIPASE C RELATED PROTEIN.

GN CAC1019.

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1488;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE=21359325; PubMed=11466286;

RA Noelling J., Berton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

RT "Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).

DR EMBL: AE007617; AAK78995.1; -.

KW Complete proteome.

SQ SEQUENCE 245 AA; 28890 MW; CF431EB9293762F2 CRC64;

Query Match 63.3%; Score 38; DB 16; Length 245;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCIVHK 8

Db 29 KVTCTIHK 36

RESULT 10

Q93367 PRELIMINARY; PRT; 553 AA.

AC Q93367;

DT 01-FEB-1997 (TREMBlrel. 02, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE C41G7.3 PROTEIN.

GN C41G7.3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Steward C.A.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;

Q9VC31 Q9VC31 PRELIMINARY; PRT; 610 AA.
 AC Q9VC31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CGI3638 PROTEIN.
 GN CGI3638.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R., G. G., Champ M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Buritis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam K.A.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -I- SIMILARITY: TO RAB PROTEINS. BELONGS TO THE RAB SUBFAMILY.
 DR EMBL; AE003749; AAF56345.1;
 DR HSP; P05713; RAB
 DR FlyBase; FBgn0039231; CGI3638.
 DR InterPro; IPR003579; Rab.
 DR InterPro; IPR001806; Ras.transfrmng.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMNG.
 DR SMART; SM00175; RAB; 1.
 DR GTP-binding; Lipoprotein.
 KW SEQUENCE 610 AA; 69826 MW; DE8BCC9BB097EC79 CRC64;
 QY 2 KTCIVHK 8

Query Match 61.7%; Score 37; DB 5; Length 610;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KTCIVHK 8

Db 418 KTCIVHR 424

RESULT 13

Q9C919 PRELIMINARY; PRT; 655 AA.
 ID Q9C919;
 AC Q9C919;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOPHETICAL 72.4 KDA PROTEIN.
 GN F26A9.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RA "Arabidopsis thaliana chromosome 1 BAC F26A9 genomic sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC016163; AAG51826.1;
 DR HSP; P24941; IHCL.
 DR InterPro; IPR000719; Euk_pkinase
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR KW ATP-binding; Hypothetical protein; Transferase.
 SQ SEQUENCE 655 AA; 72442 MW; EFC70BE1608A1F9F CRC64;

Query Match 61.7%; Score 37; DB 10; Length 655;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTCIVHKMK 10

Db 500 KVICSHKFK 509

RESULT 14

Q9GV23 PRELIMINARY; PRT; 1247 AA.
 ID Q9GV23;
 AC Q9GV23;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE 210KDA PROTEIN (FRAGMENT).
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20536508; PubMed=10965055;
 RA Fujii-Taira I., Tanaka Y., Homma K.J., Natori S.;
 RT "Hydrolysis and synthesis of substrate proteins for cathepsin L in the
 RL brain basement membranes of Sarcophaga during metamorphosis.";
 DR J. Biochem. 128:539-542(2000).
 DR EMBL; AB041729; BAB16608.1;
 FT NON_TER 1
 SQ SEQUENCE 1247 AA; 142521 MW; 12B097428B518959 CRC64;

Thu Sep 5 11:23:41 2002

Query Match 61.7%; Score 37; DB 5; Length 1247;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 TCIVHKMK 11
| | | | |
Db 1221 TCAVHKIK 1229

RESULT 15
Q95L17 PRELIMINARY; PRT; 173 AA.
AC Q95L17;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE CD80.
GN CD80.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21390213; PubMed=11498243;
RA Yang S., Sellins K.S., Powell T., Stoneman E., Sim G.K.;
RT "Novel transcripts encoding secreted forms of feline CD80 and CD86
costimulatory molecules.";
RL Vet. Immunol. Immunopathol. 81:15-21(2001).
DR EMBL; AY007703; AAC23341.1;
SQ SEQUENCE 173 AA; 19841 MW; A7AB46A71E5E97AC CRC64;

Query Match 60.0%; Score 36; DB 6; Length 173;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KKTICIVHKMK 11
| | | | |
Db 113 KYTCIIQKIEK 123

Search completed: September 4, 2002, 17:01:37
Job time: 1158 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:02 ; Search time 158.52 Seconds
(without alignments)
9.810 Million cell updates/sec

Title: US-09-821-726-3

Perfect score: 81

Sequence: 1 KKLQGGKGGPPPK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	81	100.0	185	20	AAW99667 Human secreted pro
2	81	100.0	185	21	AAW99667 Human PRO1005 prot
3	81	100.0	185	21	AAW99667 Human signal pept
4	81	100.0	185	21	AAW99667 Membrane-bound pro
5	81	100.0	185	22	AAW99667 Human PRO1005 (UNQ
6	81	100.0	185	22	AAW99667 Human PRO1005 prot
7	81	100.0	186	21	AAW99667 Human secreted pro
8	81	100.0	194	19	AAW99667 Cancer associated
9	81	100.0	194	20	AAW99667 Human ovarian tumo
10	52	64.2	103	21	AAW99667 Human ORFX ORF812
11	52	64.2	163	22	AAW99667 Human polypeptide

12	52	64.2	279	22	AAU03592 Human DNA modifca
13	52	64.2	467	22	AAW94309 Human protein sequ
14	51	63.0	108	22	AAW94309 Human polypeptide
15	51	63.0	125	22	AAO11472 Human polypeptide
16	50.5	62.3	140	22	AAW08289 Human polypeptide
17	50	61.7	673	21	AAV58042 Escherichia coli D
18	49.5	61.1	147	22	AAW06887 Human polypeptide
19	49	60.5	84	22	AAO13411 Human polypeptide
20	49	60.5	115	22	AAO08183 Human polypeptide
21	49	60.5	120	22	AAO06522 Human polypeptide
22	49	60.5	855	22	AAO08748 Human protease pol
23	48	59.3	127	22	AAO05497 Human polypeptide
24	48	59.3	128	22	AAO03588 Human polypeptide
25	48	59.3	247	20	AAW89037 Polypeptide fragme
26	48	59.3	247	22	ABW51188 Human secreted pro
27	48	59.3	532	21	AAW42542 Human ORFX ORF2306
28	48	59.3	774	22	ABW64148 Drosophila melanog
29	48	59.3	2061	22	ABW71759 Drosophila melanog
30	47.5	58.6	109	22	AAO09868 Human polypeptide
31	47	58.0	71	22	AAU41527 Propionibacterium
32	47	58.0	102	22	AAO00839 Human polypeptide
33	47	58.0	1963	22	ABW62819 Drosophila melanog
34	46.5	57.4	127	22	AAO07630 Human polypeptide
35	46	56.8	99	22	AAO11475 Human polypeptide
36	46	56.8	114	22	AAO03173 Human polypeptide
37	46	56.8	125	22	AAO12870 Human polypeptide
38	46	56.8	133	22	AAO02140 Human polypeptide
39	46	56.8	135	22	AAO01562 Human polypeptide
40	46	56.8	141	22	AAO06613 Human polypeptide
41	46	56.8	356	22	ABG21039 Novel human diagno
42	46	56.8	498	22	ABG09968 Novel human diagno
43	46	56.8	560	22	ABG21040 Drosophila melanog
44	46	56.8	1194	22	ABW59646 Chlamydia pneumoni
45	45.5	56.2	584	20	AAW34934

ALIGNMENTS

RESULT 1

AAW99667

ID AAW99667 standard; Protein: 185 AA.

AC AAW99667;

XX

XX

DT 07-JUN-1999 (first entry)

XX

XX

DE Human secreted protein clone ej90_5 protein.

XX

DE Human; secreted protein; nutritional; cytokine; cell proliferation;

XX

KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;

XX

KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;

XX

KW anti-inflammatory; cadherin; tumour invasion suppressor;

XX

XX Homo sapiens.

XX

PN WO9907840-A1.

XX

PD 18-FEB-1999.

XX

XX 06-AUG-1998; 98WO-US16318.

PF

XX

PR 04-AUG-1998; 98US-0130189.

PR

XX 06-AUG-1997; 97US-0906708.

XX

XX (GEM) GENETICS INST INC.

XX

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

PI Merberg D, Racie IA, Steininger RJ, Treacy M;

XX WPI; 1999-167419/14.

DR N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
PT or adult retina cDNA libraries
XX
PS Claim 34; Page 98-99; 107pp; English.
XX
CC The present sequence represents a human secreted protein. The secreted
CC protein can have activities such as: nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating activity,
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity, chemotactic/
CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
CC suppressor activity, and tumour inhibition activity. The secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. The
CC polynucleotides are also stated to be useful for gene therapy.
XX
SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGKGGGPPPK 14
| | | | | | | | | | | | | | | |
DB 104 kklqkgpggpppk 117

RESULT 2
ID AAB24067 standard; Protein; 185 AA.
XX
AC AAB24067;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1005 protein sequence SEQ ID NO:34.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW immunosuppressant; antineoplastic; immunosuppressive;
KW immunostimulant; antineoplastic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
XX 14-SEP-2000.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 30-NOV-1999; 99WO-US28313.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX

DR WPI; 2000-572270/53.
XX N-PSDB; AAC58377.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
XX Claim 61; Fig 22; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO639, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1133, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the
CC treatment, diagnosis and prevention of cancer. The antibodies and other
CC anti-tumour compounds may be used to treat various conditions, including
CC those characterised by overexpression and/or activation of the amplified
CC PRO genes. Exemplary conditions or disorders to be treated with such
CC antibodies and other compounds include benign or malignant tumours
CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic,
CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC leukaemias and lymphoid malignancies, and other disorders such as neuronal,
CC glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC epithelial, stromal and blastocoele disorders, and inflammatory,
CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC primers and hybridisation probes used in the isolation of the human PRO
CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC PRO polynucleotide and protein sequences given in the exemplification of
CC the present invention.
XX
SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGKGGGPPPK 14
| | | | | | | | | | | | | | | |
DB 104 kklqkgpggpppk 117

RESULT 3
AAY87272
ID AAY87272 standard; Protein; 185 AA.
XX
AC AAY87272;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
XX
XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; neutropenic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
XX
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14484.
XX
XX 26-JUN-1998; 98US-0090762.
XX

PR 31-JUL-1998; 98US-0094983.
 PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX
 DR WPI: 2000-160673/14.
 DR N-PSDB; AA298157.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease
 XX
 PS Claim 1; Page 193-194; 327pp; English.
 XX
 CC AA298109 to AA298242 encode AA298724 to AA298737 which represent the
 CC human signal peptide-containing proteins HSPp-1 to HSPp-134. HSPps have
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can
 CC be used in gene therapy. HSPps can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSPp. Antagonists of
 CC HSPp are used to treat or prevent disorders associated with increased
 CC activity or function of HSPp. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPp
 CC nucleic acids can be used for the recombinant production of HSPp, for
 CC detecting HSPp in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSPp are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSPp-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSPp
 CC from natural sources.
 XX
 SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLOGKGFPGPPPK 14
 Db 104 kklqkgpggpppk 117
 |||||

RESULT 4
 AA298686
 ID AA298686 standard; protein; 185 AA.
 XX
 AC AA298686;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1005.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN W09963088-A2.
 XX

PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-US12252.
 XX
 PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 02-JUN-1998; 98US-0087759.
 PR 03-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
 PR 04-JUN-1998; 98US-0088025.
 PR 04-JUN-1998; 98US-0088028.
 PR 04-JUN-1998; 98US-0088029.
 PR 04-JUN-1998; 98US-0088030.
 PR 04-JUN-1998; 98US-0088033.
 PR 04-JUN-1998; 98US-0088326.
 PR 05-JUN-1998; 98US-0088167.
 PR 05-JUN-1998; 98US-0088202.
 PR 05-JUN-1998; 98US-0088212.
 PR 05-JUN-1998; 98US-0088217.
 PR 05-JUN-1998; 98US-0088655.
 PR 10-JUN-1998; 98US-0088722.
 PR 10-JUN-1998; 98US-0088730.
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 PR 10-JUN-1998; 98US-0088741.
 PR 10-JUN-1998; 98US-0088742.
 PR 10-JUN-1998; 98US-0088810.
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 PR 10-JUN-1998; 98US-0088825.
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 PR 11-JUN-1998; 98US-0088863.
 PR 11-JUN-1998; 98US-0088876.
 PR 12-JUN-1998; 98US-0089090.
 PR 12-JUN-1998; 98US-0089105.
 PR 16-JUN-1998; 98US-0089440.
 PR 16-JUN-1998; 98US-0089512.
 PR 16-JUN-1998; 98US-0089514.
 PR 17-JUN-1998; 98US-0089532.
 PR 17-JUN-1998; 98US-0089538.
 PR 17-JUN-1998; 98US-0089598.
 PR 17-JUN-1998; 98US-0089599.
 PR 17-JUN-1998; 98US-0089600.
 PR 17-JUN-1998; 98US-0089653.
 PR 18-JUN-1998; 98US-0089801.
 PR 18-JUN-1998; 98US-0089907.
 PR 18-JUN-1998; 98US-0089908.
 PR 19-JUN-1998; 98US-0089947.
 PR 19-JUN-1998; 98US-0089948.
 PR 19-JUN-1998; 98US-0089952.
 PR 22-JUN-1998; 98US-0090246.
 PR 22-JUN-1998; 98US-0090252.
 PR 22-JUN-1998; 98US-0090254.
 PR 23-JUN-1998; 98US-0090349.
 PR 23-JUN-1998; 98US-0090355.
 PR 24-JUN-1998; 98US-0090429.
 PR 24-JUN-1998; 98US-0090431.
 PR 24-JUN-1998; 98US-0090435.
 PR 24-JUN-1998; 98US-0090444.
 PR 24-JUN-1998; 98US-0090445.
 PR 24-JUN-1998; 98US-0090461.
 PR 24-JUN-1998; 98US-0090472.
 PR 24-JUN-1998; 98US-0090535.
 PR 24-JUN-1998; 98US-0090538.
 PR 24-JUN-1998; 98US-0090540.
 PR 24-JUN-1998; 98US-0090557.
 PR 25-JUN-1998; 98US-0090676.
 PR 25-JUN-1998; 98US-0090678.
 PR 25-JUN-1998; 98US-0090688.
 PR 25-JUN-1998; 98US-0090690.

PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 07-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
PR (GETH) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX

DR WPI; 2000-072883/06.
DR N-PSDB; AA265023.
XX Membrane-bound proteins and related nucleotide sequences
PT
XX
PS claim 12; Fig 139; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, RIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SQ Sequence 185 AA;

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLOGKGGGPPPK 14
Db 104 kklgkgpggpppk 117
|||||
|||||

RESULT 5
AAB65209
ID AAB65209 standard; Protein; 185 AA.
XX
AC AAB65209;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO2000073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB: AAF44169.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA;
 XX
 Query Match 100.0%; Score 81; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLOGKGGGPPPK 14
 Db 104 kklqgkpggpppk 117
 XX
 RESULT 6
 AAB50957
 ID AAB50957 standard; Protein; 185 AA.
 AC
 XX AAB50957;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human PRO1005 protein.
 XX
 KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200073348-A2.
 PN
 XX 07-DEC-2000.
 PD
 XX 30-MAY-2000; 2000WO-US14941.
 PF

XX 02-JUN-1999; 99WO-US12352.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-0187202.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-016509/02.
 DR N-PSDB: AAC91559.
 XX
 PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeleic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA;
 XX
 Query Match 100.0%; Score 81; DB 22; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKLOGKGGGPPPK 14
 Db 104 kklqgkpggpppk 117
 XX
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 9 clone HNSAD53.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytosstatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;
 KW vulnery; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX WO200061623-A1.
 XX 19-OCT-2000.
 XX 06-APR-2000; 2000WO-US08979.
 XX 09-APR-1999; 99US-0128693.
 XX 26-APR-1999; 99US-0130991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX WPI; 2000-647418/62.
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX Claim 11; Page 598; 716pp; English.
 XX Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX Sequence 186 AA;
 Query Match 100.0%; Score 81; DB 21; Length 186;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLOGKGGGPPPK 14
 Db 104 kklqgkpgpgppk 117
 RESULT 8
 AAW69974
 ID AAW69974 standard; Protein: 194 AA.
 XX AAW69974;
 XX 16-NOV-1998 (first entry)
 XX Cancer associated protein.
 XX Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX Synthetic.
 OS
 XX

PN WO9837187-A1.
 XX 27-AUG-1998.
 XX 18-FEB-1998; 98WO-JP00667.
 XX 21-FEB-1997; 97JP-0052508.
 XX (TAKI) TAKARA SHUZO CO LTD.
 XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 PI WPI; 1998-467552/40.
 XX Detection of cancer cells in tissue samples - by changes in mRNA
 PT expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 XX Claim 14; Page 64-65; 92pp; Japanese.
 XX The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX Sequence 194 AA;
 Query Match 100.0%; Score 81; DB 19; Length 194;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKLOGKGGGPPPK 14
 Db 113 kklqgkpgpgppk 126
 RESULT 9
 AAY76591
 ID AAY76591 standard; Protein: 194 AA.
 XX AAY76591;
 XX 10-APR-2000 (first entry)
 XX Human ovarian tumor EST fragment encoded protein 87.
 DE Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX Homo sapiens.
 XX DE19817557-A1.
 XX 21-OCT-1999.
 XX 09-APR-1998; 98DE-1017557.
 XX 09-APR-1998; 98DE-1017557.
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 PA Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
 PI

DR WPI; 1999-591920/51.
 DR N-PSDB; AA277487.
 XX
 PT New nucleic acid sequences expressed in ovarian, and some other, cancer
 PT tissues, and derived polypeptides, for treatment of ovarian cancer and
 PT identification of therapeutic agents -
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-277572.
 XX
 CC Sequence 194 AA;
 CC
 CC Query Match 100.0%; Score 81; DB 20; Length 194;
 CC Best Local Similarity 100.0%; Pred. No. 0.003;
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 KKLOGKGGPGGPPPK 14
 CC |||||
 CC DB 113 KKlqgkgpggpppk 126
 CC
 CC RESULT 10
 CC AAB41048
 CC ID AAB41048 standard; Protein; 103 AA.
 CC
 CC AC AAB41048;
 CC
 CC XX 08-FEB-2001 (first entry)
 CC
 CC DE Human ORFX ORF812 polypeptide sequence SEQ ID NO:1624.
 CC
 CC KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 CC KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 CC KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 CC KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 CC KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 CC KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 CC KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 CC KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 CC KW cholesterol ester storage; systemic lupus erythematosus; infection;
 CC KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 CC KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 CC KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 CC KW thrombosis; contraceptive.
 CC
 CC XX Homo sapiens.
 CC OS
 CC PN WO200058473-A2.
 CC
 CC XX 05-OCT-2000.
 CC
 CC PD
 CC XX 31-MAR-2000; 2000WO-US08621.
 CC
 CC PF
 CC XX 31-MAR-1999; 99US-0127607.
 CC
 CC PR

PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 PA (CURA-) CURAGEN CORP.
 XX
 XX Shimkets RA, Leach M;
 PI
 XX WPI; 2000-602362/57.
 DR N-PSDB; AAC75257.
 XX
 CC Novel nucleic acids and peptides derived from open reading frame X,
 CC useful for treating e.g. cancers, proliferative disorders,
 CC neurodegenerative disorders and cardiovascular disease -
 CC
 CC Claim 11; Page 1306; 5507pp; English.
 CC
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 CC XX Sequence 103 AA;
 CC
 CC Query Match 64.2%; Score 52; DB 21; Length 103;
 CC Best Local Similarity 64.3%; Pred. No. 9.8;
 CC Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 KKLOGKGGPGGPPPK 14
 CC :| ||||| | |
 CC DB 61 rkssgkgpgnprpk 74
 CC
 CC RESULT 11
 CC ID AA001151 standard; Protein; 163 AA.
 CC
 CC XX AA001151;
 CC
 CC DT 06-NOV-2001 (first entry)
 CC
 CC XX Human polypeptide SEQ ID NO 15043.
 CC DE
 CC KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 CC KW vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;
 CC KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 CC KW nervous system disorders; arthritis; inflammation.
 CC
 CC XX Homo sapiens.
 CC OS
 CC PN WO200164835-A2.
 CC
 CC XX 07-SEP-2001.
 CC
 CC PD
 CC XX 26-FEB-2001; 2001WO-US04927.
 CC
 CC PR

XX 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX N-PSDB; AAI81082.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-514838/56.
 XX N-PSDB; AAI81082.
 XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX Claim 20; SEQ ID NO 15043; 1399pp + Sequence Listing; English.
 XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 163 AA;

Query Match 64.2%; Score 52; DB 22; Length 163;
 Best Local Similarity 69.2%; Pred. No. 15;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLQKGGGPGPP 13
 || :||| |||
 Db 57 kkgqgkgnppp 69

RESULT 12
 AAU03592
 ID AAU03592 standard; Protein; 279 AA.
 XX AAU03592;
 AC AAU03592;
 DT 24-OCT-2001 (first entry)
 XX Human DNA modification protein, DNAMP-7.
 DE Human; DNA modification protein; DNAMP-7; developmental disorder;
 XX seizure disorder; hyperproliferative disorder; cancer; gene therapy;
 KW DNA repair disorder.
 XX Homo sapiens.
 XX WO200151642-A2.
 PN 19-JUL-2001.
 XX 10-JAN-2001; 2001WO-US00870.
 XX 13-JAN-2000; 2000US-0176178.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Tang YT, Lal P, Hillman JL, Yue H, Azimzai Y, Lu DAM, Baughn MR;
 XX WPI; 2001-442149/47.

DR N-PSDB; AAS05998.

XX New isolated human DNA modification protein, useful for diagnosing,
 PT preventing and treating diseases associated with the protein such as
 PT developmental disorders, cancers and DNA repair disorders -
 XX Claim 1; Page 91-92; 101pp; English.

XX The present sequence represents the human DNA modification protein,
 CC DNAMP-7, which is 1 of 9 novel DNAMPs (AAU03586-AAU03594). The DNAMPs
 CC and their (ant)agonist are useful for treating a disease or
 CC condition associated with decreased expression or overexpression of
 CC functional DNAMP in a patient, where the disorder is selected
 CC from developmental disorders (e.g. renal tubular acidosis, anaemia,
 CC Cushing's syndrome, epilepsy, hereditary neuropathies, hypothyroidism,
 CC hyperproliferative disorders (e.g. cancer), and DNA repair disorders
 CC (e.g. xeroderma pigmentosum, Bloom's syndrome). DNAMPs are useful for
 CC screening a compound that specifically binds to them or modulates their
 CC activity, for screening libraries of compounds in a variety of drug
 CC screening techniques, and for analysing the proteome of a tissue or cell
 CC type. The polynucleotides encoding DNAMPs are useful for creating knockin
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model
 CC human disease, for therapeutic or diagnostic purposes, for somatic or
 CC germline gene therapy, to generate hybridisation probes useful in
 CC mapping the naturally occurring genomic sequence, and in molecular
 CC biological techniques. Antibodies to DNAMPs are useful as elements on a
 CC microarray, for diagnosing disorders associated with expression of DNAMP,
 CC and in assays to monitor patients being treated with DNAMP.
 XX Sequence 279 AA;

Query Match 64.2%; Score 52; DB 22; Length 279;
 Best Local Similarity 64.3%; Pred. No. 23;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKLQKGGGPGPPK 14
 :| ||||| |||
 Db 25 rkssgkgnprpk 38

RESULT 13
 AAB94309
 ID AAB94309 standard; Protein; 467 AA.
 XX AAB94309;
 AC AAB94309;
 XX 26-JUN-2001 (first entry)
 DT Human protein sequence SEQ ID NO:14777.
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 DE Homo sapiens.
 XX EP1074617-A2.
 PN 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 14777; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 467 AA;

Query Match 64.2%; Score 52; DB 22; Length 467;
 Best Local Similarity 64.3%; Pred. No. 36;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKQCKGPGGPPK 14
 :| ||||| |
 Db 213 rkssgkggnprk 226

RESULT 14
 AA004166
 ID AA004166 standard; Protein: 108 AA.

XX AA004166;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 18058.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-514838/56.
 DR N-PSDB; AAI184097.

XX Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -
 XX

PS Claim 20; SEQ ID NO 18058; 1399pp + Sequence Listing; English.

XX

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 108 AA;

Query Match 63.0%; Score 51; DB 22; Length 108;
 Best Local Similarity 80.0%; Pred. No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QCKGPGGPPP 13
 :| |||||
 Db 56 rgggpggppp 65

RESULT 15

AA011472

ID AA011472 standard; Protein: 125 AA.

XX AA011472;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 25364.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.

XX 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AAI191403.

XX

PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX
PS Claim 20; SEQ ID NO 25364; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 125 AA;

Query Match 63.0%; Score 51; DB 22; Length 125;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGPGGPPP 13
Db ||| | |||||
58 lgpgnggppp 68

Search completed: September 4, 2002, 16:45:03
Job time: 379 sec

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:06 ; Search time 57.74 Seconds
(without alignments)
5.922 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQGGPGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	50	61.7	673	4	US-09-078-347A-2
2	49	60.5	855	4	US-09-813-819-2
3	49	60.5	855	4	US-09-920-048-2
4	45	55.6	402	2	US-08-709-979A-3
5	45	55.6	402	3	US-08-709-974A-1
6	45	55.6	402	3	US-08-709-974A-5
7	45	55.6	415	2	US-08-833-642A-5
8	45	55.6	415	3	US-08-709-974A-4
9	45	55.6	415	4	US-09-069-632-1
10	45	55.6	435	1	US-08-361-920-27
11	45	55.6	435	1	US-08-479-939-27
12	45	55.6	435	1	US-08-483-432-27
13	45	55.6	435	4	US-09-069-632-3
14	45	55.6	752	4	US-09-817-180-2
15	45	55.6	822	4	US-09-817-180-4
16	44	54.3	18	3	US-08-630-916A-9
17	44	54.3	218	1	US-08-247-946A-3
18	44	54.3	218	5	PCT-US95-06420-3
19	44	54.3	1205	1	US-07-908-245-2
20	44	54.3	1205	4	US-08-319-866-10
21	44	54.3	1205	4	US-09-123-708-6
22	44	54.3	1205	4	US-09-123-624-6
23	43	53.1	265	2	US-08-484-905-119
24	43	53.1	265	3	US-08-481-585B-119
25	43	53.1	265	4	US-08-370-476-119
26	43	53.1	298	2	US-08-207-481-39
27	43	53.1	298	5	PCT-US95-02689-41

28	43	53.1	311	2	US-08-318-837-9	Sequence 9, Appli
29	42	51.9	118	1	US-08-393-985-14	Sequence 14, Appl
30	42	51.9	298	3	US-08-767-942A-25	Sequence 25, Appl
31	41	50.6	107	3	US-08-478-097A-19	Sequence 19, Appl
32	41	50.6	124	1	US-08-455-559-11	Sequence 11, Appl
33	41	50.6	124	4	US-09-145-060-11	Sequence 11, Appl
34	41	50.6	124	5	PCT-US94-00657-11	Sequence 11, Appl
35	41	50.6	147	4	US-09-347-833-10	Sequence 10, Appl
36	41	50.6	437	2	US-08-935-450-8	Sequence 8, Appli
37	41	50.6	629	3	US-08-464-258B-6	Sequence 6, Appli
38	41	50.6	3025	6	5223423-3	Patent No. 5223423
39	40	49.4	112	2	US-08-301-915-3	Sequence 3, Appli
40	40	49.4	112	3	US-08-524-694A-3	Sequence 3, Appli
41	40	49.4	112	5	PCT-US93-04301-3	Sequence 3, Appli
42	40	49.4	133	1	US-07-917-722-3	Sequence 3, Appli
43	40	49.4	256	2	US-08-727-688-33	Sequence 33, Appl
44	40	49.4	269	2	US-07-857-224B-14	Sequence 14, Appl
45	40	49.4	269	2	US-07-857-224B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-078-347A-2
; Sequence 2, Application US/09078347A
; Patent No. 6132968
; GENERAL INFORMATION:
; APPLICANT: Le, Xiao-Chun
; APPLICANT: Weinfield, Michael
; APPLICANT: Xing, James Z.
; TITLE OF INVENTION: Methods for Quantitating Low Level
; TITLE OF INVENTION: Modifications of Nucleotide Sequences
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,347A
; FILING DATE: 13-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cartoll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UALB-03283
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-078-347A-2

Query Match 61.7%; Score 50; DB 4; Length 673;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGPGGPPPK 13
| | | | |

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DB 313 LSGRGPGEPPP 323
RESULT 2
US-09-813-819-2
; Sequence 2, Application US/09813819
; Patent No. 6294368
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001177
; CURRENT APPLICATION NUMBER: US/09/813,819
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-813-819-2

Query Match 60.5%; Score 49; DB 4; Length 855;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPP 13
|:|:|:|:|:|
DB 797 KRLQSQGPAKPPPP 809

RESULT 3
US-09-920-048-2
; Sequence 2, Application US/09920048
; Patent No. 6344352
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001177DV
; CURRENT APPLICATION NUMBER: US/09/920,048
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/813,819
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Human
US-09-920-048-2

Query Match 60.5%; Score 49; DB 4; Length 855;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPP 13
|:|:|:|:|:|
DB 797 KRLQSQGPAKPPPP 809

RESULT 4
US-08-709-979A-3
; Sequence 3, Application US/08709979A
; Patent No. 5912157
; GENERAL INFORMATION:
; APPLICANT: Claus von der Osten
; APPLICANT: Martin Sch lein
; TITLE OF INVENTION: No. 5912157el Alkaline Cellulases
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; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5912157o No. 5912157disk of No. 5912157th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,979A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4160.404-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-979A-3

Query Match 55.6%; Score 45; DB 2; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLGKGGPGG-----PPPK 14
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DB 42 RAEGLGPGCGDGNPPPK 60

RESULT 5
US-08-709-974A-1
; Sequence 1, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
```

REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.414-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 6

US-08-709-974A-5
; Sequence 5, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten,Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127Y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 55.6%; Score 45; DB 3; Length 402;
Best Local Similarity 47.4%; Pred. No. 82;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 7
US-08-833-642A-5
; Sequence 5, Application US/08833642A
; Patent No. 5883066
; GENERAL INFORMATION:
; APPLICANT: Ivan M. A. J. Herbots et al.
; TITLE OF INVENTION: Liquid Detergent Compositions
; TITLE OF INVENTION: Containing Cellulase and Amine
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jackie Ann Zurcher
; ADDRESSEE: Dinsmore & Shohl LLP
; STREET: 255 E. Fifth Street
; STREET: 1900 Chemed Center
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: USA
; ZIP: 45202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,642A
; FILING DATE: April 8, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zurcher, J. A.
; REGISTRATION NUMBER: P42,251
; REFERENCE/DOCKET NUMBER: CM551C
; TELEPHONE: (513) 977-8377
; TELEFAX: (513) 977-8141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 47.4%; Pred. No. 84;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
: : | | | |
Db 42 RAELGPGGCGDGNPPPK 60

RESULT 8

US-08-709-974A-4
; Sequence 4, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten,Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York

```

; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-974A-4

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Query Match 55.6%; Score 45; DB 3; Length 415;
 Best Local Similarity 47.4%; Pred. No. 84;
 Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

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QY 2 KLOGKPGG-----PPPK 14
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Db 42 RAELGPGGCGDGNPPPK 60

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RESULT 9
; Sequence 1, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123

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; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-1

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Query Match 55.6%; Score 45; DB 4; Length 415;
 Best Local Similarity 47.4%; Pred. No. 84;
 Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

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QY 2 KLOGKPGG-----PPPK 14
   : : | | | | |
Db 42 RAELGPGGCGDGNPPPK 60

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RESULT 10
; Sequence 27, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sved, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; TITLE OF INVENTION: or Hemicellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5457046o No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-361-920-27

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Query Match 55.6%; Score 45; DB 1; Length 435;

Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 62 RAELGPGCGDGNPPPK 80

RESULT 11
US-08-479-939-27
; Sequence 27, Application US/08479939
; Patent No. 5686593
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56865930 No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-939-27

Query Match 55.6%; Score 45; DB 1; Length 435;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKPGG-----PPPK 14
Db 62 RAELGPGCGDGNPPPK 80

RESULT 13
US-09-069-632-3
; Sequence 3, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 62618280 No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue

```
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

Query Match 55.6%; Score 45; DB 4; Length 435;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKGGG-----PPPK 14
   :| |||||
Db 62 RAEGLGPGCGDGNPPPK 80

RESULT 14
US-09-817-180-2
; Sequence 2, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-2

Query Match 55.6%; Score 45; DB 4; Length 752;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
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QY 2 KLOGKGGG-----PPPK 14
   :| |||||
Db 62 RAEGLGPGCGDGNPPPK 80
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RESULT 14
US-09-817-180-2
; Sequence 2, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-2
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Query Match 55.6%; Score 45; DB 4; Length 752;
Best Local Similarity 47.4%; Pred. No. 88;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLOGKGGG-----PPPK 14
   :| |||||
Db 62 RAEGLGPGCGDGNPPPK 80
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RESULT 15
US-09-817-180-4
; Sequence 4, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Human
; US-09-817-180-4

Query Match 55.6%; Score 45; DB 4; Length 822;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLOGKGGGPPPP 13
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Db 387 KLEHLGFGPPPP 398

Search completed: September 4, 2002, 16:46:07
Job time: 328 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model
Run on: September 4, 2002, 16:59:19 ; Search time 704.77 Seconds
(without alignments)
6.992 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQKGGPGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 3502263 seqs, 351980561 residues 3502263
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	81	100.0	18	22	US-09-821-726-7
3	81	100.0	21	22	US-09-821-726-8
4	81	100.0	25	22	US-09-821-726-10
5	81	100.0	42	22	US-09-821-726-6
6	81	100.0	150	13	US-08-906-708-24
7	81	100.0	182	20	US-09-684-524-212
					Sequence 212, App
					Sequence 3, Appli
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 10, Appli
					Sequence 6, Appli
					Sequence 24, Appli

8	81	100.0	182	24	US-10-050-704-212	Sequence 212, App
9	81	100.0	185	1	PCT-US98-16318-18	Sequence 18, Appl
10	81	100.0	185	15	US-09-130-189-18	Sequence 18, Appl
11	81	100.0	185	20	US-09-684-524-105	Sequence 105, App
12	81	100.0	185	21	US-09-709-238-211	Sequence 211, App
13	81	100.0	185	21	US-09-746-783-146	Sequence 146, App
14	81	100.0	185	22	US-09-821-726-13	Sequence 13, Appl
15	81	100.0	185	22	US-09-821-726-18	Sequence 18, Appl
16	81	100.0	185	23	US-09-941-992-211	Sequence 211, App
17	81	100.0	185	23	US-09-989-279-211	Sequence 211, App
18	81	100.0	185	23	US-09-989-293A-211	Sequence 211, App
19	81	100.0	185	23	US-09-989-722-211	Sequence 211, App
20	81	100.0	185	23	US-09-989-723-211	Sequence 211, App
21	81	100.0	185	23	US-09-989-724-211	Sequence 211, App
22	81	100.0	185	23	US-09-989-725-211	Sequence 211, App
23	81	100.0	185	23	US-09-989-726-211	Sequence 211, App
24	81	100.0	185	23	US-09-989-727-211	Sequence 211, App
25	81	100.0	185	23	US-09-989-728-211	Sequence 211, App
26	81	100.0	185	23	US-09-989-729A-211	Sequence 211, App
27	81	100.0	185	23	US-09-989-730-211	Sequence 211, App
28	81	100.0	185	23	US-09-989-731-211	Sequence 211, App
29	81	100.0	185	23	US-09-989-732-211	Sequence 211, App
30	81	100.0	185	23	US-09-989-734-211	Sequence 211, App
31	81	100.0	185	23	US-09-989-735-211	Sequence 211, App
32	81	100.0	185	23	US-09-989-862-211	Sequence 211, App
33	81	100.0	185	23	US-09-990-427-211	Sequence 211, App
34	81	100.0	185	23	US-09-990-436-211	Sequence 211, App
35	81	100.0	185	23	US-09-990-437-211	Sequence 211, App
36	81	100.0	185	23	US-09-990-438-211	Sequence 211, App
37	81	100.0	185	23	US-09-990-439-211	Sequence 211, App
38	81	100.0	185	23	US-09-990-440-211	Sequence 211, App
39	81	100.0	185	23	US-09-990-441-211	Sequence 211, App
40	81	100.0	185	23	US-09-990-442-211	Sequence 211, App
41	81	100.0	185	23	US-09-990-443-211	Sequence 211, App
42	81	100.0	185	23	US-09-990-444-211	Sequence 211, App
43	81	100.0	185	23	US-09-990-456-211	Sequence 211, App
44	81	100.0	185	23	US-09-990-562-211	Sequence 211, App
45	81	100.0	185	23	US-09-990-562-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-3
; Sequence 3, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-3

Query Match 100.0%; Score 81; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGPPPK 14
DB 1 KKLQKGGPGPPPK 14

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RESULT 2
US-09-821-726-7
; Sequence 7, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-7

Query Match      100.0%; Score 81; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
Db 1 KKLOGKGGGPPPK 14

RESULT 3
US-09-821-726-8
; Sequence 8, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-8

Query Match      100.0%; Score 81; DB 22; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
Db 8 KKLOGKGGGPPPK 21

RESULT 4
US-09-821-726-10
; Sequence 10, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-10

Query Match      100.0%; Score 81; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
Db 8 KKLOGKGGGPPPK 21

RESULT 5
US-09-821-726-6
; Sequence 6, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-6

Query Match      100.0%; Score 81; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
Db 27 KKLOGKGGGPPPK 40

RESULT 6
US-08-906-708-24
; Sequence 24, Application US/08906708
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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Thu Sep 5 11:23:37 2002

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-708-24

Query Match 100.0%; Score 81; DB 13; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 7
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match 100.0%; Score 81; DB 20; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 8
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,708
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-906-708-24

Query Match 100.0%; Score 81; DB 13; Length 150;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 7
US-09-684-524-212
; Sequence 212, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-212

Query Match 100.0%; Score 81; DB 20; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 8
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 100.0%; Score 81; DB 24; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 9
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 100.0%; Score 81; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGPGGPPPK 14
Db 104 KKLQKGPGGPPPK 117

RESULT 10
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
```

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; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match      100.0%; Score 81; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGPPPK 14
Db 104 KKLQKGGPGPPPK 117

RESULT 11
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match      100.0%; Score 81; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLQKGGPGPPPK 14
Db 104 KKLQKGGPGPPPK 117

RESULT 12
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Chen, Jian
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2730R1C1
; CURRENT APPLICATION NUMBER: US/09/709,238
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
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us-09-821-726-3.rapm

Thu Sep 5 11:23:37 2002

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; PRIOR APPLICATION NUMBER: US 60/089,514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: US 60/089,532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 60/089,801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 60/089,947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/089,952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 60/090,246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: US 60/090,355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/090,429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: US 60/090,444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,461
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 60/090,676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,696
; PRIOR FILING DATE: 1998-06-25

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,862
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,863
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/091,358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,486
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,646
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,673
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/091,982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/092,182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
DB 104 KKLOGKGGGPPPK 117

RESULT 13
US-09-746-783-146
; Sequence 146, Application US/09746783
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Lavallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.
; Howes, Steven H.
; Fechtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,783
; FILING DATE: 21-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Milasincic, Debra J.
; REGISTRATION NUMBER: 46,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
US-09-746-783-146

Query Match 100.0%; Score 81; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 14
US-09-821-726-13
; Sequence 13, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-13

Query Match 100.0%; Score 81; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 15
US-09-821-726-18
; Sequence 18, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS

;
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Porcine sp.
US-09-821-726-18

Query Match 100.0%; Score 81; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 100.0%; Score 81; DB 5; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKLOGKGGGPPPK 14
|||||
Db 104 KKLOGKGGGPPPK 117

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

us-09-821-726-3.rapn

Thu' Sep 5 11:23:37 2002

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match      100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKGKGPGGPPPK 14
Db 104 KKGKGPGGPPPK 117

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match      100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKGKGPGGPPPK 14
Db 104 KKGKGPGGPPPK 117

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

```

```

Query Match      100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KKLOGKGGGPPPK 14
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DB 104 KKLOGKGGGPPPK 117

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RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC7
; CURRENT APPLICATION NUMBER: US/10/216.165
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148

```

```

Query Match      100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 KKLOGKGGGPPPK 14
   |||||
DB 104 KKLOGKGGGPPPK 117

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RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC9
; CURRENT APPLICATION NUMBER: US/10/216.166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148

```

```

Query Match      100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KKLOGKGGGPPPK 14
   |||||
DB 104 KKLOGKGGGPPPK 117

```

```

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

```


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```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

```

```

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

Qy 1 KKLQKGPGGPPPK 14
    |||
Db 104 KKLQKGPGGPPPK 117

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```

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

```

```

; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

```

```

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

Qy 1 KKLQKGPGGPPPK 14
    |||
Db 104 KKLQKGPGGPPPK 117

```

```

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

```

```

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

Qy 1 KKLQKGPGGPPPK 14
    |||
Db 104 KKLQKGPGGPPPK 117

```

RESULT 13
 US-10-218-849-148
 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 100.0%; Score 81; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
 |||||

Db 104 KKLOGKGGGPPPK 117

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-930-148

Query Match 100.0%; Score 81; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLOGKGGGPPPK 14
 |||||

Db 104 KKLOGKGGGPPPK 117

RESULT 15
 US-10-219-003-148
 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application Number: 10/119,480
 ; Prior Filing Date: 2002-04-09
 ; Prior Application Number: 60/059113
 ; Prior Filing Date: 1997-09-17
 ; Prior Application Number: 60/062287
 ; Prior Filing Date: 1997-10-17
 ; Prior Application Number: 60/063549
 ; Prior Filing Date: 1997-10-28
 ; Prior Application Number: 60/064103
 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
 ; Prior Application Number: 60/079294
 ; Prior Filing Date: 1998-03-25
 ; Prior Application Number: 60/079656
 ; Prior Filing Date: 1998-03-26
 ; Prior Application Number: 60/079728
 ; Prior Filing Date: 1998-03-27
 ; Prior Application Number: 60/081819
 ; Prior Filing Date: 1998-04-15
 ; Prior Application Number: 60/081955
 ; Prior Filing Date: 1998-04-15
 ; Prior Application Number: 60/082804
 ; Prior Filing Date: 1998-04-22
 ; Prior Application Number: 60/084441
 ; Prior Filing Date: 1998-05-06
 ; Prior Application Number: 60/085323
 ; Prior Filing Date: 1998-05-13
 ; Prior Application Number: 60/085579
 ; Prior Filing Date: 1998-05-15
 ; Prior Application Number: 60/086392
 ; Prior Filing Date: 1998-05-22
 ; Prior Application Number: 60/089532
 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089538
 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089905
 ; Prior Filing Date: 1998-06-18
 ; Prior Application Number: 60/090472
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090557
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090691
 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 100.0%; Score 81; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLOGKGGPPPK 14
|||||
Db 104 KKLOGKGGPPPK 117

Search completed: September 4, 2002, 17:04:23

Thu Sep 5 11:23:37 2002

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Page 8

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:30 : Search time 75.48 Seconds
(without alignments)
17.823 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLQKGGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	60	74.1	1677	2 T14267	Xin protein, stage
2	50	61.7	673	1 BVEUCB	excinuclease ABC C
3	50	61.7	673	2 A93736	excision nuclease
4	50	61.7	673	2 B85586	DNA repair, excisi
5	50	61.7	673	2 AD0597	excision nuclease
6	47	58.0	22	2 C42856	hypothetical prote
7	47	58.0	669	2 D82739	excinuclease ABC s
8	46	56.8	377	2 E87022	probable conserved
9	46	56.8	426	2 A93695	transforming prote
10	46	56.8	551	2 S57447	HPBR11-7 protein -
11	46	56.8	561	2 T16148	hypothetical prote
12	46	56.8	830	2 T18860	hypothetical prote
13	46	56.8	1105	1 S40243	DNA-directed DNA p
14	46	56.8	1315	2 T32734	myosin-IA - Acanth
15	46	56.8	1357	2 T29265	hypothetical prote
16	45.5	56.2	579	2 D72092	conserved hypotet
17	45.5	56.2	579	2 C86532	CT082 hypotet
18	45	55.6	171	2 H96833	hypothetical prote
19	45	55.6	477	1 TVMVCS	protein-tyrosine k
20	45	55.6	609	1 TVMVGC	protein-tyrosine k
21	45	55.6	820	1 TVCTFF	protein-tyrosine k
22	45	55.6	822	1 THUUFF	protein-tyrosine k
23	45	55.6	2715	2 T13049	eyelid - fruit fly
24	44	54.3	142	2 D32880	hypothetical prote
25	44	54.3	149	2 T31446	plastoquinol--plas
26	44	54.3	182	2 B86462	hypothetical prote
27	44	54.3	218	1 TVHURR	transforming prote
28	44	54.3	230	2 I56979	nitric-oxide synth
29	44	54.3	347	2 E97487	hypothetical prote

ALIGNMENTS

RESULT 1

T14267

Xin protein, stage early embryo - mouse

C:Species: Mus musculus (house mouse)

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R:Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1677 <WAN>

A:Cross-references: EMBL:AF051945; NID:g2970645; PID:g2970645; PIDN:AAC06023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match 74.1%; Score 60; DB 2; Length 1677;

Best Local Similarity 81.8%; Pred. No. 1.9;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 QKGKGGGPPPK 14

:|||||:

Db 574 EGKGGGPPPE 584

RESULT 2

BVEUCB

excinuclease ABC chain B - Escherichia coli

N:Alternate names: uvrB protein

N:Contains: excision endonuclease ABC (EC 3.1.-.-) chain B

C:Species: Escherichia coli

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 19-Jan-2001

C:Accession: A93612; C64814; A23765; A24939

R:Backendorf, C.; Spaink, H.; Barbeiro, A.P.; van de Putte, P.

Nucleic Acids Res. 14, 2877-2890, 1986

A:Title: Structure of the uvrB gene of Escherichia coli. Homology with other DNA repa

A:Reference number: A93613; MUID:86176773

A:Accession: A93613

A:Molecule type: DNA

A:Residues: 1-673 <BAC>

A:Cross-references: GB:X03722; NID:g43285; PIDN:CAA27357.1; PID:g43286

R:Arikan, E.; Kulkarni, M.S.; Thomas, D.C.; Sancar, A.

Nucleic Acids Res. 14, 2637-2650, 1986

A:Title: Sequences of the E. coli uvrB gene and protein.

A:Reference number: A93612; MUID:86176755

A:Accession: A93612

A:Molecule type: DNA

A:Residues: 1-476, 'R', 478-673 <ARI>

A:Cross-references: GB:X03678; GB:J01722; GB:J01723; GB:M24329; GB:V00374; GB:V00375;

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

ABC transporter, s
conserved hypotet
hypothetical prote
cell division cycl
excinuclease ABC s
ABC-type multidrug
hypothetical prote
nitric-oxide synth
nitric-oxide synth
nitric-oxide synth
collagen alpha 1(I
collagen alpha 1(I
vpx protein - simi
hypothetical prote
hypothetical prote
hypothetical prote

30 44 54.3 347 2 AE2705
31 44 54.3 558 2 B81711
32 44 54.3 560 2 D71560
33 44 54.3 593 2 T43323
34 44 54.3 670 2 A83255
35 44 54.3 706 2 D97303
36 44 54.3 996 2 A71080
37 44 54.3 1202 2 S71424
38 44 54.3 1203 1 A47501
39 44 54.3 1205 1 A38943
40 44 54.3 1464 2 S59856
41 43.5 53.7 1049 1 GCB07S
42 43 53.1 140 2 S46351
43 43 53.1 189 2 A86369
44 43 53.1 221 2 G72665
45 43 53.1 224 2 B72710

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: C64814

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-673 <BLAT>

A:Cross-references: GB:AB000180; GB:U00096; NID:gl1786988; PIDN:AAC73866.1; PID:gl1786996;

A:Experimental source: strain K-12, substrain MG1655

C:Comment: uvrA, uvrB, and uvrC function together as excision nuclease.

C:Genetics:

A:Gene: uvrB

A:Map position: 18 min

C:Function:

A:Description: stimulates the ATPase activity of uvrA protein in the presence of UV-irradiation

C:Superfamily: excinuclease ABC chain B

C:Keywords: ATP; DNA repair; hydrolase; nucleotide binding; P-loop

F:39-46/Region: nucleotide-binding motif A (P-loop)

F:334-339/Region: nucleotide-binding motif B

F:338-341/Region: DEXH motif

Query Match 61.7%; Score 50; DB 1; Length 673;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : |||| |||

Db 313 LSGRGGGPPPP 323

RESULT 3

A99736

excision nuclease subunit B [imported] - *Escherichia coli* (strain O157:H7, substrain RIM)

C:Species: *Escherichia coli*

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C:Accession: A99736

R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic islands

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: A99736

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <HAY>

A:Cross-references: GB:BA000007; PIDN:BA34280.1; PID:gl1360316; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 050952

C:Genetics:

A:Gene: Ecs0857

C:Superfamily: excinuclease ABC chain B

Query Match

Best Local Similarity 61.7%; Score 50; DB 2; Length 673;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : |||| |||

Db 313 LSGRGGGPPPP 323

RESULT 4

B85586

DNA repair, excision nuclease subunit B [imported] - *Escherichia coli* (strain O157:H7, substrain RIM)

C:Species: *Escherichia coli*

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: B85586

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85586

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <STO>

A:Cross-references: GB:AE005174; NID:gl12513768; PIDN:AAG55150.1; GSPDB:GN00145; UWGP:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: uvrB

C:Superfamily: excinuclease ABC chain B

Query Match

Best Local Similarity 61.7%; Score 50; DB 2; Length 673;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : |||| |||

Db 313 LSGRGGGPPPP 323

RESULT 5

AD0597

excision nuclease ABC chain B STY0831 [imported] - *Salmonella enterica* subsp. enteric

C:Species: *Salmonella enterica* subsp. enterica serovar Typhi

A:Note: this species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AD0597

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se

A:Reference number: AB0502; PMID:11677608

A:Accession: AD0597

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-673 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD05246.1; PID:gl6502016; GSPDB:GN00176

C:Genetics:

A:Gene: STY0831

C:Superfamily: excinuclease ABC chain B

Query Match

Best Local Similarity 61.7%; Score 50; DB 2; Length 673;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LOGKGGGPPPP 13

| : |||| |||

Db 313 LSGRGGGPPPP 323

RESULT 6

C42856

hypothetical protein 3 EPF-region [Imported] - human (fragment)

C:Species: *Homo sapiens* (man)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C:Accession: C42856

R:Li, Z.; Diaz, L.A.; Haas, A.L.; Giudice, G.J.

J. Biol. Chem. 267, 15829-15835, 1992

A:Title: cDNA cloning of a novel human ubiquitin carrier protein. An antigenic domain

this human epidermal transcript.

A:Reference number: A42856; MUID:92348449

A:Accession: C42856

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-22 <LIU>

A:Experimental source: keratinocyte

A:Note: sequence extracted from NCBI backbone (NCBI:109895, NCBI:109899)

Thu' Sep 5 11:23:37 2002

Query Match 58.0%; Score 47; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
QY 2 KLOGKGPGGPPP 13
I :||||| I
DB 6 KNAGRGPGGPAP 17

RESULT 7
D82739
excinuclease ABC subunit B XF0967 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C:Accession: D82739
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82739
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-669 <STM>
A:Cross-references: GB:AE003935; GB:AE003849; NID:g9105894; PIDN:AAF83777.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briões, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P
as-Nelo, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshakho, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
C:Gene: XF0967
C:Superfamily: excinuclease ABC chain B

Query Match 58.0%; Score 47; DB 2; Length 669;
Best Local Similarity 61.5%; Pred. No. 50;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;
QY 1 KKLQKGPGGPPP 13
: ||| ||| |||
DB 311 RHLTGKAPGEP 323

RESULT 8
E87022
probable conserved membrane protein ML0907 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: E87022
R:Coile, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: E87022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <STO>
A:Cross-references: GB:AL450380; NID:g13092977; PIDN:CAC31288.1; GSPDB:GN00147
C:Genetics:

A:Gene: ML0907

Query Match 56.8%; Score 46; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GPGGPPP 13
|||||
DB 254 GPGGPPP 260

RESULT 9
A39695
transforming protein (N-myc) - common canary
C:Species: Serinus canaria (common canary)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997
C:Accession: A39695
R:Collum, R.G.; Clayton, D.F.; Alt, F.W.
Mol. Cell. Biol. 11, 1770-1776, 1991
A:Title: Structure and expression of canary myc family genes.
A:Reference number: A39695; MUID:91141534
A:Accession: A39695
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <COL>
A:Cross-references: GB:M64251; GB:M64598
C:Superfamily: myc transforming protein; myc transforming protein homology
C:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein
F:11-426/Domain: myc transforming protein homology <MYC>
F:395-423/Region: leucine zipper motif

Query Match 56.8%; Score 46; DB 2; Length 426;
Best Local Similarity 61.5%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KKLQKGPGGPPP 13
: ||| ||| |||
DB 144 EKLQNKTPAAP 156

RESULT 10
S57447
HPBRII-7 protein - human
N:Alternate names: HPBRII-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S57447; S57489
R:Fleischhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <FL>
A:Cross-references: EMBL:X67336; NID:g871300; PIDN:CAA47751.1; PID:g871301
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299
C:Genetics:
A:Introns: 231/3
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleopro
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 56.8%; Score 46; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GPGGPPP 13

Db 222 GPGGPPP 228

|||||||

RESULT 11

T16148 hypothetical protein F25B5.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16148

R:Taich, A.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid F25B5.

A:Reference number: Z18458

A:Accession: T16148

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-561 <TAI>

A:Cross-references: EMBL:U23172; NID:q726388; PID:g726394; PIDN:AAC46528.1; CESP:F25B5.7

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F25B5.7

A:Introns: 39/2; 157/3; 258/2; 290/2; 356/1; 531/1

Query Match 56.8%; Score 46; DB 2; Length 561;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

|||||||

Db 409 GPGGPPP 415

RESULT 12

T18860 hypothetical protein C02C6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T18860

R:Swinburne, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19032

A:Accession: T18860

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-830 <WIL>

A:Cross-references: EMBL:Z79596; PIDN:CAB01857.1; GSPDB:GN000028; CESP:C02C6.1

A:Experimental source: clone C02C6

C:Genetics:

A:Gene: CESP:C02C6.1

A:Map position: X

A:Introns: 56/2; 131/1; 333/2; 501/2; 593/2; 686/3; 815/2

C:Superfamily: human dynamin II; pleckstrin repeat homology

Query Match 56.8%; Score 46; DB 2; Length 830;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

|||||||

Db 818 GPGGPPP 824

RESULT 13

S40243

DNA-directed DNA polymerase (EC 2.7.7.7) delta chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S40243; JT0670

R:Cullmann, G.; Hindges, R.; Burchtold, M.W.; Huebscher, U.

submitted to the EMBL Data Library, March 1993

A:Reference number: S40243

A:Accession: S40243

A:Molecule type: mRNA

A:Residues: 1-1105 <CUL>

A:Cross-references: EMBL:Z21848; NID:q438133; PIDN:CAA79895.1; PID:q438134

R:Cullmann, G.; Hindges, R.; Burchtold, M.W.; Huebscher, U.

Gene 134, 191-200, 1993

A:Title: Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of the hom

A:Reference number: JT0670; MUID:94085777

A:Accession: JT0670

A:Molecule type: DNA

A:Residues: 1-1111, 'G', 113, 'P', 115-1034, 'Y', 1036-1105 <CU2>

A:Cross-references: EMBL:Z21848

A>Note: the sequence translated from Z21848 is inconsistent with that from this sequ

C:Comment: Three DNA polymerases alpha, delta and epsilon chains are essential. This

C:Genetics:

A:Gene: poldelta

C:Superfamily: herpesvirus DNA-directed DNA polymerase

C:Keywords: DNA replication; heterodimer; nucleotidyltransferase

Query Match 56.8%; Score 46; DB 1; Length 1105;

Best Local Similarity 57.1%; Pred. No. 1.1e+02;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLOGKGGGPPPK 14

| : | | | | | | | :

Db 4 KRRQGGGPGVPPKR 17

RESULT 14

T32734

myosin-IA - Acanthamoeba castellanii

C:Species: Acanthamoeba castellanii

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000

C:Accession: T32734

R:Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.

submitted to the EMBL Data Library, August 1998

A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA G

A:Reference number: Z21216

A:Accession: T32734

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1215 <LEE>

A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1

A:Experimental source: strain Neff

C:Genetics:

A:Gene: MIA

A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 5

C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 hom

F:14-674/Domain: myosin motor domain homology <MMO>

Query Match 56.8%; Score 46; DB 2; Length 1215;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GPGGPPP 13

| | | | | | | |

Db 1075 GPGGPPP 1081

RESULT 15

T29265

hypothetical protein C01G8.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29265

R:Du, Z.; Gattung, S.

submitted to the EMBL Data Library, November 1996

A:Description: The sequence of C. elegans cosmid C01G8.

A:Reference number: Z20597

A:Accession: T29265

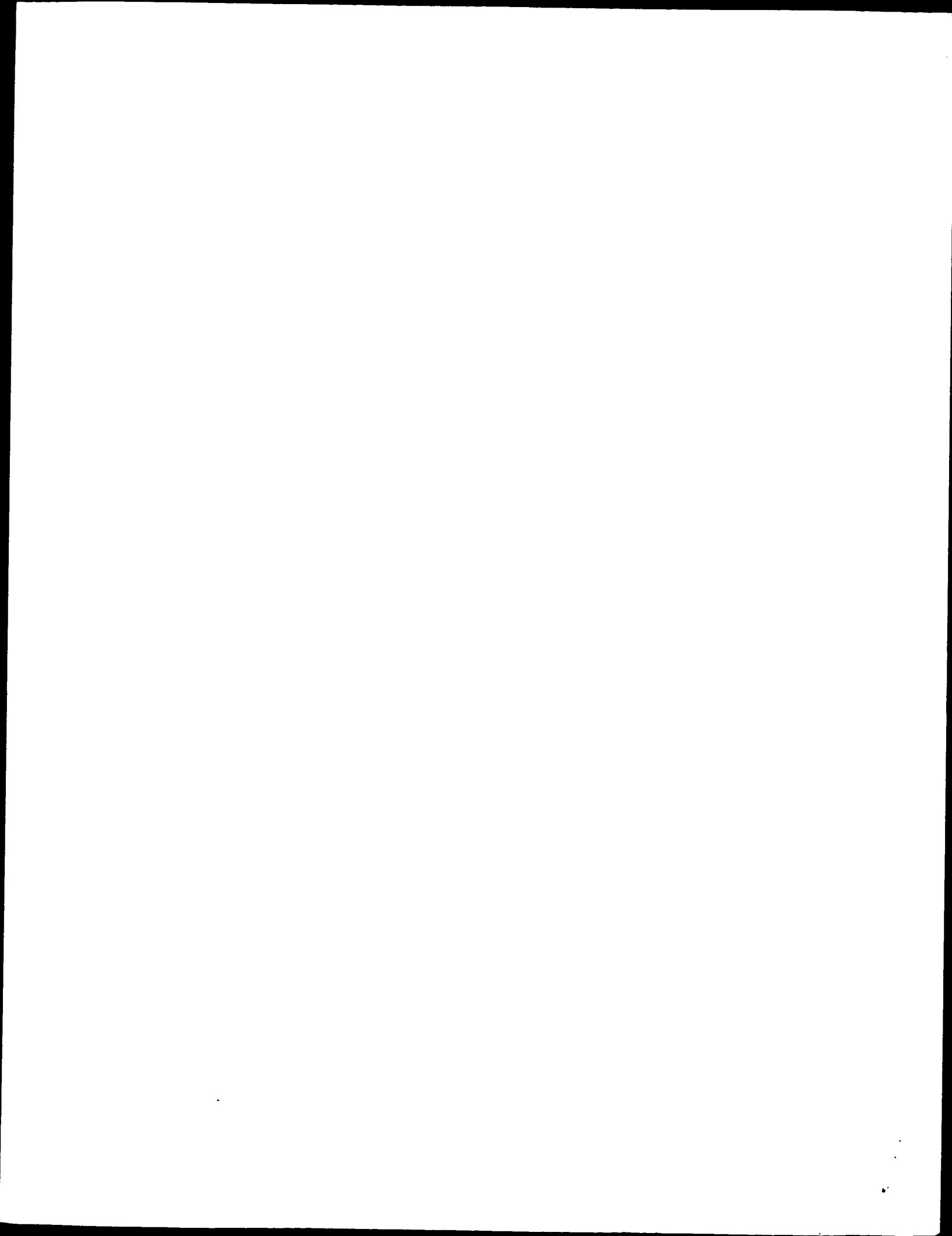
Thu Sep 5 11:23:37 2002

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1357 <DUZ>
A;Cross-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7
A;Experimental source: strain Bristol N2; clone C01G8
C;Genetics:
A;Gene: CESP:C01G8.7
A;Map position: 1
A;Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3

Query Match 56.8%; Score 46; DB 2; Length 1357;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GPGGPPP 13
|||||
Db 153 GPGGPPP 159

Search completed: September 4, 2002, 16:47:31
Job time: 367 sec



Thủ Sep 5 11:23:38 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:04 ; Search time 34.18 Seconds
(without alignments)
15.859 Million cell updates/sec

Title: US-09-821-726-3

Perfect score: 81

Sequence: 1 KKLOGKGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	81	100.0	199	1 C11P_HUMAN	Q9ns71 homo sapien
2	59	72.8	184	1 C11P_MOUSE	Q9cr36 mus musculu
3	50	61.7	673	1 UVRB_ECOLI	P07025 escherichia
4	48	59.3	532	1 CG48_HUMAN	Q9y5j1 homo sapien
5	46	56.8	427	1 MYCN_SERCA	P26014 serinus can
6	46	56.8	830	1 DYNL_CAEEL	P39055 caenorhabdi
7	46	56.8	1103	1 DPOD_MOUSE	P97283 mesocricetu
8	46	56.8	1105	1 DPOD_MOUSE	P52431 mus musculu
9	45	55.6	402	1 GUN1_HUMAN	P56680 humicola in
10	45	55.6	477	1 PES_FSVST	P00543 feline sarc
11	45	55.6	609	1 PES_FELCA	P00542 feline sarc
12	45	55.6	820	1 PES_HUMAN	P14238 felis silve
13	44	54.3	142	1 YPUB_KLEPN	P20775 klebsiella
14	44	54.3	218	1 RRAS_HUMAN	P10301 homo sapien
15	44	54.3	593	1 CC23_SCHPO	O42709 schizosach
16	44	54.3	670	1 UVRB_PSEAE	P72174 pseudomonas
17	44	54.3	919	1 NOS3_RAT	Q62600 rattus norv
18	44	54.3	1048	1 AGO1_ARATH	Q04379 arabidopsis
19	44	54.3	1201	1 NOS3_MOUSE	P70313 mus musculu
20	44	54.3	1202	1 NOS3_HUMAN	P29474 homo sapien
21	44	54.3	1204	1 NOS3_BOVIN	P29473 bos taurus
22	44	54.3	1204	1 NOS3_PIG	Q28969 sus scrofa
23	44	54.3	1464	1 CA13_MOUSE	P08121 mus musculu
24	44	54.3	1049	1 CA13_BOVIN	P04258 bos taurus
25	43.5	53.7	1049	1 CA13_MOUSE	P06341 rattus norv
26	43	53.1	233	1 HB2A_RAT	P06346 mus musculu
27	43	53.1	252	1 CRH1_BOVIN	P29826 rattus norv
28	43	53.1	252	1 HB2F_MOUSE	P06343 mus musculu
29	43	53.1	263	1 HB2B_RAT	P06344 mus musculu
30	43	53.1	263	1 HB2K_MOUSE	P14483 mus musculu
31	43	53.1	263	1 HB2S_MOUSE	
32	43	53.1	263	1 HB2U_MOUSE	
33	43	53.1	265	1 HB2A_MOUSE	

34	43	53.1	265	1 HB2D_MOUSE	P01921 mus musculu
35	43	53.1	265	1 HB2Q_MOUSE	P06342 mus musculu
36	43	53.1	268	1 HB2X_HUMAN	P05538 homo sapien
37	43	53.1	360	1 OC3A_HUMAN	O01860 homo sapien
38	43	53.1	379	1 Y671_CHLMO	Q9pk02 chlamydia m
39	43	53.1	423	1 TBX2_CAEEL	Q19691 caenorhabdi
40	43	53.1	736	1 DVL2_MOUSE	O60838 mus musculu
41	43	53.1	860	1 ELS_MOUSE	P54320 mus musculu
42	43	53.1	864	1 ELS_RAT	Q99372 rattus norv
43	43	53.1	886	1 SM6B_MOUSE	O54951 mus musculu
44	43	53.1	887	1 SM6B_RAT	O70141 rattus norv
45	43	53.1	994	1 C1C1_MOUSE	Q64347 mus musculu

ALIGNMENTS

RESULT 1					
ID C11P_HUMAN	STANDARD:	PRT:	199 AA.		
AC O9NS71:					
DT 01-MAR-2002 (Rel. 41, Created)					
DT 01-MAR-2002 (Rel. 41, Last sequence update)					
DT 01-MAR-2002 (Rel. 41, Last annotation update)					
DE Call protein.					
GN CALL.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=Stomach;					
RX MEDLINE=20296773; PubMed=10835488;					
RA Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;					
RT "Isolation of two novel genes, down-regulated in gastric cancer."					
RL Jpn. J. Cancer Res. 91:459-463(2000).					
CC -I- TISSUE SPECIFICITY: Expressed in stomach. No expression is					
CC detected in cancer tissue or gastric cancer cell lines.					
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CC -----					
DR EMBL: AB039886; BAA92433.1; -					
DR MIM: 606402; -					
SO SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;					

Query Match 100.0%; Score 81; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKLOGKGGPPPK 14

Db 118 KKLOGKGGPPPK 131

RESULT 2

ID C11P_MOUSE	STANDARD:	PRT:	184 AA.
AC Q9CR36:			
DT 01-MAR-2002 (Rel. 41, Created)			
DT 01-MAR-2002 (Rel. 41, Last sequence update)			
DT 01-MAR-2002 (Rel. 41, Last annotation update)			
DE Call protein homolog.			
GN CALL.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AK008990; BAB26010.1; -
 DR EMBL; AK008622; BAB25784.1; -
 DR EMBL; AK008641; BAB25801.1; -
 DR EMBL; AK008647; BAB25805.1; -
 DR EMBL; AK008672; BAB25856.1; -
 DR EMBL; AK008745; BAB25872.1; -
 DR EMBL; AK008933; BAB25975.1; -
 DR EMBL; AK008956; BAB25988.1; -
 DR EMBL; AK009145; BAB26103.1; -
 DR EMBL; AK019050; BAB31525.1; -
 FT CONFLICT 113 113 P -> L (IN REF. 1: BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;
 Query Match 72.8%; Score 59; DB 1; Length 184;
 Best Local Similarity 71.4%; Pred. No. 0.18;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KKIQKGKGGGPPPK 14
 Db 102 KEQKGGKGGGPPPK 115
 I: :||||| |||
 RESULT 3
 ID UVRB_ECOLI STANDARD; PRT; 673 AA.
 AC P07025;
 DT 01-APR-1998 (Rel. 07, Created)
 DT 01-APR-1998 (Rel. 07, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Exonuclease ABC subunit B.
 GN UVRB OR B0779 OR Z0998 OR ECS0857.
 OS Escherichia coli, and
 OS Escherichia coli, O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562, 83334;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=86176773; PubMed=3008099;
 RA Backendorf C., Spaik H., Barbeiro A.P., van de Putte P.;
 RT "Structure of the uvrB gene of Escherichia coli. Homology with other
 RL DNA repair enzymes and characterization of the uvrB5 mutation.";
 RN Nucleic Acids Res. 14:2877-2890(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86176755; PubMed=3515321;
 RA Arkan E., Kulkarni M.S., Thomas D.C., Sancar A.;
 RT "Sequences of the E. coli uvrB gene and protein.";
 RN Nucleic Acids Res. 14:2637-2650(1986).
 [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:12453-1474(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postell G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 [5]
 RP SEQUENCE FROM N.A.
 RX STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RL O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 [6]
 RP SEQUENCE OF 168-673 FROM N.A.
 RX STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K.,
 RA Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S.,
 RA Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
 RA Nashimoto H., Nishio Y., Saito N., Sempel G., Seki Y., Tagami H.,
 RA Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RL corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 619-673.
 RX MEDLINE=20123894; PubMed=10631326;
 RA Sohi M., Alexandrovich A., Moolenaar G., Visse R., Goosen N.,
 RA Vernede X., Fontecilla-Camps J.C., Champness J., Sanderson M.R.;
 RT "Crystal structure of Escherichia coli UvrB C-terminal domain, and a
 RL model for UvrB-uvrC interaction.";
 RL FEBS Lett. 465:161-164(2000).
 [8]
 RP STRUCTURE BY NMR OF 619-673
 RX MEDLINE=99257571; PubMed=10371161;
 RA Alexandrovich A., Sanderson M.R., Moolenaar G.F., Goosen N.,
 RA Lane A.N.;
 RT "NMR assignments and secondary structure of the UvrC binding domain of
 UvrB.";

```

[2]
SEQUENCE OF 138-532 FROM N.A.
Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
Margolin J.F.:
Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE CGI-48 FAMILY OF WD-REPEAT PROTEINS.
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-----
EMBL; AF151806; AAD34043.1; -.
EMBL; AY007138; AAG01999.1; ALT_INIT.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 4.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Hypothetical protein; Repeat; WD repeat.
KW REPEAT 225 264 WD 1.
FT REPEAT 269 309 WD 2.
FT REPEAT 315 356 WD 3.
FT REPEAT 357 395 WD 4.
FT REPEAT 397 438 WD 5.
FT REPEAT 447 488 WD 6.
FT REPEAT 519 532 GKALMYELHHYSDF -> ARP (IN REF. 1).
FT CONFLICT 519 532
SEQUENCE 532 AA; 59103 MW; 2DA86DFASDDF7A1 CRC64;

Query Match 59.3%; Score 48; DB 1; Length 532;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 KGKGGGPPPK 14
| | | | | | |
DB 8 GAGGPGPPQK 17

RESULT 5
MYCN_SERCA STANDARD; PRT; 427 AA.
ID MYCN_SERCA
AC P26014;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE N-myc proto-oncogene protein.
GN MYCN.
OS Serinus canaria (Canary).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Fringillidae;
OC Carduelinae; Serinus.
OX NCBI_TaxID=9135;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=91141534; PubMed=1996121;
RA Collum R.G., Clayton D.F., Alt F.W.;
RT "Structure and expression of canary myc family genes.";
RL Mol. Cell. Biol. 11:1770-1776(1991).
CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BLH1 PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
-----
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CC -----
 CC EMBL; M64598; AAA49540.1; -.
 CC EMBL; M64251; AAA49540.1; JOINED.
 CC PIR; A39695; A39695.
 CC HSP; P25912; IHLO.
 CC TRANSFAC; T02381; -.
 CC InterPro; IPR003015; HLH_Myc.
 CC InterPro; IPR001092; HLH_dlm.
 CC InterPro; IPR002418; Myc.
 CC Pfam; PF00010; HLH; 1.
 CC Pfam; PF01056; Myc_N_term; 1.
 CC PRINTS; PR00044; LEUZIPRMVC.
 CC SMART; SM00353; HLH; 1.
 CC PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
 CC Nuclear protein; DNA-binding; proto-oncogene; phosphorylation.
 CC DOMAIN 212 219 POLY-SER.
 CC FT DOMAIN 220 242 ASP/GLU-RICH (ACIDIC).
 CC FT DNA_BIND 343 356 BASIC DOMAIN.
 CC FT DOMAIN 357 397 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CC FT DOMAIN 396 417 LEUCINE-ZIPPER (POTENTIAL).
 CC FT MOD_RES 224 224 PHOSPHORYLATION (BY CK2).
 CC FT MOD_RES 226 226 (BY SIMILARITY).
 CC FT PHOSPHORYLATION (BY CK2).
 CC FT (BY SIMILARITY).
 CC SEQUENCE 427 AA; 47140 MW; 5631FFEF615AE54B CRC64;

Query Match 56.8%; Score 46; DB 1; Length 427;
 Best Local Similarity 61.5%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 KKLQKGGPGPPP 13
 Db 144 EKLQKTPAAPPP 156
 :||| | | | |

RESULT 6
 ID DYNL_CAEEL STANDARD; PRT; 830 AA.
 AC P39055;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dyanamin (EC 3.6.1.50).
 GN DYN-1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=97439883; PubMed=9294229;
 RA Clark S.G., Shurland D.L., Meyerowitz E.M., Bargmann C.I.,
 RA van der Bliek A.M.;
 RT "A dyanamin GTPase mutation causes a rapid and reversible temperature-
 RT inducible locomotion defect in *C. elegans*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:10438-10443(1997).
 RN [2]
 RP REVISIONS TO C-TERMINUS.
 RC STRAIN=BRISTOL N2;
 RA van der Bliek A.M.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MICROTUBULE-ASSOCIATED FORCE-PRODUCING PROTEIN INVOLVED
 CC IN PRODUCING MICROTUBULE BUNDLES AND ABLE TO BIND AND HYDROLYZE
 CC GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICKING PROCESSES, IN
 CC PARTICULAR ENDOCYTOSIS.
 CC -!- CATALYTIC ACTIVITY: GTP + H(2)O = GDP + phosphate.
 CC -!- SUBCELLULAR LOCATION: MICROTUBULE-ASSOCIATED.
 CC -!- SIMILARITY: BELONGS TO THE DYANAMIN FAMILY.

CC -----
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -----
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CC -----
 CC EMBL; L29031; AAB72228.2; -.
 CC HSP; Q05193; 2DYN.
 CC InterPro; IPR001401; Dyanamin.
 CC InterPro; IPR000375; Dyanamin_central.
 CC InterPro; IPR001330; GED.
 CC InterPro; IPR001849; PH.
 CC Pfam; PF00350; dyanamin; 1.
 CC Pfam; PF01031; dyanamin_2; 1.
 CC Pfam; PF02212; GED; 1.
 CC Pfam; PF00169; PH; 1.
 CC PRINTS; PR00195; DYANAMIN.
 CC SMART; SM00053; DYNC; 1.
 CC SMART; SM00302; GED; 1.
 CC SMART; SM00233; PH; 1.
 CC PROSITE; PS00410; DYANAMIN; 1.
 CC PROSITE; PS00003; PH_DOMAIN; 1.
 CC Hydrolase; Motor protein; GTP-binding; Microtubules; Multigene family;
 KW Endocytosis.
 FT NP_BIND 40 47 GTP (BY SIMILARITY).
 FT NP_BIND 138 142 GTP (BY SIMILARITY).
 FT NP_BIND 207 210 GTP (BY SIMILARITY).
 FT DOMAIN 519 624 PH.
 FT SEQUENCE 830 AA; 93348 MW; FC3D7106D079EDC5 CRC64;

Query Match 56.8%; Score 46; DB 1; Length 830;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GPGGPPP 13
 Db 818 GPGGPPP 824
 :||| | | | |

RESULT 7
 ID DPOD_MESAU STANDARD; PRT; 1103 AA.
 AC P97283; P97284;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).
 GN POLD1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Mishra N.C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSESSES TWO ENZYMATIC ACTIVITIES: DNA SYNTHESIS
 CC (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT DGRADATES SINGLE
 CC STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS
 CC ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND
 CC REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND
 CC SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED
 CC BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).
 CC -!- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa,
 CC 66 kDa and 12 kDa. The 125 kDa SUBUNIT CONTAINS THE POLYMERASE

STRANDED DNA IN THE 3' TO 5' DIRECTION. REQUIRED WITH ITS ACCESSORY PROTEINS (PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) AND REPLICATION FACTOR C (RFC) OR ACTIVATOR 1) FOR LEADING STRAND SYNTHESIS. ALSO INVOLVED IN COMPLETING OKAZAKI FRAGMENTS INITIATED BY THE DNA POLYMERASE ALPHA/PRIMASE COMPLEX.

-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + (DNA)(N).

-!- SUBUNIT: HETEROTETRAMER COMPOSED OF SUBUNITS OF 125 kDa, 50 kDa, 66 kDa and 12 kDa. The 125 kDa SUBUNIT CONTAINS THE POLYMERASE ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5' EXONUCLEASE ACTIVITY.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES: ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS OF DNA SYNTHESIS.

-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

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EMBL: Z21848; CAA79895.1; -
EMBL: AF024570; AAB99910.1; -
MGI: 97741; Poldi.
InterPro: IPR002064; DNA_pol_B.
Pfam: PF00136; DNA_pol_B; 1.
Pfam: PF03104; DNA_pol_B_exo; 1.
PRINTS: PR00106; DNAPOLB.
SMART: SM00486; POLB; 1.
PROSITE: PS00116; DNA_POLYMERASE_B; 1.
Transferase: DNA-directed DNA polymerase; DNA replication;
DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein.
DOMAIN 4 19 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ZN_FING 1010 1027 C4-TYPE (POTENTIAL).
ZN_FING 1056 1074 RPL -> GPP (IN REF. 2).
CONFLICT 112 114 E -> K (IN REF. 2).
CONFLICT 793 793 L -> F (IN REF. 2).
CONFLICT 1000 1000 S -> Y (IN REF. 2).
CONFLICT 1035 1035 LEERSRL -> WKNGSLRF (IN REF. 2).
CONFLICT 1045 1052
SEQUENCE 1105 AA; 123783 MW; 53556C7620400564 CRC64;

Query Match 56.8%; Score 46; DB 1; Length 1105;
Best Local Similarity 57.1%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLQKGPGGPPPK 14
Db 4 KRRQGPVGVPK 17
I: || ||| || :
: || ||| || :
: || ||| || :
: || ||| || :

RESULT 9
GUNI_HUMIN STANDARD; PRT; 402 AA.
ID GUNI_HUMIN
AC P56680;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
GN CEL7B.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=34413;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
RX MEDLINE=97475713; PubMed=9335168;
RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schulein M.;
CC -!- FUNCTION: POSSESSES TWO ENZYMATIC ACTIVITIES: DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT DEGRADES SINGLE

ACTIVE SITE AND MOST LIKELY THE ACTIVE SITE FOR THE 3'-5' EXONUCLEASE ACTIVITY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Nuclear.

-!- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES: ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS OF DNA SYNTHESIS.

-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.

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EMBL: U83704; AAB47254.1; -
EMBL: U83705; AAB47255.1; -
InterPro: IPR002064; DNA_pol_B.
Pfam: PF00136; DNA_pol_B; 1.
Pfam: PF03104; DNA_pol_B_exo; 1.
PRINTS: PR00106; DNAPOLB.
SMART: SM00486; POLB; 1.
PROSITE: PS00116; DNA_POLYMERASE_B; 1.
Transferase: DNA-directed DNA polymerase; DNA replication;
DNA-binding; Hydrolyase; Exonuclease; Zinc-finger; Nuclear protein.
DOMAIN 4 19 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ZN_FING 1008 1025 C4-TYPE (POTENTIAL).
ZN_FING 1054 1072 C4-TYPE (POTENTIAL).
VARIANT 64 64 MISSING (IN DELTA').
VARIANT 386 386 P -> S (IN DELTA').
SEQUENCE 1103 AA; 123465 MW; 34B5BF72DE53011 CRC64;

Query Match 56.8%; Score 46; DB 1; Length 1103;
Best Local Similarity 57.1%; Pred. No. 57;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KKLQKGPGGPPPK 14
Db 4 KRRQGPVGVPK 17
I: || ||| || :
: || ||| || :
: || ||| || :
: || ||| || :

RESULT 8
DPOD_MOUSE STANDARD; PRT; 1105 AA.
ID DPOD_MOUSE
AC P52431; O54883;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase delta catalytic subunit (EC 2.7.7.7).
GN POLD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=94085777; PubMed=82623377;
RA Cullmann G., Hindges R., Berchtold M.W., Huebscher U.;
RT "Cloning of a mouse cDNA encoding DNA polymerase delta: refinement of the homology boxes";
RL Gene 134:191-200(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98096600; PubMed=9434960;
RA Goldsby R.E., Singh M., Preston B.D.;
RT "Mouse DNA polymerase delta gene (Pold1) maps to chromosome 7";
RL Mamm. Genome 9:92-93(1998).
CC -!- FUNCTION: POSSESSES TWO ENZYMATIC ACTIVITIES: DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT DEGRADES SINGLE

RT of potential sugar-binding subsites.";

RL J. Biotechnol. 57:91-100(1997).

RN [2]

RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.

RA MacKenzie L.F., Sulzenbacher G., Divne C., Jones T.A., Woeldike H.F.,

RA Schuelin M., Withers S.G., Davies G.J.;

RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from

RT Humicola insolens at 2.2 A resolution and identification of the

RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme

RT intermediate.";

RL Biochem. J. 335:409-416(1998).

CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE

CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:

CC (1) ENDOLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;

CC (2) EXOCELLULOBIODOLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE

CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;

CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER

CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

CC linkages in cellulose.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL

CC HYDROLASES).

DR PDB; 1A39; 02-MAR-99.

DR PDB; 2A39; 16-FEB-99.

DR InterPro: IPR001722; Glyco_hydro_7.

DR Pfam; PF00840; Glyco_hydro_7; 1.

DR PRINTS; PR00734; GLHYDRIASE7.

DR ProDom; PD186135; Glyco_hydro_7; 1.

KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;

KW 3D-structure.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT ACT_SITE 197 197 NUCLEOPHILE.

FT ACT_SITE 202 202 PROTON DONOR.

FT DISULFID 18 24

FT DISULFID 51 73

FT DISULFID 63 69

FT DISULFID 140 365

FT DISULFID 172 195

FT DISULFID 176 194

FT DISULFID 215 234

FT DISULFID 223 228

FT DISULFID 239 315

FT CARBOHYD 89 89 N-LINKED (GLCNAC: . . .).

FT CARBOHYD 247 247 N-LINKED (GLCNAC: . . .).

SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

Query Match 55.6%; Score 45; DB 1; Length 402;

Best Local Similarity 47.4%; Pred. No. 29;

Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 KLGKGGG-----PPPK 14

Db : : | | | | |

42 RAELGGCGGDWGNPPPK 60

RESULT 10

FES_FSVST

ID FES_FSVST STANDARD; PRT; 477 AA.

AC P00543;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).

GN V-FES.

OS Feline sarcoma virus (strain Snyder-Theilen).

OC Viruses; Retroviral viruses; Retroviridae; Mammalian type C retroviruses.

OX NCBI_Taxid=11780;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83050963; PubMed=6183005;

RX MEDLINE=83050963; PubMed=6183005;

RA Hampe A., Laprevotte I., Galibert F., Fedele L.A., Sherr C.J.;

RT "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide

RT evidence for a family of tyrosine-specific protein kinase genes.";

RL Cell 30:775-785(1982).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.

CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES

CC POLYPEPTIDE.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC

CC DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -----

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CC -----

DR EMBL; J02088; AAA43046.2; -.

DR PIR; A00652; TMVCS.

DR HSP; P11362; IFGK.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR000980; SH2_pkinase.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00017; SH2; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

KW Polyprotein; Tyrosine-protein kinase; Oncogene; Transferase;

KW ATP-binding; phosphorylation; SH2 domain.

FT DOMAIN 115 204 SH2.

FT NP_BIND 216 477 PROTEIN KINASE.

FT BINDING 222 230 ATP (BY SIMILARITY).

FT ACT_SITE 245 245 ATP (BY SIMILARITY).

FT MOD_RES 338 338 BY SIMILARITY.

SQ SEQUENCE 477 AA; 53756 MW; BB87EDB4E7A3BEB5 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 477;

Best Local Similarity 66.7%; Pred. No. 35;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLGKGGGPPPP 13

Db : : | | | | |

42 KLEQLGPGGPPPP 53

RESULT 11

FES_FSVGA

ID FES_FSVGA STANDARD; PRT; 609 AA.

AC P00542;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase transforming protein FES (EC 2.7.1.112).

GN V-FES.

OS Feline sarcoma virus (strain Gardner-Arnstein) (Ga-FesV) (Gardner-

OS Arnstein feline leukemia oncovirus B).

OC Viruses; Retroviral viruses; Retroviridae; Gammaretrovirus.

OX NCBI_Taxid=11774;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83050963; PubMed=6183005;

Thu Sep 5 11:23:38 2002

Hampe A., Laprevotte I., Galibert F., Fedele L.A., Sherr C.J.;
 "Nucleotide sequences of feline retroviral oncogenes (v-fes) provide
 evidence for a family of tyrosine-specific protein kinase genes.";
 Cell 30:775-785(1982).
 RT CATLYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FES
 POLYPROTEIN.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 DOMAIN BELONGS TO THE FES/FPS SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J02087; AAA43041.1; -
 CC PIR; A0651; TVMVGK.
 CC HSP; P11362; IFGK.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR001060; FCH.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00611; FCH; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00017; SH2; 1.
 CC PRINTS; PR00401; SH2DOMAIN.
 CC PRINTS; PR00109; TYRKINASE.
 CC SMART; SM00252; SH2; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS500011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS500011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC PolyProtein; Tyrosine-protein kinase; Oncogene; Transferase;
 KW ATP-binding; Phosphorylation; SH2 domain.
 FT DOMAIN 247 336 PROTEIN KINASE.
 FT NP_BIND 348 609 ATP (BY SIMILARITY).
 FT BINDING 377 377 ATP (BY SIMILARITY).
 FT ACT_SITE 470 470 BY SIMILARITY.
 FT MOD_RES 500 500 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 609 AA; 68769 MW; 53D491975CF73A3 CRC64;
 Query Match 55.6%; Score 45; DB 1; Length 609;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 2 KLOGKGGPGGPPP 13
 Db 174 KLEQLGPGGPPP 185
 ||: ||| |||
 RESULT 12
 FES_FELCA STANDARD; PRT; 820 AA.
 AC P14238;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
 GN FES OR FPS.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=87198954; PubMed=3553615;
 RX Roebroek A.J.M., Schalken J.A., Onnekink C., Bloemers H.P.J.,
 RA van de Ven W.J.M.;
 RT "Structure of the feline c-fes/fps proto-oncogene: genesis of a
 retroviral oncogene";
 RL J. Virol. 61:2009-2016(1987).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 DOMAIN BELONGS TO THE FES/FPS SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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 CC
 CC EMBL; M16705; AAA30808.1; -
 CC EMBL; M16666; AAA30808.1; JOINED.
 CC EMBL; M16667; AAA30808.1; JOINED.
 CC EMBL; M16668; AAA30808.1; JOINED.
 CC EMBL; M16669; AAA30808.1; JOINED.
 CC EMBL; M16670; AAA30808.1; JOINED.
 CC EMBL; M16671; AAA30808.1; JOINED.
 CC EMBL; M16706; AAA30808.1; JOINED.
 CC EMBL; M16672; AAA30808.1; JOINED.
 CC EMBL; M16673; AAA30808.1; JOINED.
 CC EMBL; M16674; AAA30808.1; JOINED.
 CC EMBL; M16698; AAA30808.1; JOINED.
 CC EMBL; M16700; AAA30808.1; JOINED.
 CC EMBL; M16701; AAA30808.1; JOINED.
 CC EMBL; M16702; AAA30808.1; JOINED.
 CC EMBL; M16704; AAA30808.1; JOINED.
 CC PIR; A27824; TVCTFF.
 CC HSP; P11362; IFGK.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR001060; FCH.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR001245; Tyr_pkinase.
 CC Pfam; PF00611; FCH; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00017; SH2; 1.
 CC PRINTS; PR00109; TYRKINASE.
 CC SMART; SM00055; FCH; 1.
 CC SMART; SM00252; SH2; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS500011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS50001; SH2; 1.
 CC Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 KW Phosphorylation; SH2 domain.
 FT DOMAIN 458 547 SH2
 FT NP_BIND 559 820 PROTEIN KINASE.
 FT BINDING 565 573 ATP (BY SIMILARITY).
 FT ACT_SITE 588 588 ATP (BY SIMILARITY).
 FT MOD_RES 711 711 BY SIMILARITY.
 SQ SEQUENCE 820 AA; 92974 MW; F3A52B750236834E CRC64;
 Query Match 55.6%; Score 45; DB 1; Length 820;
 Best Local Similarity 66.7%; Pred. No. 58;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 2 KLOGKGGPGGPPP 13
 Db 385 KLEQLGPGGPPP 396
 ||: ||| |||

```

RESULT 13
FES_HUMAN
ID FES_HUMAN STANDARD; PRT; 822 AA.
AC P07332;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase FES/FPS (EC 2.7.1.112) (C-FES).
GN FES OR FPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90191711; PubMed=2179816;
RA Alcalay M., Antolini F., van de Ven W.J., Lanfranccone L.,
RA Grignani F., Pelicci P.G.;
RT "Characterization of human and mouse c-fes cDNA clones and
RT identification of the 5' end of the gene.";
RL Oncogene 5:267-275(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86055727; PubMed=4065096;
RA Roebroek A.J.M., Schalken J.A., Verbeek J.S., van den Ouweland A.M.W.,
RA Onnekink C., Bloemers H.P.J., van de Ven W.J.M.;
RT "The structure of the human c-fes/fps proto-oncogene.";
RL EMBO J. 4:2897-2903(1985).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE FES/FPS SUBFAMILY.
CC
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CC
CC EMBL; X52192; CAA36438.1; -
CC EMBL; X06292; CAA29619.1; -
CC PIR; A24673; TVHUFF.
CC PIR; A60188; A60188.
CC HSSP; P11362; 1FGK.
CC MIM; 190030;
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR001060; FCH.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00611; FCH; 1.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00017; SH2; 1.
CC PRINTS; PR00401; SH2DOMAIN.
CC PRINTS; PR00109; TYRKINASE.
CC SMART; SM00055; FCH; 1.
CC SMART; SM00252; SH2; 1.
CC SMART; SM00219; TyrKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50001; SH2; 1.
CC Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain.
FT DOMAIN 460 549
FT DOMAIN 561 822
FT NP_BIND 567 575
FT BINDING 590 590
FT ACT_SITE 683 683
FT MOD_RES 713 713
FT
FT (BY SIMILARITY).

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FT CONFLICT 719 719 S -> L (IN REF. 2).
SQ SEQUENCE 822 AA; 93470 MW; ADA0B8F7D2666356 CRC64;

Query Match
Best Local Similarity 55.6%; Score 45; DB 1; Length 822;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLOGKPGGGPPP 13
Db 387 KLEHLGPGGPPPP 398
||: ||| |||
||: ||| |||

RESULT 14
YPUB_KLEPN
ID YPUB_KLEPN STANDARD; PRT; 142 AA.
AC P20775;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PULS 3'-region (Fragment).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89291709; PubMed=2661532;
RA D'Enfert C., Pugsley A.P.;
RT "Klebsiella pneumoniae puls gene encodes an outer membrane
RT lipoprotein required for pullulanase secretion.";
RL J. Bacteriol. 171:3673-3679(1989).
CC
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CC
CC EMBL; M29097; AAA61979.1; -
CC PIR; D32880; D32880.
CC KW Hypothetical protein.
CC FT NON_TER 142 142
CC SQ SEQUENCE 142 AA; 16447 MW; 03ED03BFB63242D0 CRC64;

Query Match
Best Local Similarity 54.3%; Score 44; DB 1; Length 142;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QGKPGGGGPPPK 14
Db 50 KGKGGKGGKPPR 60
||| ||| |||
||| ||| |||

RESULT 15
RRAS_HUMAN
ID RRAS_HUMAN STANDARD; PRT; 218 AA.
AC P10301;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ras-related protein R-Ras (P23).
OS RRAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87078390; PubMed=3098437;

```

Thu Sep 5 11:23:38 2002

RA Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L.,
 RA Goeddel D.V.;
 RT "Structure of the human and murine R-ras genes, novel genes closely
 RL related to ras proto-oncogenes.";
 RL Cell 48:137-146(1987).
 CC -!- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY
 CC WITH ATTACHMENT REQUIRING ACYLATION OF THE C-TERMINAL CYSTEINE
 CC (BY SIMILARITY WITH RAS).
 CC -!- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; M14949; AAA60256.1; -.
 DR EMBL; M14948; AAA60256.1; JOINED.
 DR PIR; A26159; TVHURR.
 DR HSPP; P01112; 1PLL.
 DR SWISS-2DPAGE; P10301; HUMAN.
 DR MIM; 165090; -.
 DR InterPro; IPR003577; Ras.
 DR InterPro; IPR001806; Ras_trnstrmng.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMNG.
 DR SMART; SM00173; RAS; 1.
 DR GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 36 43 GTP (BY SIMILARITY).
 FT NP_BIND 83 87 GTP (BY SIMILARITY).
 FT NP_BIND 142 145 GTP (BY SIMILARITY).
 FT DOMAIN 58 66 EFFECTOR REGION (BY SIMILARITY).
 FT LIPID 215 215 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 218 AA; 23480 MW; 437F73170670EB28 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 218;
 Best Local Similarity 77.8%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GKGGGPPPP 13
 DB 18 GPGGDPPPP 26

Search completed: September 4, 2002, 17:05:05
 Job time: 1131 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:33 ; Search time 124.34 Seconds
(without alignments)
19.478 Million cell updates/sec

Title: US-09-821-726-3
Perfect score: 81
Sequence: 1 KKLOGKPGGPPPK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	60	74.1	1677	11 070373	070373 mus musculus
2	52	64.2	467	4 QH9F1	QH9F1 homo sapien
3	50	61.7	333	2 Q9APQ3	Q9APQ3 uncultured
4	49	60.5	212	2 Q9APJ1	Q9APJ1 methylobact
5	48	59.3	547	11 P97472	P97472 mus musculus
6	48	59.3	547	11 Q91XC0	Q91XC0 mus musculus
7	48	59.3	774	5 Q9V620	Q9V620 drosophila
8	48	59.3	813	5 Q95TY2	Q95TY2 drosophila
9	48	59.3	1289	10 Q9FLQ7	Q9FLQ7 arabidopsis
10	48	59.3	1292	3 Q96WLO	Q96WLO ustilago ma
11	48	59.3	2061	5 Q9VUH9	Q9VUH9 drosophila
12	47	58.0	262	12 Q9DWB2	Q9DWB2 rat cytoleg
13	47	58.0	669	16 Q9PER1	Q9PER1 xylella fas
14	47	58.0	673	2 Q9RBK2	Q9RBK2 xanthomonas
15	47	58.0	1963	5 Q9VSK5	Q9VSK5 drosophila
16	47	58.0	1966	5 Q9NHX6	Q9NHX6 drosophila

17	46	56.8	241	4 095542	095542 homo sapien
18	46	56.8	250	4 075894	075894 homo sapien
19	46	56.8	281	5 095QJ0	095QJ0 caenorhabdi
20	46	56.8	322	13 Q9PTB4	Q9PTB4 brachydanio
21	46	56.8	377	16 069559	069559 mycobacteri
22	46	56.8	495	5 095YB0	095YB0 caenorhabdi
23	46	56.8	549	5 098IB7	098IB7 caenorhabdi
24	46	56.8	551	4 016630	016630 homo sapien
25	46	56.8	561	5 009542	009542 caenorhabdi
26	46	56.8	588	4 098W18	098W18 homo sapien
27	46	56.8	830	5 093176	093176 caenorhabdi
28	46	56.8	1105	11 091VT0	091VT0 mus musculu
29	46	56.8	1194	5 09W485	09W485 drosophila
30	46	56.8	1215	5 077202	077202 acanthamoeb
31	46	56.8	1256	5 095YA9	095YA9 caenorhabdi
32	46	56.8	1284	5 0960F1	0960F1 drosophila
33	46	56.8	1761	5 091019	091019 caenorhabdi
34	45.5	56.2	579	16 0928K7	0928K7 chlamydia p
35	45	55.6	153	11 09CTM4	09CTM4 mus musculu
36	45	55.6	171	10 09SSB8	09SSB8 arabidopsis
37	45	55.6	316	15 0998S7	0998S7 chimpanzee
38	45	55.6	976	6 09MZT1	09MZT1 canis fami
39	45	55.6	2703	5 09VEG7	09VEG7 drosophila
40	45	55.6	2715	5 061603	061603 drosophila
41	44.5	54.9	439	4 09H874	09H874 homo sapien
42	44.5	54.9	459	4 096BH1	096BH1 homo sapien
43	44	54.3	149	2 092GG1	092GG1 heliobacill
44	44	54.3	172	11 09CU12	09CU12 mus musculu
45	44	54.3	182	10 09C8U3	09C8U3 arabidopsis

ALIGNMENTS

RESULT 1

ID 070373 PRELIMINARY: PRT; 1677 AA.
AC 070373:
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX PubMed=9159189;
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;
RT "Differential display of mRNAs from the atrioventricular region of
developing chicken hearts at stages 15 and 21.";
RL Front. Biosci. 1:al-a15(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART MUSCLE;
RX MEDLINE=99146891; PubMed=10021346;
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,
Krob S.L., Schultheiss T.M., Evans S., Lin J.J.-C.;
RT "Requirement of a novel gene, Xin, in cardiac morphogenesis.";
RL Development 126:1281-1294(1999).
DR EMBL: AF051945; AAC06023.1; -;
DR MGD: MGI:1333878; Xin.
SO SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;

Query Match 74.1%; Score 60; DB 11; Length 1677;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QGKPGGPPPK 14

Db 574 EKGPGGPPPE 584
:|||||

RESULT 2
Q9H9F1 ID Q9H9F1 PRELIMINARY; PRT; 467 AA.
AC Q9H9F1;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE CDNA FLJ12800 FIS, CLONE NT2P2002079, WEAKLY SIMILAR TO HISTONE H1,
DE GONADAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK02862; BAB14278.1; -.
DR InterPro; IPR000637; AT_hook.
DR SMART; SM00384; AT_hook; 1.
SQ SEQUENCE 467 AA; 49648 MW; 287B1BF4CF30B1A1 CRC64;

Query Match 64.2%; Score 52; DB 4; Length 467;
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KKLQGGGPGPPK 14
:|||||

RESULT 3
Q9APQ3 ID Q9APQ3 PRELIMINARY; PRT; 333 AA.
AC Q9APQ3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE EXCISION NUCLEASE SUBUNIT B (FRAGMENT).
GN UVRB.
OS uncultured bacterium pCosHEL.
OC Bacteria; environmental samples.
OX NCBI_TaxID=143796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20575196; PubMed=11133432;
RA Entcheva P., Liebl W., Johann A., Hartsch T., Streit W.R.;
RT "Direct cloning from enrichment cultures, a reliable strategy for
RT isolation of complete operons and genes from microbial consortia."
RL Appl. Environ. Microbiol. 67:89-99(2001).
DR EMBL; AF250772; AAG60567.1; -.
DR HSSP; P56981; 1D9X.
DR InterPro; IPR001410; DEAD.
FT NON_TER 1
FT NON_TER 333
SQ SEQUENCE 333 AA; 38152 MW; E6401C01A8A46DEF CRC64;

Query Match 61.7%; Score 50; DB 2; Length 333;
Best Local Similarity 72.7%; Pred. No. 8.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LOGKGGGPPPP 13

Db 135 LSGRGGPPPP 145
:|||||

RESULT 4
Q9APJ1 ID Q9APJ1 PRELIMINARY; PRT; 212 AA.
AC Q9APJ1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PUTATIVE REGULATOR FOR GRANULA-ASSOCIATED PROTEIN.
OS Methylobacterium extorquens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AM1;
RX MEDLINE=21142531; PubMed=11208803;
RA Korotkova N., Lidstrom M.E.;
RT "Connection between Poly-beta-Hydroxybutyrate Biosynthesis and Growth
RT on C1 and C2 Compounds in the Methylophilic Methylobacterium extorquens
RT AM1."
RL J. Bacteriol. 183:1038-1046(2001).
DR EMBL; AF287907; AAK11535.1; -.
SQ SEQUENCE 212 AA; 23141 MW; 4121BD0E8A3FBAC3 CRC64;

Query Match 60.5%; Score 49; DB 2; Length 212;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GKGGGPPPP 13
:|||||

RESULT 5
P97472 ID P97472 PRELIMINARY; PRT; 547 AA.
AC P97472;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE AJUBA.
GN JUB OR AJUBA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99263009; PubMed=10330178;
RA Goyal R.K., Lin P., Kanungo J., Payne A.S., Muslin A.J.,
RA Longmore G.D.;
RT "Ajuba, a novel LIM protein, interacts with Grb2, augments mitogen-
RT activated protein kinase activity in fibroblasts, and promotes meiotic
RT maturation of Xenopus oocytes in a Grb2- and Ras-dependent manner."
RL Mol. Cell. Biol. 19:4379-4389(1999).
CC -1- SIMILARITY: CONTAINS 3 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC TONS.
DR EMBL; U79776; AAB38287.1; -.
DR HSSP; Q05159; 1QLI.
DR MGD; MGI:1341886; Jub.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 3.
DR ProDom; PD000094; LIM; 3.
DR SMART; SM00132; LIM; 3.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS0023; LIM_DOMAIN_2; 3.
KW LIM domain; Metal-binding; Zinc.
SQ SEQUENCE 547 AA; 57901 MW; C326772AC1C441B2 CRC64;

RA Apili J.R., Agbayani, B. 1990
RA Baller R.M., Basu A.P., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.K., Cusum D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov G.C., Dunn P.,

Db 405 QKSPGPGCPPP 417

RESULT 9

Q9FLQ7 ID Q9FLQ7 PRELIMINARY; PRT; 1289 AA.
 AC Q9FLQ7
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE GB|AAD23008.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneo T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 DR EMBL: AB010070; BAB11454.1; -;
 DR InterPro: IPR002965; P_rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENS.
 SO SEQUENCE 1289 AA; 137558 MW; 898E55A2A618F5E0 CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 10; Length 1289;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GKPGGPP 13

|:|:|:|:|

Db 1142 GRGPGAPP 1150

RESULT 10

Q96WLO ID Q96WLO PRELIMINARY; PRT; 1292 AA.
 AC Q96WLO
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE TPR-CONTAINING PROTEIN MQL1.
 GN MQL1.
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=5270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loubradou G., Kahmann R.;
 RT "Involvement of the TPR containing protein Mql1 in filamentous growth
 RT of Ustilago maydis.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF268097; AAK58576.1; -;
 SO SEQUENCE 1292 AA; 135886 MW; 543A2702C4E0D610 CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 3; Length 1292;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LQKPGGPP 13

|:|:|:|:|

Db 716 LAAAGPGPP 726

RESULT 11

Q9VUH9 ID Q9VUH9 PRELIMINARY; PRT; 2061 AA.
 AC Q9VUH9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CG9425 PROTEIN.
 GN CG9425.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Balles R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003533; AAF49702.1; -;
 DR FlyBase: FBgn0036451; CG9425.
 DR InterPro: IPR002965; P_rich_extensn.
 DR InterPro: IPR001412; tRNA-synt.1.
 DR InterPro: IPR000571; zf-CCCH.
 DR InterPro: IPR000822; znf-C2H2.
 DR Pfam: PF00642; zf-CCCH; 1.
 DR PRINTS: PR01217; PRICHEXTENS.
 DR SMART: SM00355; znf-C2H2; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE-I; UNKNOWN.1.
 DR PROSITE: PS00028; ZINC-FINGER-C2H2.1; UNKNOWN.1.
 SO SEQUENCE 2061 AA; 225386 MW; B6A155395B5CC0E CRC64;

Query Match

Best Local Similarity 59.3%; Score 48; DB 5; Length 2061;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RA	Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.M., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madalena A.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.R., Nascimento A.L.T.O., Netto L.E.S., Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira B.C., de Oliveira R.C., Palmieri D.A., Paris A.B., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quagão V.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa R.F. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meldanis J., Setubal J.C.; The genome sequence of the plant pathogen Xylella fastidiosa."
RL	"Nature 406:151-159(2000).
CC	-I- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
DR	EMBL; AE003935; AA833777.1; -.
DR	HSSP; P56981; ID9X.
DR	InterPro; IPR001410; DPAD.
DR	InterPro; IPR001650; Helicase_C.
DR	InterPro; IPR001943; UVR.
DR	Pfam; PF00271; helicase_C; 1.
DR	Pfam; PR02151; UVR; 1.
DR	SMART; SM00487; DEXDC; 1.
DR	SMART; SM00490; HELICC; 1.
KW	ATP-binding; Complete proteome; Helicase.
SQ	SEQUENCE 669 AA; 75557 MW; 26BA460383A7125E CRC64;
Qy	Query Match 58.0%; Score 47; DB 16; Length 669; Best Local Similarity 61.5%; Pred. No. 46; Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0
Db	1 KKLQGKGGGPPPP 13 : 311 RHLTGRAPGEPPP 323
RESULT 14	
Q9RBK2	PRELIMINARY; PRT; 673 AA.
AC Q9RBK2;	
DT 01-MAY-2000 (TrEMBLrel. 13; Created)	
DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update)	
DT 01-DEC-2001 (TrEMBLrel. 19; Last annotation update)	
DE EXCINUCLEASE ABC SUBUNIT B.	
GN UVRB.	
OS Xanthomonas campestris (pv. campestris).	
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;	
OC Xanthomonas.	
OX NCBI_TaxID=340;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=XCI7;	
RA Tseng Y.H.;	
RT "Cloning and characterization of the uvrB of Xanthomonas campestris pv. campestris";	
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF102847; AAD46146.2; -.	
DR HSSP; P56981; ID9X.	
DR InterPro; IPR001410; DEAD.	
DR InterPro; IPR001650; Helicase_C.	
DR InterPro; IPR001943; UVR.	
DR Pfam; PF00271; helicase_C; 1.	
DR Pfam; PF02151; UVR; 1.	
DR SMART; SM00487; DEXDC; 1.	
DR SMART; SM00490; HELICC; 1.	
KW ATP-binding; Helicase.	
SQ SEQUENCE 673 AA; 75855 MW; 976441B101DE3897 CRC64;	

QY	3	LQKGGGPGPPP	13
ID	:	:	
DB	1361	LRGMPPGGPPP	1371
RESULT	12		
Q9DWB2	PRELIMINARY;	PRT;	262 AA.
ID	Q9DWB2		
AC	Q9DWB2;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	PR90.		
OS	Rat cytomegalovirus (strain Maastricht).		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
CC	Betaherpesvirinae; Muromegalovirus.		
OX	NCBI_TaxID=79700;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MAASTRICHT;		
RC	MEDLINE=20366325; PubMed=10906222;		
RA	Vink C., Beuken E., Bruggeman C.A.;		
RT	"Complete DNA sequence of the rat cytomegalovirus genome.";		
RL	J. Virol. 74:7656-7665(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MAASTRICHT;		
RC	MEDLINE=20473137; PubMed=11018281;		
RA	Gruithuijsen Y.K., Beuken E., Bruggeman C.A.;		
RT	"Rat cytomegalovirus R89 is a highly conserved gene which expresses a		
RL	spliced transcript.";		
RL	Virus Res. 69:119-130(2000).		
DR	EBU; AF232689; AAF99178.1; -.		
SQ	SEQUENCE 262 AA; 27742 MW; 7C8063857113D7B7 CRC64;		
Query Match	58.0%;	Score 47;	DB 12; Length 262;
Best Local Similarity	70.0%;	Pred. No. 18;	
Matches	7; Conservative	2; Mismatches	1; Indels 0; Gaps 0;
QY	4	OQKGPGGPPP	13
ID	:	:	
DB	18	RRGPGGPSP	27
RESULT	13		
Q9PER1	PRELIMINARY;	PRT;	669 AA.
ID	Q9PER1		
AC	Q9PER1;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
GN	EXCINUCLEASE ABC SUBUNIT B.		
DN	XF0967.		
OS	Xylella fastidiosa.		
OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;		
CC	Xylella.		
OX	NCBI_TaxID=2371;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=9A5C;		
RC	MEDLINE=20365717; PubMed=10910347;		
RA	Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,		
RA	Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,		
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,		
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,		
RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,		
RA	Coutinho L.P., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,		
RA	Faciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,		
RA	Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,		
RA	Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,		

Query Match 58.0%; Score 47; DB 2; Length 673;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KKLGKGGGGPPP 13
 Db 311 RHLTGKAGCGPPP 323

RESULT 15
 Q9VSK5 PRELIMINARY; PRT; 1963 AA.

AC Q9VSK5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CG6964 PROTEIN.
 GN GUG OR CG6964.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003555; AAF50413.1; -;
 DR FlyBase; FBgn0020427; GUG.
 DR InterPro; IPR000949; ELM2.
 DR InterPro; IPR001005; Myb_DNA_bind.
 DR Pfam; PF01448; ELM2; 1.
 DR Pfam; PF00249; myb_DNA-binding; 1.

DR SMART; SM00395; SANT; 1.
 SQ SEQUENCE 1963 AA; 207927 MW; 8F386DE56E66CB68 CRC64;

Query Match 58.0%; Score 47; DB 5; Length 1963;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GPGGPPPK 14
 Db 1156 GPGGPPPK 1163

Search completed: September 4, 2002, 17:01:35
 Job time: 1156 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:01 : Search time 158.52 seconds
(without alignments)
16.116 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDTWVKEQKGGPGAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	72.0	185	20 AAW99667	Human secreted pro
2	90	72.0	185	21 AAB24067	Human PRO1005 prot
3	90	72.0	185	21 AAY87272	Human signal pepti
4	90	72.0	185	21 AAY66686	Membrane-bound pro
5	90	72.0	185	22 AAB65209	Human PRO1005 (UNQ
6	90	72.0	185	22 AAB50957	Human PRO1005 prot
7	90	72.0	186	21 AAB38329	Human secreted pro
8	90	72.0	194	19 AAW69974	Cancer associated
9	90	72.0	194	20 AAY76591	Human ovarian tumo
10	54	43.2	194	22 ABB59646	Drosophila melanog
11	51	40.8	298	16 AAB79655	Human UBC/CDC34 pr

12	51	40.8	298	20 AAY39971	Human UBC/CDC34 p
13	51	40.8	298	21 AAB03179	Human UBC/CDC34 .
14	51	40.8	307	22 ABB07765	Novel human diagno
15	51	40.8	307	22 ABB08168	Novel human diagno
16	51	40.8	378	22 ABB72035	Drosophila melanog
17	51	40.8	465	22 AAG67296	Amino acid sequenc
18	50.5	40.4	127	22 AAO07630	Human polypeptide
19	49	39.2	109	22 AAO05707	Human polypeptide
20	49	39.2	170	11 AAR04129	Stem cell leukaemi
21	49	39.2	206	11 AAR04127	Stem cell leukaemi
22	49	39.2	214	11 AAR05857	Stem cell leukaemi
23	49	39.2	418	22 ABB03314	Novel human diagno
24	49	39.2	1518	22 ABB64829	Drosophila melanog
25	48.5	38.8	415	16 AAW01500	50 kD endogluanas
26	48.5	38.8	435	12 AAR15240	Humicola insolens
27	48.5	38.8	3080	22 ABB64877	Drosophila melanog
28	48	38.4	140	22 AAO08289	Human polypeptide
29	48	38.4	145	22 ABB71381	Drosophila melanog
30	48	38.4	147	22 AAO06887	Human polypeptide
31	48	38.4	163	22 AAO01151	Human polypeptide
32	48	38.4	367	22 AAM78403	Human protein SEQ
33	48	38.4	417	21 AAB25777	Human secreted pro
34	48	38.4	417	22 AAB75363	Human secreted pro
35	48	38.4	540	21 AAY57930	Human transmembran
36	48	38.4	1024	21 AAG42350	Arabidopsis thalia
37	48	38.4	1105	21 AAG42349	Arabidopsis thalia
38	48	38.4	1189	21 AAG42348	Arabidopsis thalia
39	47	37.6	52	21 AAB59108	Breast and ovarian
40	47	37.6	85	22 AAU47437	Propionibacterium
41	47	37.6	132	22 AAO05991	Human polypeptide
42	47	37.6	136	22 AAM96230	Human reproductive
43	47	37.6	136	22 AAU18917	Novel prostate gla
44	46.5	37.2	921	22 ABB68780	Drosophila melanog
45	46	36.8	97	21 AAB56449	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAW99667
ID AAW99667 standard; Protein; 185 AA.

XX
AC AAW99667;

XX
DT 07-JUN-1999 (first entry)

XX
DE Human secreted protein clone ej90_5 protein.

XX
KW Human; secreted protein; nutritional; cytokine; cell proliferation;
KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

XX
OS Homo sapiens.

XX
PN WO9907840-A1.

XX
PD 18-FEB-1999.

XX
PF 06-AUG-1998; 98WO-US16318.

XX
PR 04-AUG-1998; 98US-0130189.

XX
PR 06-AUG-1997; 97US-0906708.

XX
PA (GEM) GENETICS INST INC.

XX
PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

XX
PI Merberg D, Racie LA, Steininger RJ, Treacy M;

XX
XX WPI; 1999-167419/14.

DR
N-PSDB; AAX19493.

XX New polynucleotides encoding secreted human proteins - derived from
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
 PT or adult retina cDNA libraries
 XX
 PS Claim 34; Page 98-99; 107pp; English.
 XX
 CC The present sequence represents a human secreted protein. The secreted
 CC protein can have activities such as: nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. The
 CC polynucleotides are also stated to be useful for gene therapy.
 XX
 SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 20; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 ldalvkekklgkgpggppkglmly 121

RESULT 2
 AAB24067
 ID AAB24067 standard; Protein; 185 AA.
 XX
 AC AAB24067;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO1005 protein sequence SEQ ID NO:34.
 XX

XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glioma disorder; astrocytic disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immunologic disorder.
 XX

XX Homo sapiens.
 OS
 XX WO2000053755-A2.
 PN

XX 14-SEP-2000.
 PD

XX 06-JAN-2000; 2000WO-US00376.
 XX

XX 08-MAR-1999; 99WO-US05028.
 PR

XX 02-JUN-1999; 99WO-US12252.
 PR

XX 23-JUN-1999; 99US-0141037.
 PR

XX 07-JUL-1999; 99US-0143048.
 PR

XX 26-JUL-1999; 99US-0145698.
 PR

XX 30-NOV-1999; 99WO-US28313.
 PR

XX 20-DEC-1999; 99WO-US30911.
 PR

XX 05-JAN-2000; 2000WO-US00219.
 PR

XX (GETH) GENENTECH INC.
 PA

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX

DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58377.
 XX

PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer -
 XX

PS Claim 61; Fig 22; 286pp; English.
 XX

XX The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO233, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic,
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glial, astrocytic, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoele disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.
 XX

SQ Sequence 185 AA;

Query Match 72.0%; Score 90; DB 21; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 ldalvkekklgkgpggppkglmly 121

RESULT 3
 AAY87272
 ID AAY87272 standard; Protein; 185 AA.
 XX

AC AAY87272;
 XX

XX 11-MAY-2000 (first entry)
 DT

XX Human signal peptide containing protein HSPP-49 SEQ ID NO:49.
 DE

XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neutropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX

OS Homo sapiens.
 XX

XX WO200000610-A2.
 PN

XX 06-JAN-2000.
 PD

XX 25-JUN-1999; 99WO-US14484.
 XX

XX 26-JUN-1998; 98US-0090762.
 PR

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us-09-821-726-2.rag

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PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
PA (INCYTE) INCYTE PHARM INC.
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX WPI; 2000-160673/14.
DR N-PSDB; AAZ98157.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and
XX cardiovascular disease
XX
XX Claim 1: Page 193-194; 327pp; English.
XX
XX AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
XX anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
XX neuroprotective, cardiovascular and antitachymatic activities, and can
XX be used in gene therapy. HSPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense,
XX triplex-forming or ribozyme therapeutics, for detecting related sequences
XX or genetic variations, and for chromosomal mapping. HSP are also used to
XX raise specific antibodies (Ab) and to screen for agonists and
XX antagonists (potential therapeutic agents). Ab are used to diagnose, or
XX monitor, HSP-related diseases (in usual immunoassays), as therapeutic
XX antagonists, in competitive drug screens, and for purification of HSP
XX from natural sources.
XX
XX Sequence 185 AA;
SQ
Query Match 72.0%; Score 90; DB 21; Length 185;
Best Local Similarity 72.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
Qy 1 LDTWVKQK--GKPGGAPKDLWY 23
Db 97 LdaivkekkigkgpggppkglmY 121
RESULT 4
AAY66686
ID AAY66686 standard; protein; 185 AA.
XX
XX AC AAY66686;
XX
XX DT 05-APR-2000 (first entry)
XX
XX DE Membrane-bound protein PRO1005.
XX
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX OS Homo sapiens.
XX
XX PN WO963088-A2.
XX

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PD 09-DEC-1999.
XX
PF
XX 02-JUN-1999; 99WO-US12252.
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 04-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088736.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 22-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.

PR 25-JUN-1998; 98US-0090691.
 PR 25-JUN-1998; 98US-0090694.
 PR 25-JUN-1998; 98US-0090695.
 PR 25-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 26-JUN-1998; 98US-0090863.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 02-JUL-1998; 98US-0091544.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 02-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091578.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 10-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 17-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 PR (GETH) GENENTECH INC.
 PR Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PR Wood WI, Yuan J;
 PR XX

DR WPI: 2000-072883/06.
 DR N-PSDB; AAZ65023.
 XX
 PT Membrane-bound proteins and related nucleotide sequences -
 XX
 PS claim 12; Fig 139; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX Sequence 185 AA;
 SQ

Query Match 72.0%; Score 90; DB 21; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMYKEQK--GKPGGAPPKDLMY 23
 II :III:II IIIII III III
 Db 97 ldalvkekklqgpgppkglmy 121

RESULT 5
 AAB65209
 ID AAB65209 standard; Protein; 185 AA.
 XX
 AC AAB65209;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1005 (UNQ489) protein sequence SEQ ID NO:211.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.

18-FEB-2000; 2000WO-US04341.
 22-FEB-2000; 2000WO-US04414.
 24-FEB-2000; 2000WO-US04914.
 24-FEB-2000; 2000WO-US05004.
 02-MAR-2000; 2000WO-US05841.
 15-MAR-2000; 2000WO-US06884.
 20-MAR-2000; 2000WO-US07377.
 (GETH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrera N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 Zhang Z;
 WPI: 2001-032160/04.
 N-PSDB: AAF44169.
 PRO polynucleotides used to produce polypeptides used to target
 bioactive molecules such as toxins, radiolabels or antibodies, to
 specific cells, to cause targeted cell death -
 Claim 12; Fig 139; 935pp; English.
 The present invention describes human secreted and transmembrane PRO
 proteins. The PRO proteins have cytostatic activity. The PRO proteins
 can be used for targeted delivery of bioactive molecules, such as
 toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 sequences, and their fragments, can be used as hybridisation probes, in
 chromosomal and gene mapping, and in the generation of anti-sense RNA
 and DNA. They may also be used to produce transgenic animals which are
 used to develop and screen therapeutically useful reagents. The PRO
 nucleotide and protein sequence can be used for tissue typing and in
 treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 sequences given in the exemplification of the present invention.
 Sequence 185 AA;
 Query Match 72.0%; Score 90; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 Db 97 Idalvkekklgkgpgpppgkglmy 121
 RESULT 6
 ID AAB50957 standard; Protein; 185 AA.
 AC AAB50957;
 XX
 XX 21-MAR-2001 (first entry)
 DT
 DE Human PRO1005 protein.
 KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 XX
 XX Homo sapiens.
 XX WO200073348-A2.
 PN
 XX
 XX 07-DEC-2000.
 PD
 XX 30-MAY-2000; 2000WO-US14941.
 PF

11-SEP-1999; 99WO-US20111.
 08-SEP-1999; 99WO-US20594.
 29-OCT-1999; 99US-0162506.
 30-NOV-1999; 99WO-US28313.
 01-DEC-1999; 99WO-US28634.
 02-DEC-1999; 99WO-US28551.
 16-DEC-1999; 99WO-US30095.
 20-DEC-1999; 99WO-US30999.
 06-JAN-2000; 2000WO-US00376.
 11-FEB-2000; 2000WO-US03565.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 02-MAR-2000; 2000WO-US05841.
 03-MAR-2000; 2000US-0187202.
 10-MAR-2000; 2000WO-US06319.
 15-MAR-2000; 2000WO-US06884.
 30-MAR-2000; 2000WO-US08439.
 17-MAY-2000; 2000WO-US13705.
 (GETH) GENENTECH INC.
 Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 Shelton DL, Smith V, Watanabe CK, Wood WI;
 WPI: 2001-016509/02.
 N-PSDB: AAC91559.
 Twenty eight nucleic acids encoding PRO polypeptides which are useful
 for treating various tumors, e.g. breast cancer, and other
 inflammatory, angiogenic and immunological disorders -
 Claim 31; Fig 14; 188pp; English.
 The present sequence is one of twenty eight novel PRO polypeptides. The
 PRO polypeptides and their agonists, including antibodies, peptides, and
 small molecule agonists, may be used to treat various tumors, e.g.,
 cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 central nervous system cancer, melanoma or leukaemia. They are also
 useful for treating other disorders such as neuronal, glial, astrocytal,
 hypothalamic and other glandular, macrophagal, epithelial, stromal and
 blastocoeleic disorders, and inflammatory, angiogenic and immunological
 disorders.
 Sequence 185 AA;
 Query Match 72.0%; Score 90; DB 22; Length 185;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGPGGAPPKDLMY 23
 Db 97 Idalvkekklgkgpgpppgkglmy 121
 RESULT 7
 ID AAB38329 standard; Protein; 186 AA.
 AC AAB38329;
 XX
 XX 31-JAN-2001 (first entry)
 DT
 DE Human secreted protein encoded by gene 9 clone HNSA53.
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective;

KW nootropic; antibacterial; virucide; fungicide; opthalmological; human;
 KW vulnary; gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX WO200061623-A1.
 XX 19-OCT-2000.
 XX 06-APR-2000; 2000WO-US08979.
 XX 09-APR-1999; 99US-0128693.
 XX 26-APR-1999; 99US-0130991.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX WPI; 2000-647418/62.
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX Claim 11; Page 598; 716pp; English.
 XX Sequences AAB3821-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX SQ Sequence 186 AA;

Query Match 72.0%; Score 90; DB 21; Length 186;
 Best Local Similarity 72.0%; Pred. No. 1.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
 || :|||: ||||| ||| |||
 Db 97 ldlvkeklqgkpgpgppkglmly 121

RESULT 8
 ID AAW69974 standard; Protein; 194 AA.
 XX AAW69974;
 AC AAW69974;
 XX 16-NOV-1998 (first entry)
 DT Cancer associated protein.
 DE Cancer; PCR; Northern blotting; ribonuclease protection assay;
 KW diagnosis; metastatic cancer.
 XX Synthetic.
 OS Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX

PN WO9837187-A1.
 XX 27-AUG-1998.
 PD 18-FEB-1998; 98WO-JP00667.
 XX 21-FEB-1997; 97JP-0052508.
 PR (TAKI) TAKARA SHUZO CO LTD.
 XX Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;
 PI WPI; 1998-467552/40.
 DR Detection of cancer cells in tissue samples - by changes in mRNA
 XX expression compared to normal tissue of specific cancer-associated
 PT gene sequences
 PT Claim 14; Page 64-65; 92pp; Japanese.
 PS The cancer associated proteins AAW69974-W69976 where used in the method
 CC of the invention to detect cancer cells in tissue samples or biological
 CC fluids. They are detected by monitoring the change in mRNA expression
 CC as compared to normal tissue of one or more cancer-associated genes
 CC whose cDNA stringently hybridises to cancer associated gene nucleic acid
 CC fragments. The change in expression may be an increase or a decrease
 CC compared to normal tissue. The mRNA expression may be determined by
 CC PCR, Northern blotting or ribonuclease protection assay, or by
 CC determining the change in the amount of protein encoded by the gene(s) as
 CC compared to normal tissue, for example by using a labelled antibody
 CC recognising the protein. Detection of cancer cells for cancer diagnosis,
 CC including detection of metastatic cancer cells in tissues other than the
 CC primary tumour site.
 XX SQ Sequence 194 AA;
 Query Match 72.0%; Score 90; DB 19; Length 194;
 Best Local Similarity 72.0%; Pred. No. 1.8e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
 || :|||: ||||| ||| |||
 Db 106 ldlvkeklqgkpgpgppkglmly 130
 RESULT 9
 AAY76591
 ID AAY76591 standard; Protein; 194 AA.
 XX AAY76591;
 AC AAY76591;
 XX 10-APR-2000 (first entry)
 DT Human ovarian tumor EST fragment encoded protein 87.
 DE Expressed sequence tag; EST; human; ovarian tumor; anticancer;
 KW gene therapy; treatment.
 XX Homo sapiens.
 OS DE19817557-A1.
 PN 21-OCT-1999.
 PD 09-APR-1998; 98DE-1017557.
 XX 09-APR-1998; 98DE-1017557.
 PR (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 PI
 XX

DR WPI: 1999-591920/51.
 DR N-PSDB; AAZ77487.
 XX
 CC New nucleic acid sequences expressed in ovarian, and some other, cancer
 CC tissues, and derived polypeptides, for treatment of ovarian cancer and
 CC identification of therapeutic agents.
 PT
 XX
 PS Claim 25; Page 279; 310pp; German.
 XX
 CC This invention describes novel nucleic acid (cDNA) sequences (A) which
 CC have anticancer activity and are highly expressed in ovarian tumor
 CC tissue (and some also in testis and breast cancer tissue). The products
 CC of the invention can be used for gene therapy. (A) are used (i) for
 CC recombinant expression of polypeptides (B) and (ii) to isolate complete
 CC genes. (B) are used (i) to identify agents suitable for treatment of
 CC ovarian cancer; (ii) directly for treating this form of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AAY76505-Y76638 represent protein
 CC fragments encoded by the human ovarian tumor cDNA library derived EST
 CC fragments represented in AAZ77450-Z77572.
 XX
 SQ Sequence 194 AA;
 Query Match 72.0%; Score 90; DB 20; Length 194;
 Best Local Similarity 72.0%; Pred. No. 1.8e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GRGPGGAPPKDLMY 23
 Db 106 ldlvkekklqgkgpggpppgkglmy 130
 ||:||||:| ||||| ||| |||
 RESULT 10
 ABB59646
 ID ABB59646 standard; Protein; 1194 AA.
 XX
 AC ABB59646;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 5730.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR
 XX 11-JUL-2000; 2000US-0614150.
 PR
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR
 XX N-PSDB; ABL03749.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 5730; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABE01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1194 AA;
 Query Match 43.2%; Score 54; DB 22; Length 1194;
 Best Local Similarity 64.3%; Pred. No. 24;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 5 VKEQKKGKGGPGAPP 18
 Db 613 mkspngngpggapp 626
 :| | |||||
 RESULT 11
 AAR79655
 ID AAR79655 standard; Protein; 298 AA.
 XX
 AC AAR79655;
 XX
 DT 06-DEC-1995 (first entry)
 DT
 XX Human UBC/CDC34 protein.
 DE
 XX Ubiquitin-conjugating enzyme; UBC/CDC34; cell cycle;
 KW cell proliferation; cancer; psoriasis; fibrosis.
 KW
 XX Homo sapiens.
 OS
 XX WO9518974-A.
 PN
 XX 13-JUL-1995.
 PD
 XX 04-JAN-1995; 95WO-US00164.
 PF
 XX 13-SEP-1994; 94US-0305520.
 PR
 XX 04-JAN-1994; 94US-0176937.
 PR
 XX 23-MAY-1994; 94US-0247904.
 PR
 XX 27-MAY-1994; 94US-0250795.
 PR
 XX (MITO-) MITOTIX INC.
 PA
 XX Cottarel G, Draetta G, Eckstein JW, Gyuris J, Rolfe M;
 PI
 XX WPI; 1995-255137/33.
 DR
 XX N-PSDB; AAQ97845.
 DR
 XX Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
 PT regulatory proteins - also new ubiquitin conjugating enzymes, their
 PT related nucleic acid, vectors, antibodies etc., useful for regulating
 PT e.g. cell proliferation
 PT
 XX Disclosure; Page 107-108; 157pp; English.
 PS
 XX Human UBC3/CDC34 cDNA (given in AAQ97845) was amplified from a HeLa
 CC cell cDNA library. The gene was subcloned into a baculovirus or
 CC PGEX vector for expression of recombinant UBC/CDC34 in Sf9 insect
 CC or E. coli cells for use as a component of an in vitro ubiquitin
 CC conjugating system.
 CC

SQ Sequence 298 AA;

Query Match 40.8%; Score 51; DB 16; Length 298;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGKGGGAPP 18
 : : | : : : :
 Db 21 eeeagggpggsp 33

RESULT 12

AA39971
 ID AAY39971 standard; Protein; 298 AA.

XX AC AAY39971;

XX DT 15-DEC-1999 (first entry)

XX DE Human UBC3/CDC34 protein sequence.

XX KW Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis;
 KW cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
 KW proliferative disorder; cancer; restenosis; tissue connective disorder;
 KW wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma;
 KW insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
 KW diagnosis; therapy; UBC3/CDC34.

XX OS Homo sapiens.

XX PN US5968761-A.

XX PD 19-OCT-1999.

XX PF 07-JUN-1995; 95US-0486663.

XX PR 04-JAN-1994; 94US-0176937.

XX PR 23-MAY-1994; 94US-0247904.

XX PR 27-MAY-1994; 94US-0250795.

XX PR 13-SEP-1994; 94US-0305520.

XX PA (MITO-) MITOTIX INC.

XX PI Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;

XX DR WPI; 1999-590402/50.

XX DR N-PSDB; AAZ27573.

XX PT Identifying ubiquitination inhibitors using novel ubiquitin conjugating enzymes -

XX PS Example 2; Column 99-102; 61pp; English.

XX CC This sequence is the human UBC3/CDC34 protein. The invention relates
 CC to assays for identifying an inhibitor of ubiquitin-mediated proteolysis
 CC of a cell-cycle regulatory protein comprising contacting a candidate
 CC agent with an ubiquitin-conjugating system and measuring the level of
 CC ubiquitination. The ubiquitin-conjugating system comprises:
 CC (a) a reconstituted protein mixture including a ubiquitin conjugating
 CC enzyme (UbCE) produced by the expression of a nucleic acid which
 CC hybridizes under high stringency conditions to human UbCE, Candida
 CC albicans UbCE, or Schizosaccharomyces pombe UbCE coding sequences;
 CC (b) a regulatory protein; and (c) ubiquitin. The polynucleotides are
 CC useful for identifying ubiquitination inhibitors. The polynucleotides are
 CC polypeptides, antisense compounds and antibodies against them may also be
 CC useful for the treatment and/or diagnosis of proliferative disorders
 CC (e.g. cancer, atherosclerosis, or restenosis), tissue connective
 CC disorders, controlling wound healing, and disorders characterized by
 CC fibrosis (e.g. rheumatoid arthritis, insulin dependent diabetes mellitus,
 CC glomerulonephritis, cirrhosis, and scleroderma).

XX SQ Sequence 298 AA;

Query Match 40.8%; Score 51; DB 20; Length 298;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGKGGGAPP 18
 : : | : : : :
 Db 21 eeeagggpggsp 33

RESULT 13

AA3179
 ID AAB03179 standard; Protein; 298 AA.

XX AC AAB03179;

XX DT 23-OCT-2000 (first entry)

XX DE Human UBC/CDC34.

XX KW UBC/CDC34; ubiquitin conjugating enzyme; ubiquitin mediated proteolysis;
 KW human; cellular protein half life; ubiquitination inhibitor; p53;
 KW cyclin; cell cycle regulator; myc deregulation; human papillomavirus;
 KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
 KW epidermal neoplasia; psoriasis; connective tissue disorder;
 KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.

XX OS Homo sapiens.

XX PN US6068982-A.

XX PD 30-MAY-2000.

XX PF 17-DEC-1996; 96US-0767942.

XX PR 07-JUN-1995; 95US-0486663.

XX PR 04-JAN-1994; 94US-0176937.

XX PR 23-MAY-1994; 94US-0247904.

XX PR 27-MAY-1994; 94US-0250795.

XX PR 13-SEP-1994; 94US-0305520.

XX PA (MITO-) MITOTIX INC.

XX PI Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;

XX DR WPI; 2000-410854/35.

XX DR N-PSDB; AAA61626.

XX PT Identifying an inhibitor of ubiquitin mediated proteolysis of
 PT regulatory protein for treating cancers involves measuring
 PT ubiquitination levels of the protein in the presence of candidate agent
 PT in an eukaryotic cell -

XX PS Example 2; Column 117-118; 73pp; English.

XX CC The invention relates to a method of identifying an inhibitor of
 CC ubiquitin-mediated proteolysis of a cell cycle regulatory protein
 CC comprising contacting an engineered eukaryotic cell with a candidate
 CC agent. The eukaryotic cells is engineered to express a recombinant
 CC human, Candida albicans or Schizosaccharomyces pombe ubiquitin-
 CC conjugating enzyme (AAB03169-H03171), a cell cycle regulatory protein
 CC (such as p53) and ubiquitin. The specification also discloses novel
 CC Candida albicans and Schizosaccharomyces pombe ubiquitin-conjugating
 CC enzymes, caUbCE and spUbCE (AAB03170, AAB03171), and two novel human
 CC ubiquitin-conjugating enzymes, hUbCE and rapUBC (AAB03169, AAB03173).
 CC The ubiquitin-mediated proteolysis system is the major pathway for the
 CC selective, controlled degradation of intracellular proteins in
 CC eukaryotic cells. In particular, this system controls the half-lives of
 CC cellular proteins, and is important in controlling the levels of proteins
 CC involved in cell cycle progression. Alterations in the ubiquitination of
 CC these proteins may therefore play a role in the development of cancers.
 CC For example, human papillomaviruses such as HPV-18 encode a transforming

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protein, E6 (AAB03176), which combines with a cellular E6-associated protein (E6-AP; AAB03177) to stimulate the ubiquitination of p53, thus targeting it for degradation. The ubiquitination inhibitors identified according to the method of the invention are useful for treatment of cervical cancers and connective tissue disorders and for controlling the wound healing process. They are also useful in treatment of hyperplastic epidermal conditions such as psoriasis, neoplastic epidermal conditions, skin cancers e.g., basal cell carcinomas, squamous cell carcinomas. The inhibitors are useful for deregulating myc expression and rendering the cells sensitive to chemotherapeutic treatment or to upset the balance of transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-mediated degradation of cyclins are useful as antiproliferative agents. The present sequence represents human UBC/CDC34.

XX Sequence 298 AA;

Query Match 40.8%; Score 51; DB 21; Length 298;

Best Local Similarity 61.5%; Pred. No. 16;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKKGKGGGAPP 18

:|: | ||||:|

Db 21 eeeagggpgspp 33

RESULT 14

ABG07765

ID ABG07765 standard; Protein; 307 AA.

XX AC

XX ABG07765;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #7756.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB; AAS71952.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX PS Claim 20; SEQ ID NO 38124; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 307 AA;

Query Match 40.8%; Score 51; DB 22; Length 307;

Best Local Similarity 61.5%; Pred. No. 16;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKKGKGGGAPP 18

:|: | ||||:|

Db 21 eeeagggpgspp 33

RESULT 15

ABG08168

ID ABG08168 standard; Protein; 307 AA.

XX AC

XX ABG08168;

XX DT 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #8159.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI: 2001-639362/73.

XX DR N-PSDB; AAS72355.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

XX PS Claim 20; SEQ ID NO 38527; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations in
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 307 AA;

Query Match 40.8%; Score 51; DB 22; Length 307;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 KEQKGGGGGAPP 18
 Db :|: | |||:|
 21 eeeaggggggsgpp 33

Search completed: September 4, 2002, 16:45:02
 Job time: 378 sec

Thu Sep 5 11:23:34 2002

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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:46:05 ; Search time 57.74 seconds
(without alignments)
9.730 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDTWKEQKKGPGGAPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA*
1: /cgn2.6/ptodata/2/1aa/5A-COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B-COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/6A-COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B-COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCTUS-COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	40.8	298	3	US-08-767-942A-25
2	46	36.8	467	4	US-09-002-361-3
3	46	36.8	496	4	US-09-002-361-2
4	45.5	36.4	402	3	US-08-709-974A-1
5	45.5	36.4	402	3	US-08-709-974A-5
6	45.5	36.4	415	2	US-08-833-642A-5
7	45.5	36.4	415	3	US-08-709-974A-4
8	45.5	36.4	415	4	US-09-069-632-1
9	45.5	36.4	435	1	US-08-361-920-27
10	45.5	36.4	435	1	US-08-479-939-27
11	45.5	36.4	435	1	US-08-483-432-27
12	45.5	36.4	435	1	US-08-069-632-3
13	45	36.0	265	2	US-08-484-905-119
14	45	36.0	265	3	US-08-481-985B-119
15	45	36.0	265	4	US-08-370-476-119
16	45	36.0	298	5	PCT-US95-02689-41
17	45	36.0	298	2	US-08-207-481-39
18	45	36.0	992	4	US-08-890-865A-1
19	44	35.2	402	2	US-08-709-979A-3
20	43	34.4	9	2	US-08-460-890A-57
21	43	34.4	9	3	US-08-167-641C-57
22	43	34.4	9	4	US-08-460-971A-57
23	43	34.4	9	4	US-08-462-040-57
24	43	34.4	321	1	US-08-362-670B-26
25	43	34.4	321	3	US-08-333-576C-26
26	43	34.4	321	4	US-08-808-324-26
27	43	34.4	321	5	PCT-US94-14030A-26

28	43	34.4	456	2	US-08-709-979A-1	Sequence 1, Appli
29	43	34.4	456	3	US-08-709-974A-11	Sequence 11, Appl
30	43	34.4	880	4	US-09-378-255-6	Sequence 6, Appli
31	43	34.4	880	4	US-09-141-212-2	Sequence 2, Appli
32	43	34.4	880	4	US-09-141-212-4	Sequence 4, Appli
33	43	34.4	880	4	US-09-552-351-4	Sequence 4, Appli
34	43	34.4	880	4	US-09-251-372-6	Sequence 6, Appli
35	43	34.4	880	4	US-09-561-138-2	Sequence 2, Appli
36	43	34.4	880	4	US-09-561-138-4	Sequence 4, Appli
37	43	34.4	880	4	US-09-715-336-6	Sequence 6, Appli
38	43	34.4	880	4	US-09-811-241-6	Sequence 4, Appli
39	43	34.4	880	4	US-09-802-839-4	Sequence 2, Appli
40	42	33.6	246	3	US-08-675-885-2	Sequence 4, Appli
41	42	33.6	295	2	US-08-700-637-4	Sequence 2, Appli
42	42	33.6	307	1	US-07-982-112-2	Sequence 4, Appli
43	42	33.6	378	4	US-09-500-569-10	Sequence 2, Appli
44	42	33.6	819	4	US-09-651-856-15	Sequence 10, Appl
45	42	33.6	1060	3	US-09-931-820-3	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-767-942A-25
; Sequence 25, Application US/08767942A
; Patent No. 6068982
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Chiu, M. Isabel
; APPLICANT: Berlin, Vivian
; APPLICANT: Damagnez, Veronique
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume, Cottarel
; TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-767-942A-25

Query Match 40.8%; Score 51; DB 3; Length 298;
Best Local Similarity 61.5%; Pred. No. 4.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 KEQKGGPGGAPP 18
::: | |||||

Db 21 EEEAGGGGGPP 33

RESULT 2
US-09-002-361-3
; Sequence 3, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
; TITLE OF INVENTION: Channels
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-002-361-3

Query Match 36.8%; Score 46; DB 4; Length 467;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGGAPPKD 20
I: : : || || || |
Db 380 LENTINGARGPAGPAPPAD 399

RESULT 3
US-09-002-361-2
; Sequence 2, Application US/09002361
; Patent No. 6329516
; GENERAL INFORMATION:
; APPLICANT: Halling, Blaik
; TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
; TITLE OF INVENTION: Channels
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,361
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-002-361-2

Query Match 36.8%; Score 46; DB 4; Length 496;
Best Local Similarity 40.0%; Pred. No. 44;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGGAPPKD 20
I: : : || || || |
Db 409 LENTINGARGPAGPAPPAD 428

RESULT 4
US-08-709-974A-1
; Sequence 1, Application US/08709974A
; Patent No. 6117664
; GENERAL INFORMATION:
; APPLICANT: Sch lein, Martin
; APPLICANT: Rosholm, Peter
; APPLICANT: Nielsen, Jack Bech
; APPLICANT: Hansen, Svend Aage
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117664o No. 6117664disk of No. 6117664th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-1

Query Match 36.4%; Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 42;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 5

US-08-709-974A-5
Sequence 5, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch lein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08709,974A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta
REGISTRATION NUMBER: 35,127Y
REFERENCE/DOCKET NUMBER: 4160.414-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-974A-5

Query Match 36.4%; Score 45.5; DB 3; Length 402;
Best Local Similarity 36.7%; Pred. No. 42;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 6
US-08-833-642A-5
Sequence 5, Application US/08833642A
Patent No. 5883066
GENERAL INFORMATION:
APPLICANT: Ivan M. A. J. Herbots et al.
TITLE OF INVENTION: Liquid Detergent Compositions
Containing Cellulase and Amine
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jackie Ann Zurcher
ADDRESSEE: Dinsmore & Shohl LLP
STREET: 255 E. Fifth Street
STREET: 1900 Chemed Center
CITY: Cincinnati
STATE: Ohio
COUNTRY: USA
ZIP: 45202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,642A
FILING DATE: April 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Zurcher, J. A. P42,251
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: CM551C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 977-8377
TELEFAX: (513) 977-8141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-642A-5

Query Match 36.4%; Score 45.5; DB 2; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
DB 33 LDSLSHPHRAEGLGPGCGDGNPPPKDV 62

RESULT 7

US-08-709-974A-4
Sequence 4, Application US/08709974A
Patent No. 6117664
GENERAL INFORMATION:
APPLICANT: Sch lein, Martin
APPLICANT: Rosholm, Peter
APPLICANT: Nielsen, Jack Bech
APPLICANT: Hansen, Svend Aage
APPLICANT: von der Osten, Claus
TITLE OF INVENTION: No. 6117664el Alkaline Cellulases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117664o No. 6117664th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,974A
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127Y
; REFERENCE/DOCKET NUMBER: 4160.414-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-974A-4

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Query Match          36.4%; Score 45.5; DB 3; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
   |||: : : |||||
Db 33 LDSLSPHIAHRAEGLPGCGDGNPPPKDV 62

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RESULT 8
US-09-069-632-1
; Sequence 1, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desiging
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 415 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-069-632-1

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Query Match          36.4%; Score 45.5; DB 4; Length 415;
Best Local Similarity 36.7%; Pred. No. 43;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKKGPGGA-----PPKDL 21
   |||: : : |||||
Db 33 LDSLSPHIAHRAEGLPGCGDGNPPPKDV 62

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RESULT 9
US-08-361-920-27
; Sequence 27, Application US/08361920
; Patent No. 5457046
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5457046o No. 5457046disk of No. 5457046th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-361-920-27

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Query Match          36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

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Thu Sep 5 11:23:34 2002

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QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
; Sequence 27, Application US/08479939
; Patent No. 5686593
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5763254o No. 5763254disk of No. 5763254th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,432
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE:
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-432-27

Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA

RESULT 12
US-09-069-632-3
; Sequence 3, Application US/09069632
; Patent No. 6261828
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA

QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
; Sequence 27, Application US/08479939
; Patent No. 5686593
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82
; GENERAL INFORMATION:
; APPLICANT: Woeldike, Helle F.
; APPLICANT: Hagen, Frederick
; APPLICANT: Hjort, Carsten M.
; APPLICANT: Sven, Hastrup
; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5686593o No. 5686593disk of No. 5686593th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,939
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,920
; FILING DATE: 22-DEC-1994
; APPLICATION NUMBER: US 07/940,860
; FILING DATE: 28-OCT-1992
; APPLICATION NUMBER: DK 1158/90
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK91/00124
; FILING DATE: 08-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 3435.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-867-0298
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-939-27

Query Match 36.4%; Score 45.5; DB 1; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM---VKEQKGGGGA-----PPKDL 21
Db 53 LDSLSHPHRAEGLGPGCGDGNPPPKDV 82
; GENERAL INFORMATION:
; APPLICANT: Lund, Henrik
; TITLE OF INVENTION: A Process For Combined Desizing
; TITLE OF INVENTION: And Stone-Washing of Dyed Denim
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6261828o No. 6261828disk of No. 6261828th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA

RESULT 11
US-08-483-432-27
; Sequence 27, Application US/08483432
; Patent No. 5763254
; GENERAL INFORMATION:
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; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,632
; FILING DATE: 29-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK96/00469
; FILING DATE: 15-NOV-1996
; APPLICATION NUMBER: 1278/95
; FILING DATE: 15-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeta
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 4588.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-069-632-3

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Query Match 36.4%; Score 45.5; DB 4; Length 435;
Best Local Similarity 36.7%; Pred. No. 46;
Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

QY 1 LDTM--VKEQKGKGGGA-----PPKDL 21
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Db 53 LDSLSHPHRAEGLPGGCGDNGNPPPKDV 82

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RESULT 13
US-08-484-905-119
; Sequence 119, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-pierre
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-905-119

Query Match 36.0%; Score 45; DB 2; Length 265;
Best Local Similarity 36.4%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 LDTMVKQKQKGGGAPPKDL 22
   |::: ||| | | |
Db 243 LGLFIRHSQKGRGPPAGLL 264

RESULT 14
US-08-481-985B-119
; Sequence 119, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:

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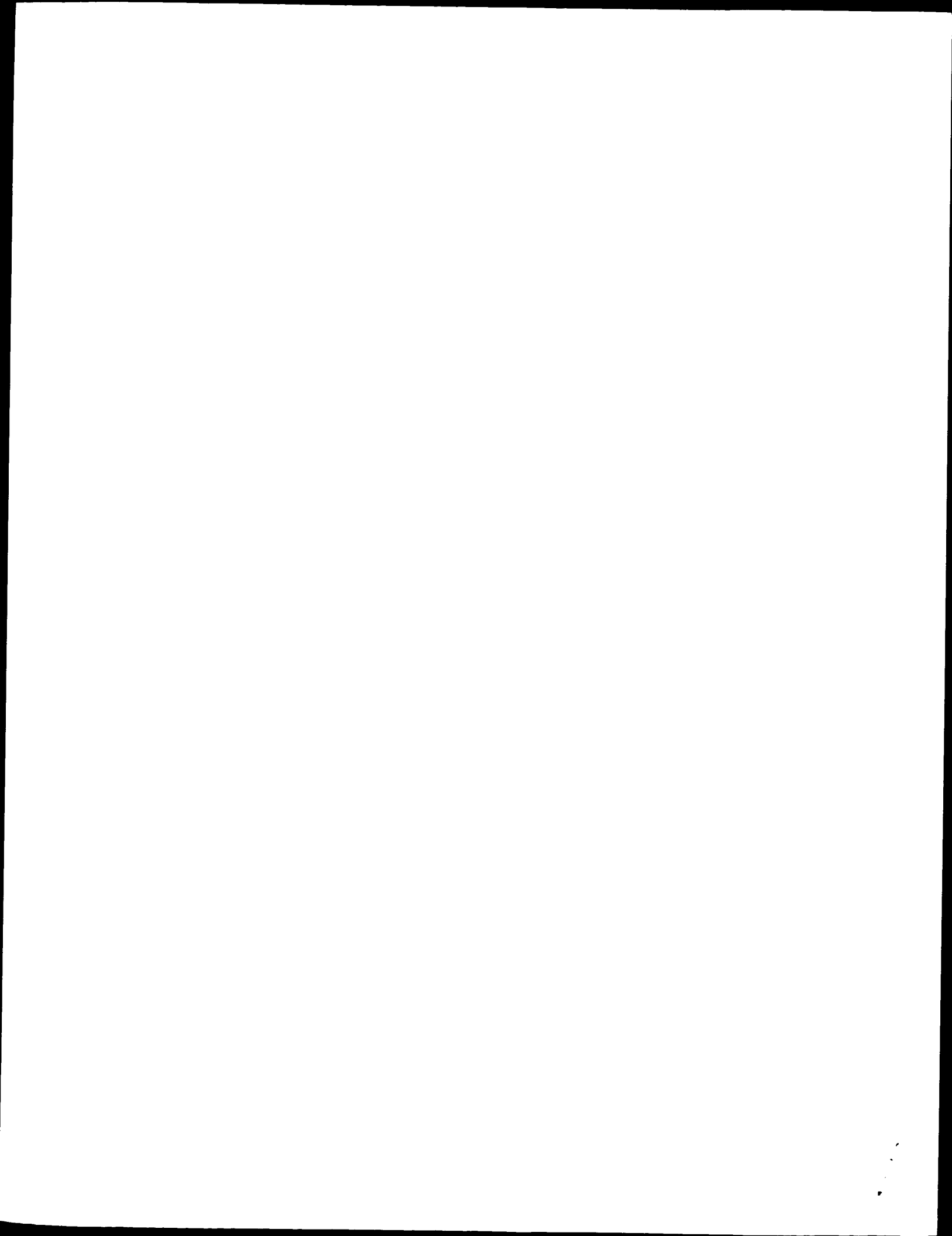
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 Best Local Similarity 36.4%; Pred. No. 32;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 LDTMVKEQKGGGAPPKDL 22
 Db 243 LGLFIRHRQKGGPRGPPAGLL 264

Search completed: September 4, 2002, 16:46:06
 Job time: 327 sec

LENGTH: 265 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-481-985B-119

Query Match 36.0%; Score 45; DB 3; Length 265;
 Best Local Similarity 36.4%; Pred. No. 32;
 Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 1 LDTMVKEQKGGGAPPKDL 22
 Db 243 LGLFIRHRQKGGPRGPPAGLL 264

RESULT 15
 US-08-370-476-119
 ; Sequence 119, Application US/08370476
 ; Patent No. 6153408
 ; GENERAL INFORMATION:
 ; APPLICANT: Mottez, Estelle
 ; APPLICANT: Abastado, Jean-Pierre
 ; APPLICANT: Kourilsky, Philippe
 ; APPLICANT: Lone, Yu-Chun
 ; APPLICANT: Ojcius, David
 ; APPLICANT: Casrouge, Armanda
 ; TITLE OF INVENTION: Altered Major Histocompatibility Complex
 ; TITLE OF INVENTION:
 ; NUMBER OF SEQUENCES: 127
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,476
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/117,575
 ; FILING DATE: 07-SEP-1993
 ; APPLICATION NUMBER: US 08/072,787
 ; FILING DATE: 06-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/801,818
 ; FILING DATE: 05-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/792,473
 ; FILING DATE: 15-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Kenneth J.
 ; REGISTRATION NUMBER: 25,146
 ; REFERENCE/DOCKET NUMBER: 05243.0001-01000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 119:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 265 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-370-476-119



us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:19 ; Search time 704.77 Seconds
(without alignments)
11.487 Million cell updates/sec

Title: US-09-821-726-2

Perfect score: 125

Sequence: 1 LDTMWKEQKGGGAPPKDLMY 23

Scoring table: BLOSUM62

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Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	125	100.0	23	22	US-09-821-726-2
2	125	100.0	184	22	US-09-821-726-16
3	90	72.0	25	22	US-09-821-726-10
4	90	72.0	150	13	US-08-906-708-24
5	90	72.0	182	20	US-09-684-524-212
6	90	72.0	182	24	US-10-050-704-212
7	90	72.0	185	1	PCT-US98-16318-18
					Sequence 2, Appli
					Sequence 16, Appl
					Sequence 10, Appl
					Sequence 24, Appl
					Sequence 212, App
					Sequence 212, App
					Sequence 18, Appl

8	90	72.0	185	15	US-09-130-189-18	Sequence 18, Appl
9	90	72.0	185	20	US-09-684-524-105	Sequence 105, App
10	90	72.0	185	21	US-09-709-238-211	Sequence 211, App
11	90	72.0	185	21	US-09-746-783-146	Sequence 146, App
12	90	72.0	185	22	US-09-821-726-13	Sequence 13, Appl
13	90	72.0	185	23	US-09-941-992-211	Sequence 211, App
14	90	72.0	185	23	US-09-989-279-211	Sequence 211, App
15	90	72.0	185	23	US-09-989-293A-211	Sequence 211, App
16	90	72.0	185	23	US-09-989-721-211	Sequence 211, App
17	90	72.0	185	23	US-09-989-722-211	Sequence 211, App
18	90	72.0	185	23	US-09-989-723-211	Sequence 211, App
19	90	72.0	185	23	US-09-989-724-211	Sequence 211, App
20	90	72.0	185	23	US-09-989-725-211	Sequence 211, App
21	90	72.0	185	23	US-09-989-726-211	Sequence 211, App
22	90	72.0	185	23	US-09-989-727-211	Sequence 211, App
23	90	72.0	185	23	US-09-989-728-211	Sequence 211, App
24	90	72.0	185	23	US-09-989-729A-211	Sequence 211, App
25	90	72.0	185	23	US-09-989-730-211	Sequence 211, App
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27	90	72.0	185	23	US-09-989-732-211	Sequence 211, App
28	90	72.0	185	23	US-09-989-734-211	Sequence 211, App
29	90	72.0	185	23	US-09-989-735-211	Sequence 211, App
30	90	72.0	185	23	US-09-989-862-211	Sequence 211, App
31	90	72.0	185	23	US-09-990-427-211	Sequence 211, App
32	90	72.0	185	23	US-09-990-436-211	Sequence 211, App
33	90	72.0	185	23	US-09-990-437-211	Sequence 211, App
34	90	72.0	185	23	US-09-990-438-211	Sequence 211, App
35	90	72.0	185	23	US-09-990-439-211	Sequence 211, App
36	90	72.0	185	23	US-09-990-440-211	Sequence 211, App
37	90	72.0	185	23	US-09-990-441-211	Sequence 211, App
38	90	72.0	185	23	US-09-990-442-211	Sequence 211, App
39	90	72.0	185	23	US-09-990-443-211	Sequence 211, App
40	90	72.0	185	23	US-09-990-444-211	Sequence 211, App
41	90	72.0	185	23	US-09-990-456-211	Sequence 211, App
42	90	72.0	185	23	US-09-990-562-211	Sequence 211, App
43	90	72.0	185	23	US-09-990-711-211	Sequence 211, App
44	90	72.0	185	23	US-09-990-726-211	Sequence 211, App
45	90	72.0	185	23	US-09-991-073-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-2
; Sequence 2, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: CASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-821-726-2

Query Match 100.0%; Score 125; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.4e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDTMWKEQKGGGAPPKDLMY 23
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Db 1 LDTMWKEQKGGGAPPKDLMY 23
|||||

RESULT 2
 US-09-821-726-16
 ; Sequence 16, Application US/09821726
 ; GENERAL INFORMATION:
 ; APPLICANT: MARTIN, TERENCE E.
 ; APPLICANT: TOBACK, F. GARY
 ; APPLICANT: POWELL, C. THOMAS
 ; APPLICANT: AGARWAL, KAN
 ; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
 ; FILE REFERENCE: 21459/90913
 ; CURRENT APPLICATION NUMBER: US/09/821,726
 ; CURRENT FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-821-726-16

Query Match 100.0%; Score 125; DB 22; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDTWVKEQK--GKGGGAPPKDLMY 23
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 Db 97 LDTWVKEQKGGGAPPKDLMY 119

RESULT 3
 US-09-821-726-10
 ; Sequence 10, Application US/09821726
 ; GENERAL INFORMATION:
 ; APPLICANT: MARTIN, TERENCE E.
 ; APPLICANT: TOBACK, F. GARY
 ; APPLICANT: POWELL, C. THOMAS
 ; APPLICANT: AGARWAL, KAN
 ; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
 ; FILE REFERENCE: 21459/90913
 ; CURRENT APPLICATION NUMBER: US/09/821,726
 ; CURRENT FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 10
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-821-726-10

Query Match 72.0%; Score 90; DB 22; Length 25;
 Best Local Similarity 72.0%; Pred. No. 4.7e-05;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGGGAPPKDLMY 23
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 Db 1 LDALVKEKKLOGKGGPPPKGLMY 25

RESULT 4
 US-08-906-708-24
 ; Sequence 24, Application US/08906708
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John M.
 ; APPLICANT: LaVallie, Edward R.
 ; APPLICANT: Racie, Lisa A.
 ; APPLICANT: Treacy, Maurice
 ; APPLICANT: Spaulding, Vikki
 ; APPLICANT: Agostino, Michael J.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 ; FILE REFERENCE: 21459/90913
 ; CURRENT APPLICATION NUMBER: US/08/906,708
 ; CURRENT FILING DATE: 1999-04-26
 ; NUMBER OF SEQ ID NOS: 344
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 212
 ; LENGTH: 182
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-08-906-708-24

NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/906,708
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne A.
 REGISTRATION NUMBER: P-41,323
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-906-708-24

Query Match 72.0%; Score 90; DB 13; Length 150;
 Best Local Similarity 72.0%; Pred. No. 0.00037;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGGGAPPKDLMY 23
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 Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

RESULT 5
 US-09-684-524-212
 ; Sequence 212, Application US/09684524
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 62 Human Secreted Proteins
 ; FILE REFERENCE: P2039P1
 ; CURRENT APPLICATION NUMBER: US/09/684,524
 ; CURRENT FILING DATE: 2000-10-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/08979
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/128,693
 ; PRIOR FILING DATE: 1999-04-09
 ; PRIOR APPLICATION NUMBER: 60/130,991
 ; PRIOR FILING DATE: 1999-04-26
 ; NUMBER OF SEQ ID NOS: 344
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 212
 ; LENGTH: 182
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-684-524-212

Query Match 72.0%; Score 90; DB 20; Length 182;
 Best Local Similarity 72.0%; Pred. No. 0.00047;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 1 LDTWVKEQK--GKGGGAPPKDLMY 23
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 Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

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RESULT 8
US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 72.0%; Score 90; DB 15; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 9
US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 72.0%; Score 90; DB 24; Length 182;
Best Local Similarity 72.0%; Pred. No. 0.00047;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 10
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 72.0%; Score 90; DB 20; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 6
US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 72.0%; Score 90; DB 24; Length 182;
Best Local Similarity 72.0%; Pred. No. 0.00047;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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RESULT 7
PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI6051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 72.0%; Score 90; DB 1; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMWKEQK--GKGPGGAPPKDLMY 23
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Db 97 LDALVKEKKLOGKGGPPPKGLMY 121

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APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jean
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,326
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: US 60/088,655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: US 60/088,722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,730
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,740
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,741
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/088,810
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: US 60/088,858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: US 60/088,861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: US 60/088,863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: US 60/088,876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: US 60/089,090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/089,105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/089,440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/089,512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: US 60/089,514
PRIOR FILING DATE: 1998-06-16
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PRIOR APPLICATION NUMBER: US 60/089,538
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,676
PRIOR FILING DATE: 1998-06-25

Db 97 LDALVKKKLOGKGGPPKGLMY 121
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US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941,992
; PRIOR FILING DATE: 2001-08-28
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; PRIOR APPLICATION NUMBER: 60/090254

us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PlC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
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; Query Match 72.0%; Score 90; DB 23; Length 185;
; Best Local Similarity 72.0%; Pred. No. 0.00048;
; Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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; ; Sequence 211, Application US/09989279

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

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Query Match          72.0%; Score 90; DB 23; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

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Db 97 LDALVKEKLOGKGGGPPKGLMY 121

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US-09-989-293A-211
; Sequence 211, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

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us-09-821-726-2.rapm

Thu Sep 5 11:23:34 2002

APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavini, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 CURRENT FILING DATE: 2001-11-20
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 PRIOR FILING DATE: 1997-06-16
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Query Match 72.0%; Score 90; DB 23; Length 185;
Best Local Similarity 72.0%; Pred. NO. 0.00048;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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Db 97 LDALVKEKKLQKGPGPPKGLMY 121
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Job time: 1040 sec

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GenCore version 4.5
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DM protein - protein search, using sw model
Run on:      September 4, 2002, 17:04:23 ; Search time 156.13 Seconds
              (without alignments)
              34.049 Million cell updates/sec

Title:
Perfect score: 125
Sequence: 1 LDYMWKEQKGKPGGAPPKDLMY 23
              US-09-821-726-2

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

```

763338

```
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45
```

Pending_Patents_AA_New: *

SUMMARIES

Result No.	Query %			Length	DB	ID	Description
	Score	Match					
1	90	72.0	185	5	US-09-991-150-211	Sequence 211, App	
2	90	72.0	185	5	US-09-720-533-49	Sequence 49, App1	
3	90	72.0	185	6	US-10-119-480-148	Sequence 148, App	
4	90	72.0	185	6	US-10-216-159A-148	Sequence 148, App	
5	90	72.0	185	6	US-10-216-162-148	Sequence 148, App	
6	90	72.0	185	6	US-10-216-163-148	Sequence 148, App	
7	90	72.0	185	6	US-10-216-164-148	Sequence 148, App	
8	90	72.0	185	6	US-10-216-165-148	Sequence 148, App	
9	90	72.0	185	6	US-10-216-166-148	Sequence 148, App	
10	90	72.0	185	6	US-10-216-167-148	Sequence 148, App	
11	90	72.0	185	6	US-10-216-168-148	Sequence 148, App	
12	90	72.0	185	6	US-10-216-160-148	Sequence 148, App	
13	90	72.0	185	6	US-10-218-849-148	Sequence 148, App	
14	90	72.0	185	6	US-10-218-930-148	Sequence 148, App	
15	90	72.0	185	6	US-10-219-003-148	Sequence 148, App	
16	90	72.0	185	6	US-10-218-612-148	Sequence 148, App	
17	90	72.0	185	6	US-10-218-956-148	Sequence 148, App	
18	90	72.0	185	6	US-10-219-010-148	Sequence 148, App	
19	90	72.0	185	6	US-10-218-765-148	Sequence 148, App	
20	90	72.0	185	6	US-10-218-784-148	Sequence 148, App	
21	90	72.0	185	6	US-10-219-061-148	Sequence 148, App	
22	90	72.0	185	6	US-10-219-062-148	Sequence 148, App	
23	90	72.0	185	6	US-10-219-063-148	Sequence 148, App	
24	90	72.0	185	6	US-10-219-064-148	Sequence 148, App	
25	90	72.0	185	6	US-10-219-065-148	Sequence 148, App	
26	90	72.0	185	6	US-10-219-066-148	Sequence 148, App	

Query Match	72.0%;	Score 90;	DB 5;	Length 185;
Best Local Similarity	72.0%;	Pred. No. 0.00012;		
			2: Indels	3: Gaps

1 DTMVKFOK--GKGGGAPPKDLMY 23

97 IDALVKEKKLOGKGGPPPKGLMY 121

```

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLOM, Ingrid E.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PF-0541 PCT
; CURRENT APPLICATION NUMBER: US/09/720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

```

```

Query Match 72.0%; Score 90; DB 5; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| ||| |||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

```

```

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Remaining Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

```

```

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| ||| |||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

```

```

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||| ||||| ||| |||
Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

```


us-09-821-726-2.rpn

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```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTWVKEOK--GKGGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-162-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTWVKEOK--GKGGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGGPPKGLMY 121

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT FILING DATE: 1998-03-20

```

```
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGGGAPPKDLMY 23
   ||:||||:|||||:|||||
Db 97 LDALVKEKKLGKGGGPPPKGLMY 121
```

```
RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC7
; CURRENT APPLICATION NUMBER: US/10/216,165
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148
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```
Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGGGAPPKDLMY 23
   ||:||||:|||||:|||||
Db 97 LDALVKEKKLGKGGGPPPKGLMY 121

RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC9
; CURRENT APPLICATION NUMBER: US/10/216,166
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148
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```
Query Match
Best Local Similarity 72.0%; Score 90; DB 6; Length 185;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGGGAPPKDLMY 23
   ||:||||:|||||:|||||
Db 97 LDALVKEKKLGKGGGPPPKGLMY 121

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
```

us-09-821-726-2.rapn

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```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGPGGPPKGLMY 121

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGPGGPPKGLMY 121

RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216,168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-167-148

```

```

; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGPGGPPKGLMY 121

RESULT 12
US-10-216-160-148
; Sequence 148, Application US/10216160
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C8
; CURRENT APPLICATION NUMBER: US/10/216,160
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-160-148

Query Match 72.0%; Score 90; DB 6; Length 185;
Best Local Similarity 72.0%; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
   ||:||||:| ||||| ||| |||
Db 97 LDALVKEKKLOGKGPGGPPKGLMY 121

```

RESULT 13
 US-10-218-849-148
 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 72.0%; Score 90; DB 6; Length 185;
 Best Local Similarity 72.0%; Pred. No. 0.00012;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 LDALVKEKKLQKGPGGPPKGLMY 121

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-930-148

Query Match 72.0%; Score 90; DB 6; Length 185;
 Best Local Similarity 72.0%; Pred. No. 0.00012;
 Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

Qy 1 LDTMVKEQK--GKGPGGAPPKDLMY 23
 || :|||:| ||||| ||| |||
 Db 97 LDALVKEKKLQKGPGGPPKGLMY 121
 RESULT 15
 US-10-219-003-148
 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; CURRENT FILING DATE: 2002-08-12
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 ; Prior Filing Date: 2002-04-09
 ; Prior Application Number: 60/059113
 ; Prior Filing Date: 1997-09-17
 ; Prior Application Number: 60/062287
 ; Prior Filing Date: 1997-10-17
 ; Prior Application Number: 60/063549
 ; Prior Filing Date: 1997-10-28
 ; Prior Application Number: 60/064103
 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
 ; Prior Application Number: 60/079294
 ; Prior Filing Date: 1998-03-25
 ; Prior Application Number: 60/079656
 ; Prior Filing Date: 1998-03-26
 ; Prior Application Number: 60/079728
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 ; Prior Application Number: 60/084441
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 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090691
 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

us-09-821-726-2.rapn

Thu 'Sep 5 11:23:35 2002

; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
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; PRIOR APPLICATION NUMBER: 60/095916
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; PRIOR APPLICATION NUMBER: 60/096146
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; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/100627
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
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; PRIOR APPLICATION NUMBER: 60/106248
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; PRIOR FILING DATE: 1998-11-17
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; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
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; PRIOR APPLICATION NUMBER: 60/113621

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; PRIOR APPLICATION NUMBER: 60/115558
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; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
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; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
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; PRIOR APPLICATION NUMBER: 60/131270
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; PRIOR FILING DATE: 1999-08-17
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; PRIOR FILING DATE: 1999-08-17
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; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 72.08; Score 90; DB 6; Length 185;
Best Local Similarity 72.08; Pred. No. 0.00012;
Matches 18; Conservative 2; Mismatches 3; Indels 2; Caps 1;

QY 1 LDTMVKEOK--GKPGGAPPKDLMY 23
|| : |||: ||||| ||| |||
Db 97 LDALVKEKKLQKGGPPPKGLMY 121

Search completed: September 4, 2002, 17:04:23

Thu Sep 5 11:23:35 2002

us-09-821-726-2.rapn

Page 8

Job time: 1154 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:03 ; Search time 34.18 Seconds
(without alignments)
26.055 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDTWKEQKGKGGAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	184	1	Q9cr36 mus musculus
2	90	72.0	199	1	Q9ns71 homo sapien
3	51	40.8	378	1	P02833 drosophila
4	49	39.2	142	1	P20775 klebsiella
5	49	39.2	331	1	P17542 homo sapien
6	47	37.6	233	1	P06341 rattus norv
7	47	37.6	263	1	P29826 rattus norv
8	46	36.8	267	1	Q9pj10 chlamydia m
9	46	36.8	267	1	O84469 chlamydia t
10	46	36.8	268	1	P05538 homo sapien
11	46	36.8	398	1	O31550 bacillus su
12	46	36.8	423	1	Q62463 mus musculus
13	45.5	36.4	402	1	P56680 humicola in
14	45	36.0	137	1	Q9qxa5 mus musculus
15	45	36.0	139	1	O9y420 homo sapien
16	45	36.0	160	1	P19586 scenedesmus
17	45	36.0	263	1	P06343 mus musculus
18	45	36.0	263	1	P06344 mus musculus
19	45	36.0	263	1	P14483 mus musculus
20	45	36.0	265	1	P01921 mus musculus
21	45	36.0	265	1	P06347 caenorhabdi
22	45	36.0	265	1	P17657 mus musculus
23	45	36.0	302	1	O35625 mus musculus
24	45	36.0	992	1	Q01299 t genome po
25	45	36.0	3414	1	P14336 t genome po
26	45	36.0	3414	1	P01201 m corticotr
27	44.5	35.6	264	1	P01189 h corticotr
28	44.5	35.6	267	1	P01192 s corticotr
29	44.5	35.6	267	1	P07184 drosophila
30	44	35.2	172	1	P57796 homo sapien
31	44	35.2	211	1	P53784 mus musculus
32	44	35.2	375	1	P78979 yarrowia li
33	44	35.2	471	1	S61A_YARLI

34	44	35.2	479	1	PGKC_LEIME
35	44	35.2	506	1	CP4B_RABIT
36	44	35.2	540	1	CH61_SYNY3
37	44	35.2	546	1	RUB1_BRANA
38	44	35.2	550	1	GPC1_CHICK
39	44	35.2	783	1	CAD5_MOUSE
40	43.5	34.8	212	1	COLI_SHEEP
41	43.5	34.8	265	1	COLI_BOVIN
42	43.5	34.8	431	1	HXB3_HUMAN
43	43.5	34.8	433	1	HXB3_MOUSE
44	43	34.4	252	1	HB2F_MOUSE
45	43	34.4	329	1	TAL_MOUSE

ALIGNMENTS

RESULT	1
CLIP_MOUSE	
ID	CLIP_MOUSE STANDARD: PRT: 184 AA.
AC	Q9CR36; Q9D7K7; Q9CTZ5;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	CALL protein homolog.
GN	CALL
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA	Kado K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA	Schrml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).

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CC	EMBL; AK008990; BAB26010.1;
CC	EMBL; AK008622; BAB25784.1;
DR	EMBL; AK008622; BAB25784.1;
DR	EMBL; AK008641; BAB25801.1;
DR	EMBL; AK008647; BAB25805.1;
DR	EMBL; AK008722; BAB25856.1;
DR	EMBL; AK008745; BAB25872.1;
DR	EMBL; AK008933; BAB25975.1;
DR	EMBL; AK008956; BAB25988.1;
DR	EMBL; AK009145; BAB26103.1;
DR	EMBL; AK019050; BAB31525.1;

FT CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 SQ SEQUENCE 184 AA; 20134 MW; 288982F0404FFA8B CRC64;

Query Match 100.0%; Score 125; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 9.8e-11;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGGPGGAPPKDLMY 23

Db 97 LDTMVKEQKGGPGGAPPKDLMY 119

RESULT 2

CLIP_HUMAN STANDARD; PRT; 199 AA.

ID Q9NS71;

OC 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE CALL protein.

GN CALL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Stomach;

RA YOSHIKAWA Y., Mukai H., Hino F., Asada K., Kato I.;

RX MEDLINE=20296773; PubMed=10835488;

RT "Isolation of two novel genes, down-regulated in gastric cancer."

RL Jpn. J. Cancer Res. 91:459-463(2000).

CC -1- TISSUE SPECIFICITY: Expressed in stomach. No expression is

CC detected in cancer tissue or gastric cancer cell lines.

CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB039886; BAA92433.1; -

SQ MIM; 606402; -

SQ SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;

Query Match

Best Local Similarity 72.0%; Score 90; DB 1; Length 199;

Matches 18; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 LDTMVKEQK--GKGGPGGAPPKDLMY 23

Db 111 LDALVKEKKLQKGGPGGPPKGLMY 135

RESULT 3

HMEN_DROME

ID HMEN_DROME

AC P02833; STANDARD; PRT; 378 AA.

OC 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE Homeotic antennapedia protein.

GN ANTP OR CG1028.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP

RA Schnewly S., Kuroiwa A., Baumgartner P., Gehring W.J.;

RT "Structural organization and sequence of the homeotic gene

RL Antennapedia of Drosophila melanogaster.";

RN EMBO J. 5:733-739(1986).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87089828; PubMed=2879222;

RA Stroehner V.L., Jorgensen E.M., Garber R.L.;

RT "Multiple transcripts from the Antennapedia gene of Drosophila

RL melanogaster.";

RN Mol. Cell. Biol. 6:4667-4675(1986).

RN [3]

RP SEQUENCE FROM N.A.

RA Ceiniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A.,

RA Palazzolo M.J.;

RT "Complete sequence of the Antennapedia complex of Drosophila.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jallali M., Jansz J., Karp G.H., Karp G.H., Karp G.H., Karp G.H.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy J., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RN Science 287:2185-2195(2000).

RN [5]

RP SEQUENCE OF 296-364 FROM N.A.

RX MEDLINE=84205674; PubMed=6327065;

RA McGinnis W., Garber R.L., Wirz J., Kuroiwa A., Gehring W.J.;

RT "A homologous protein-coding sequence in Drosophila homeotic genes

RL and its conservation in other metazoans.";

RN Cell 37:403-408(1984).

RN [6]

RP SEQUENCE OF 296-364 FROM N.A.

RX MEDLINE=84248068; PubMed=6330741;

RA Scott M.P., Weiner A.J.;

RT "Structural relationships among genes that control development:

RL sequence homology between the Antennapedia, Ultrathorax, and fushi

tarazu loci of Drosophila.";


```

RL  Proc. Natl. Acad. Sci. U.S.A. 81:4115-4119(1984).
RN  [7]
RP  SEQUENCE OF 297-357 FROM N.A.
RX  MEDLINE=86079516; PubMed=2416463;
RA  Regulski M., Harding K., Kostriken R., Karch F., Levine M.,
RA  McGinnis W.;
RT  "Homeo box genes of the Antennapedia and bithorax complexes of
RT  Drosophila.";
RL  Cell 43:71-80(1985).
RN  [8]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=90317820; PubMed=2164583;
RA  Billeter M., Qian Y.-Q., Otting G., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Determination of the three-dimensional structure of the Antennapedia
RT  homeodomain from Drosophila in solution by 1H nuclear magnetic
RT  resonance spectroscopy.";
RL  J. Mol. Biol. 214:183-197(1990).
RN  [9]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=94087721; PubMed=7903397;
RA  Qian Y.-Q., Otting G., Billeter M., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Nuclear magnetic resonance spectroscopy of a DNA complex with the
RT  uniformly 13C-labeled Antennapedia homeodomain and structure
RT  determination of the DNA-bound homeodomain.";
RL  J. Mol. Biol. 234:1070-1083(1993).
RN  [10]
RP  STRUCTURE BY NMR OF HOMEBOX.
RX  MEDLINE=94087722; PubMed=7903398;
RA  Billeter M., Qian Y.-Q., Otting G., Mueller M., Gehring W.J.,
RA  Wuethrich K.;
RT  "Determination of the nuclear magnetic resonance solution structure
RT  of an Antennapedia homeodomain-DNA complex.";
RL  J. Mol. Biol. 234:1084-1097(1993).
RN  [11]
RP  STRUCTURE BY NMR OF 279-363.
RX  MEDLINE=93066318; PubMed=1359544;
RA  Qian Y.-Q., Otting G., Furukubo-Tokinaga K., Affolter M.,
RA  Gehring W.J., Wuethrich K.;
RT  "NMR structure determination reveals that the homeodomain is
RT  connected through a flexible linker to the main body in the
RT  Drosophila Antennapedia protein.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:10738-10742(1992).
RN  [12]
RP  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 297-356.
RX  MEDLINE=98363212; PubMed=9699632;
RA  Fraenkel E., Pabo C.O.;
RT  "Comparison of X-ray and NMR structures for the Antennapedia
RT  homeodomain-DNA complex.";
RL  Nat. Struct. Biol. 5:692-697(1998).
CC  -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC  A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC  SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC  -!- FUNCTION: THIS HOMEOBOX PROTEIN CONTROLS DEVELOPMENT OF THE CELLS
CC  IN THE MESOTHORAX SEGMENTS.
CC  -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC  -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC  -----
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CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X03790; CAA27417.1; -
DR  EMBL; X03791; CAA27417.1; JOINED.
DR  EMBL; K01948; AAZ28373.1; ALT_SEQ.
DR  EMBL; AE001572; AAD19793.1; -
DR  EMBL; AE003673; AAG22205.1; -
DR  EMBL; M14496; AAA28376.1; -

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DR  EMBL; M20704; AAA70214.1; -
DR  EMBL; M20705; AAA70216.1; -
DR  EMBL; M12009; AAA79241.1; -
DR  PIR; A03318; A03318.
DR  PIR; A25399; A25399.
DR  PIR; A23450; A23450.
DR  PIR; C24780; C24780.
DR  PIR; A25400; A25400.
DR  PDB; 1HOM; 31-OCT-93.
DR  PDB; 2HOA; 31-OCT-93.
DR  PDB; 1AHD; 31-OCT-93.
DR  PDB; 1SAN; 30-APR-94.
DR  PDB; 9ANT; 18-NOV-98.
DR  TRANSFAC; T00026; -.
DR  FlyBase; FBgn0000095; Antp.
DR  InterPro; IPR001827; Antennapedia.
DR  InterPro; IPR001356; Homeobox.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00025; ANTENNAPEDIA.
DR  PRINTS; PR00024; HOMEBOX.
DR  SMART; SM00389; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00032; ANTENNAPEDIA; 1.
DR  PROSITE; PS00071; HOMEBOX_2; 1.
DR  Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW  3D-structure.
FT  DOMAIN 76 81 GLN-RICH (OPA-REPEAT).
FT  DOMAIN 110 155 GLN-RICH (OPA-REPEAT).
FT  DOMAIN 283 288 ANTP-TYPE HEXAPEPTIDE.
FT  DNA_BIND 297 356 HOMEBOX.
FT  CEFELICT 300 300 G -> E (IN REF. 7).
FT  HELIX 306 318
FT  HELIX 324 334
FT  HELIX 335 335
FT  TURN 339 350
FT  HELIX 339 350
FT  TURN 351 355
FT  TURN 358 359
SQ  SEQUENCE 378 AA; 42761 MW; D653232A8622D055 CRC64;

```

Query Match 40.8%; Score 51; DB 1; Length 378;

Best Local Similarity 45.0%; Pred. No. 5.2;

Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MVKEQKGGPGGAPPKDLMY 23

DB 230 MYQQSGVPPVPGAPPGGMMH 249

RESULT 4

YPUB_KLEPN STANDARD; PRT; 142 AA.

AC P20775;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in PULS 3' region (Fragment).

OS Klebsiella pneumoniae.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.

OX NCBI_TaxID=573;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=89291709; PubMed=2661532;

RA D'Enfert C., Pugsley A.P.;

RT "Klebsiella pneumoniae pulS gene encodes an outer membrane

RT lipoprotein required for pullulanase secretion.";

RL J. Bacteriol. 171:3673-3679(1989).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M29097; AAA61979.1; -;
 KW PIR: D32880; D32880.
 KW Hypothetical protein.
 FT NON_TER 142
 SQ SEQUENCE 142 AA; 16447 MW; 03ED03FBF63242D0 CRC64;

Query Match 39.2%; Score 49; DB 1; Length 142;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 8 QKGGKGGGAPPK 19
 Db 49 RKGKGGKGGKPPR 60
 :|||||
 :|||||

RESULT 5
 TAL_HUMAN STANDARD; PRT; 331 AA.
 AC P17542;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE T-cell acute lymphocytic leukemia-1 protein (TAL-1 protein) (STEM cell
 DE protein) (T-cell leukemia/lymphoma-5 protein).
 GN TAL1 OR SCL OR TCF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE-91061750; PubMed-2247063;
 RA Aplan P.D., Begley C.G., Bertness V., Nussmeier M., Ezquerro A.,
 RA Colligan J., Kirsch I.R.;
 RT "The SCL gene is formed from a transcriptionally complex locus";
 RL Mol. Cell. Biol. 10:6426-6435(1990).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Graham D.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 118-331 FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE-90099309; PubMed-2602361;
 RA Begley C.G., Aplan P.D., Denning S.M., Haynes B.F., Waldmann T.A.,
 RA Kirsch I.R.;
 RT "The gene SCL is expressed during early hematopoiesis and encodes a
 RT differentiation-related DNA-binding motif";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:10128-10132(1989).
 RN [4]

RP SEQUENCE OF 181-331 FROM N.A.
 RX MEDLINE-90151616; PubMed-2303035;
 RA Chen Q., Cheng J.-T., Tsai L.H., Schneider N., Buchanan G.,
 RA Carroll A., Crist W., Ozanne B., Siciliano M.J., Baer R.;
 RT "The tal gene undergoes chromosome translocation in T cell leukemia
 RT and potentially encodes a helix-loop-helix protein.";
 RL EMO J. 9:415-424(1990).
 RN [5]

RP SEQUENCE OF 106-148 FROM N.A.
 RX MEDLINE-91037802; PubMed-2230650;
 RA Chen Q., Yang C.Y.C., Tsan J.T., Xia Y., Ragab A.H., Peiper S.C.,
 RA Carroll A., Baer R.;
 RT "Coding sequences of the tal-1 gene are disrupted by chromosome
 RT translocation in human T cell leukemia.";
 RL J. Exp. Med. 172:1403-1408(1990).
 RN [6]
 RP FUNCTION.
 RX MEDLINE-93011002; PubMed-1396592;

RA Aplan P.D., Nakahara K., Orkin S.H., Kirsch I.R.;
 RT "The SCL gene product: a positive regulator of erythroid
 RT differentiation.";
 RL EMBO J. 11:4073-4081(1992).
 RN [7]
 RP PHOSPHORYLATION
 RX MEDLINE-93173511; PubMed-8437851;
 RA Cheng J.-T., Hsu H.-L., Hwang L.-Y., Baer R.;
 RT "Products of the TAL1 oncogene: basic helix-loop-helix proteins
 RT phosphorylated at serine residues.";
 RL Oncogene 8:677-683(1993).
 CC -1- FUNCTION: IMPLICATED IN THE GENESIS OF HEMOPOIETIC MALIGNANCIES.
 CC IT MAY PLAY AN IMPORTANT ROLE IN HEMOPOIETIC DIFFERENTIATION.
 CC SERVES AS A POSITIVE REGULATOR OF ERYTHROID DIFFERENTIATION. BINDS
 CC TO THE LIM DOMAIN CONTAINING PROTEIN RHOMBOTIN-2.
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. FORMS HETERODIMERS WITH EL2 AND E47. BINDS TO DRG1.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: PP42-TAL1 (SHOWN HERE),
 CC PP39-TAL1 AND PP22-TAL1; ARE PRODUCED BY ALTERNATIVE SPLICING. THE
 CC SPLICING PATTERN IS CELL-LINEAGE DEPENDENT.
 CC -1- TISSUE SPECIFICITY: LEUKEMIC STEM CELL.
 CC -1- DOMAIN: THE HELIX-LOOP-HELIX DOMAIN IS NECESSARY AND SUFFICIENT
 CC FOR THE INTERACTION WITH DRG1.
 CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
 CC -1- DISEASE: SOME T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) (A FORM
 CC OF STEM-CELL LEUKEMIA) ARE CHARACTERIZED BY A CHROMOSOMAL
 CC TRANSLOCATION T(1;4)(p32;q11) WHICH INVOLVES TAL1 AND T-CELL
 CC RECEPTOR ALPHA CHAIN (TCRA) GENES.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.

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CC EMBL; M61108; AAA36600.1; -;
 DR EMBL; M61103; -; NOT_ANNOTATED_CDS.
 DR EMBL; M61104; -; NOT_ANNOTATED_CDS.
 DR EMBL; M61105; -; NOT_ANNOTATED_CDS.
 DR EMBL; M63572; -; NOT_ANNOTATED_CDS.
 DR EMBL; AL135960; CAB72103.1; -;
 DR EMBL; M63589; AAA36599.1; -;
 DR EMBL; M63576; AAA36599.1; JOINED.
 DR EMBL; M63584; AAA36599.1; JOINED.
 DR EMBL; M29038; AAA36598.1; -;
 DR EMBL; X51990; CAA36246.1; -;
 DR EMBL; X58621; CAA41476.1; ALT_SEQ.
 DR EMBL; X58622; CAA41477.1; -;
 DR PIR; A34519; A34519.
 DR PIR; A36358; A36358.
 DR HSSP; P10085; IMDY.
 DR TRANSFAC; T00790; -;
 DR MIM; 187040; -;
 DR InterPro; IPR003015; HLH_Myc.
 DR InterPro; IPR001092; HLH_dim.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
 KW DNA-binding; Transcription regulation; Differentiation;
 KW Proto-oncogene; Chromosomal translocation; Alternative splicing;
 KW Phosphorylation.
 FT DOMAIN 89 132 PRO-RICH
 FT DNA_BIND 187 199 BASIC DOMAIN
 FT DOMAIN 200 240 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 FT DOMAIN 263 274 POLY-GLY.
 FT VARSELIC 1 25 MISSING (IN ISOFORM PP39-TAL1).
 FT VARSELIC 1 175 MISSING (IN ISOFORM PP22-TAL1).
 SQ SEQUENCE 331 AA; 34270 MW; 33BEE31589DBE7C7 CRC64;

211 I.GI.FTRHKROKGGPPAGLL 232

ID	1K0A_CHEFC	Standard,
AC	Q9PJT0;	
DT	16-OCT-2001 (Rel. 40. Created)	

211 I.GI.FTRHKROKGGPPAGLL 232

```

Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITIONS 38, 39 AND 40 IN
CC THE ANTICODON STEM AND LOOP OF TRANSFER RNAS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
CC 5'-phosphate + H(2)O.
CC -!- SIMILARITY: BELONGS TO THE TRUA FAMILY OF PSEUDOURIDINE SYNTHASES.
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CC -----
CC EMBL; AF001320; AAC68063.1; -
CC InterPro: IPR001406; Pseudou_synth_1.
CC Pfam; PF01416; Pseudou_synth_1; 1.
CC Lyase; tRNA processing; Complete proteome.
CC ACT_SITE 53 53 BY SIMILARITY.
CC SEQUENCE 267 AA; 30427 MW; 917EA49E394B3CB3 CRC64;
CC -----
Query Match 36.8%; Score 46; DB 1; Length 267;
Best Local Similarity 42.9%; Pred. No.19;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OQ 1 LDTMYKEQKGKGGGAPPKDL 21
DB 221 LDMLATKDRKGGPPSPVGYL 241
|| : : ||| ||| |
|| : : ||| ||| |
RESULT 10
HB2X_HUMAN STANDARD; PRT; 268 AA.
P05538;
01-NOV-1988 (Rel. 09, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class II histocompatibility antigen, DX beta chain precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=87250501; PubMed=3036828;
Jonsson A.K., Hyldig-Nielsen J.J., Servenius B., Larhammar D.,
Andersson G., Joergensen F., Peterson P.A., Rask L.;
"Class II genes of the human major histocompatibility complex.
Comparisons of the DQ and DX alpha and beta genes.";
J. Biol. Chem. 262:8767-8777(1987).
[2]
SEQUENCE OF 38-125 FROM N.A.
MEDLINE=85216510; PubMed=3858830;
Okada K., Boss J.M., Prentice H., Spies T., Mengler R., Auffray C.,
Lillie J.W., Grossberger D., Strominger J.L.;
"Gene organization of DC and DX subregions of the human major
histocompatibility complex.";
Proc. Natl. Acad. Sci. U.S.A. 82:3410-3414(1985).
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EMBL; M29614; -; NOT_ANNOTATED_CDS.
EMBL; M29615; -; NOT_ANNOTATED_CDS.
EMBL; M11136; -; NOT_ANNOTATED_CDS.

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GCRDB; GCR_1612; .
 DR MGD; MGI:1859216; Avprla.
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 53 76 1 (POTENTIAL).
 FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 110 2 (POTENTIAL).
 FT DOMAIN 111 125 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 126 147 3 (POTENTIAL).
 FT DOMAIN 148 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 190 4 (POTENTIAL).
 FT DOMAIN 191 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 5 (POTENTIAL).
 FT DOMAIN 242 298 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 299 318 6 (POTENTIAL).
 FT DOMAIN 319 335 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 337 356 7 (POTENTIAL).
 FT DOMAIN 357 423 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 205 BY SIMILARITY.
 FT VARIANT 41 42 PP -> RR.
 FT VARIANT 55 55 V -> F.
 SQ SEQUENCE 423 AA; 47181 MW; C75AFFID0A082CC6 CRC64;

 Query Match 36.8%; Score 46; DB 1; Length 423;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

 QY 6 KEQKKGKGGGAPPKDL 21
 DB 30 REAAGLGGGSPGDV 45

 RESULT 13
 GUNI_HUMIN STANDARD; PRT; 402 AA.
 AC P56680;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Endoglucanase I (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 GN CEL7B.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT S37W/P39W.
 RX MEDLINE=97475713; PubMed=9335168;
 RA Davies G.J., Ducros V., Lewis R.J., Borchert T.V., Schulein M.;
 RT "Oligosaccharide specificity of a family 7 endoglucanase: Insertion
 RT of potential sugar-binding subsites.";
 RL J. Biotechnol. 57:91-100(1997).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MUTAGENESIS.
 RX MEDLINE=98437137; PubMed=9761741;
 RA Mackenzie L.F., Sulzenbacher G., Davne C., Jones T.A., Woeldike H.F.,
 RA Schulein M., Withers S.G., Davies G.J.;
 RT "Crystal structure of the family 7 endoglucanase I (Cel7B) from
 RT Humicola insolens at 2.2 A resolution and identification of the
 RT catalytic nucleophile by trapping of the covalent glycosyl-enzyme
 RT intermediate.";
 RL Biochem. J. 335:409-416(1998).
 CC
 CC -!- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE

FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
 SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
 -!- SUBUNIT: MONOMER.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- SIMILARITY: BELONGS TO CELLULASE FAMILY C (FAMILY 7 OF GLYCOSYL
 HYDROLASES).
 PDB; 1A39; 02-MAR-99.
 PDB; 2A39; 16-FEB-99.
 DR InterPro: IPR001722; Glyco_hydro_7.
 DR Pfam: PF00840; Glyco_hydro_7; 1.
 DR PRINTS; PR00734; GLHYDRLASE7.
 DR ProDom; PD186135; Glyco_hydro_7; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein;
 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 197 197 NUCLEOPHILE.
 FT ACT_SITE 202 202 PROTON DONOR.
 FT DISULFID 18 24
 FT DISULFID 51 73
 FT DISULFID 63 69
 FT DISULFID 140 365
 FT DISULFID 172 195
 FT DISULFID 176 194
 FT DISULFID 215 234
 FT DISULFID 223 228
 FT DISULFID 239 315
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .).
 SQ SEQUENCE 402 AA; 44577 MW; E0C6D31375D1635F CRC64;

 Query Match 36.4%; Score 45.5; DB 1; Length 402;
 Best Local Similarity 36.7%; Pred. No. 33;
 Matches 11; Conservative 5; Mismatches 5; Indels 9; Gaps 2;

 QY 1 LDTM--VKEQKKGKGGGA-----PPKDL 21
 DB 33 LDSLHFIHRAEGLGPGCGDWGNPPPKDV 62

 RESULT 14
 LSM4_MOUSE STANDARD; PRT; 137 AA.
 AC Q9QX5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE U6 snRNA-associated Sm-like protein LSM4.
 GN LSM4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirsch E., Ohashi T., Stamm S., Paessler R.;
 RT "Peri-implantation lethality in mice lacking the Sm motif-containing
 RT protein lsm4.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
 CC SNRNA (BY SIMILARITY).
 CC -!- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGNUT SHAPE.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
 CC
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DR EMBL: AJ249439; CAB65729.1; -.
DR MGD: MGI:1354692; Lsm4.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 137 AA; 15076 MW; A917E15E61467940 CRC64;

Query Match 36.0%; Score 45; DB 1; Length 137;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGKGPCCA 16
I:||||:|
DB 95 KQKGRGMGGA 105

RESULT 15
LSM4 HUMAN
ID LSM4 HUMAN STANDARD; PRT; 139 AA.
AC Q9Y4Z0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE U6 snRNA-associated Sm-like protein LSM4 (Glycine-rich protein) (GRP).
GN LSM4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99298196; PubMed=10369684;
RA Salgado-Garrido J., Bragado-Nilsson E., Kandel-Lewis S., Seraphin B.;
RT "Sm and Sm-like proteins assemble in two related complexes of deep
RT evolutionary origin.";
RL EMBO J. 18:3451-3462(1999).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=99452783; PubMed=10523320;
RA Achsel T., Brahm H., Kastner B., Bachi A., Wilm M., Luehrmann R.;
RT "A doughnut-shaped heteromer of human Sm-like proteins binds to the
RT 3'-end of U6 snRNA, thereby facilitating U4/U6 duplex formation in
RT vitro.";
RL EMBO J. 18:5789-5802(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=20402571; PubMed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RT axis and full-length cDNA cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Chan E.K.L.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS SPECIFICALLY TO THE 3'-TERMINAL U-TRACT OF U6
CC snRNA.
CC -!- SUBUNIT: LSM SUBUNITS FORM A HETEROMER WITH A DOUGHNUT SHAPE.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE SNRNP SM PROTEINS FAMILY.
CC -----

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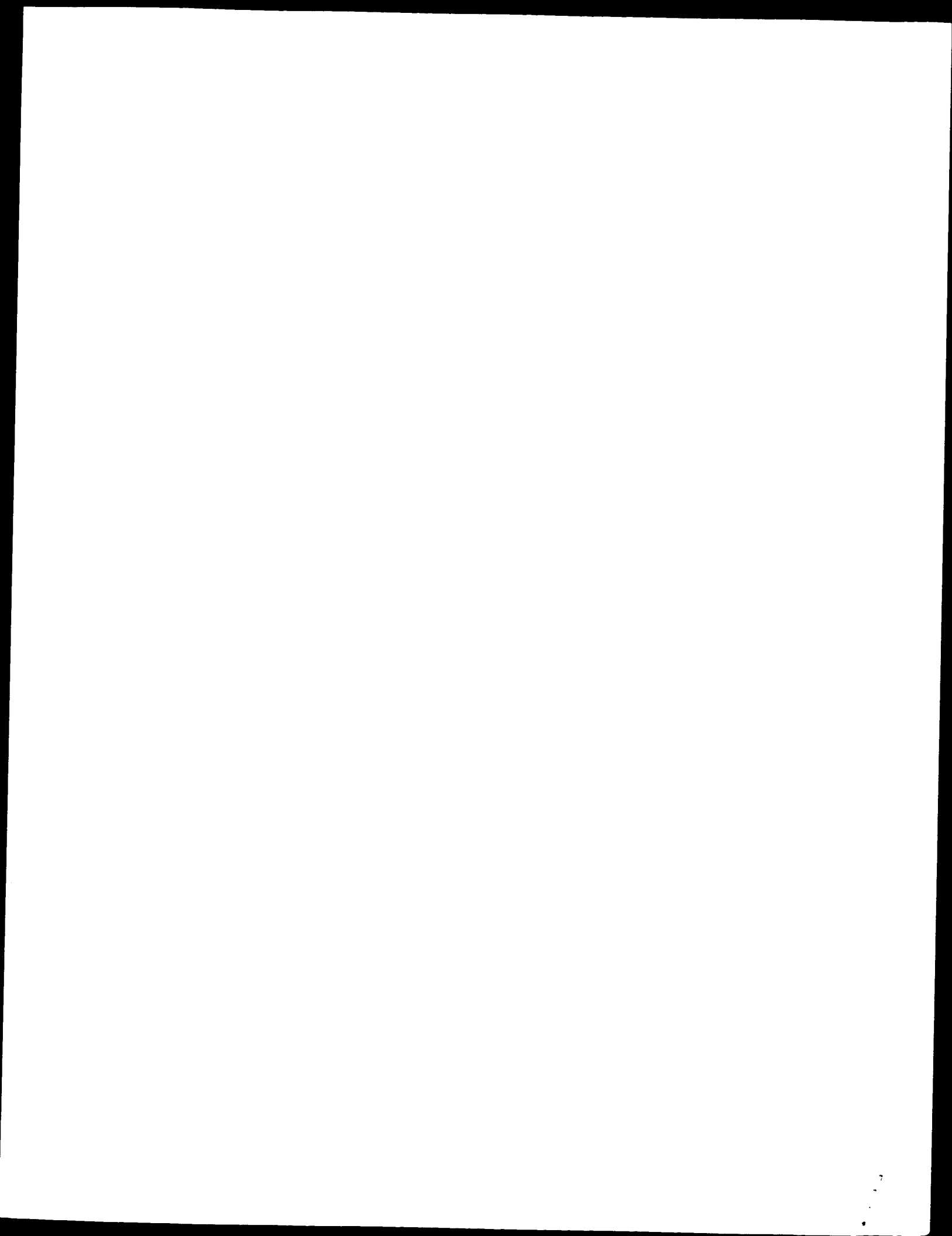
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DR EMBL: AJ238096; CAB45867.1; -.
DR EMBL: AF182290; AAD56228.1; -.
DR EMBL: AF117235; AAF17216.1; -.
DR EMBL: AF251218; AAF90055.1; -.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;
KW RNA-binding.
SQ SEQUENCE 139 AA; 15350 MW; BCEFB20247335A1B CRC64;

Query Match 36.0%; Score 45; DB 1; Length 139;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGKGPCCA 16
I:||||:|
DB 97 KQKGRGMGGA 107

Search completed: September 4, 2002, 17:05:04
Job time: 1130 sec



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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:47:29 ; Search time 75.48 Seconds
(without alignments)
29.280 Million cell updates/sec

Title: US-09-821-726-2

Perfect score: 125

Sequence: 1 LDTWKEQKGKGGAPPKDLMY 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR71:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	% Match	Length	ID	Description
1	59	47.2	1677	2 T14267	Xin protein, stage
2	51	40.8	153	2 B71226	hypothetical prote
3	51	40.8	298	2 A49630	ubiquitin conjugat
4	51	40.8	378	2 A25399	homeotic protein A
5	50	40.0	269	2 I54432	MHC class II histo
6	49	39.2	142	2 D32880	hypothetical prote
7	49	39.2	266	2 B84351	pseudouridylylate sy
8	49	39.2	331	2 A36358	T-cell acute lymph
9	48	38.4	263	2 T50596	probable oxidoredu
10	47	37.6	218	2 T51887	hypothetical prote
11	47	37.6	233	1 HURTAB	Rt1 class II histo
12	47	37.6	263	1 HURTAB	class II histocomp
13	47	37.6	798	2 T42070	protein serine/thr
14	47	37.6	539	2 T49456	hypothetical prote
15	47	37.6	4936	2 A82515	hypothetical prote
16	46.5	37.2	1240	2 T30834	nuclear protein SA
17	46	36.8	267	2 D81669	tRNA pseudouridine
18	46	36.8	267	2 C71511	probable pseudouri
19	46	36.8	268	2 D29312	MHC class II histo
20	46	36.8	315	2 T29525	hypothetical prote
21	46	36.8	398	2 F69581	acetoin dehydrogen
22	46	36.8	511	2 S24345	Balbani ring 1 pr
23	46	36.8	709	2 T34706	fatty acid oxidati
24	46	36.8	886	2 S07132	hypothetical prote
25	46	36.8	2022	2 T48818	glucan 1,4-alpha-g
26	46	36.8	4957	2 T03455	ALR protein - huma
27	46	36.8	5262	2 T03454	ALR protein - huma
28	45.5	36.4	376	2 A12339	dihydroorotate oxi
29	45.5	36.4	579	2 D72092	conserved hypothet

ALIGNMENTS

RESULT 1

T14267

Xin protein, stage early embryo - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T14267

R:Wang, D.Z.; Lin, J.J.C.

submitted to the EMBL Data Library, March 1998

A:Description: Involvement of a novel gene, Xin, in cardiac looping.

A:Reference number: Z17948

A:Accession: T14267

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1677 <W>

A:Cross-references: EMBL:AF051945; NID:g2970645; PID:g2970646; PIDN:RAC06023.1

A:Experimental source: cardiac muscle; stage early embryo

Query Match 47.2%; Score 59; DB 2; Length 1677;
Best Local Similarity 64.3%; Pred. No. 4.9;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 KEQKGKGGAPPK 19

DB 571 EEEGKGPGGPPE 584

RESULT 2

B71226

hypothetical protein PH0068 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000

C:Accession: B71226

R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil

A:Reference number: A71000; MUID:98344137

A:Accession: B71226

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <W>

A:Cross-references: GB:AF000001; NID:g3236128; PIDN:BAA29137.1; PID:g3256454

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBa

C:Genetics:

A:Gene: PH0068

C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0068

Query Match 40.8%; Score 51; DB 2; Length 153;
Best Local Similarity 60.0%; Pred. No. 6;

Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LDTMVKEQKGKGG 15
 Db 121 LDTIIEENKGVGG 135

RESULT 3

A:ubiquitin conjugating enzyme - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
 C:Accession: A49630
 R:Pilon, S.E.; Leppig, K.A.; Do, H.N.; Groudine, M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10484-10488, 1993
 A:Title: Cloning of the human homolog of the CDC34 cell cycle gene by complementation in
 A:Reference number: A49630; MUID:94068425
 A:Accession: A49630
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <RES>
 A:Cross-references: GB:I22005; NID:q388308; PIDN:AAC37534.1; PID:q388309
 C:Superfamily: human ubiquitin-protein ligase E2

Query Match 40.8%; Score 51; DB 2; Length 298;
 Best Local Similarity 61.5%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KEQKGKGGGAPP 18
 Db 21 EEEAGGGGGSP 33

RESULT 4

A25399
 homeotic protein Antennapedia - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jun-2000
 C:Accession: A23450; A25400; A25399; A03318; C24780; S02593
 R:Schneuwly, S.; Kuroiwa, A.; Baumgartner, P.; Gehring, W.J.
 EMBO J. 5, 733-739, 1986
 A:Title: Structural organization and sequence of the homeotic gene Antennapedia of Drosophila
 A:Reference number: A23450; MUID:99334708
 A:Accession: A23450
 A:Molecule type: DNA; mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:X03790; NID:q7593; PIDN:CAA27417.1; PID:e293776; PID:gl805742
 R:Laughon, A.; Boulet, A.M.; Bermingham Jr., J.R.; Laymon, R.A.; Scott, M.P.
 Mol. Cell. Biol. 6, 4676-4689, 1986
 A:Title: Structure of transcripts from the homeotic antennapedia gene of Drosophila mela
 A:Reference number: A25400; MUID:87089829
 A:Accession: A25400
 A:Molecule type: DNA
 A:Residues: 1-378 <LAU>
 A:Cross-references: GB:M14496; GB:K01950; NID:gl56945; PIDN:AAA28376.1; PID:gl56947
 R:Strother, V.L.; Jorgensen, E.M.; Garber, R.L.
 Mol. Cell. Biol. 6, 4667-4675, 1986
 A:Title: Multiple transcripts from the antennapedia gene of Drosophila melanogaster.
 A:Reference number: A25399; MUID:87089828
 A:Accession: A25399
 A:Molecule type: mRNA
 A:Residues: 1-378 <STR>
 A:Cross-references: GB:M20704; GB:M14699; GB:M14701; NID:gl56948; PIDN:AAA70214.1; PID:gl
 A:Note: the authors translated the codon TCG for residue 179 as Asp
 R:McGinnis, W.; Garber, R.L.; Wirz, J.; Kuroiwa, A.; Gehring, W.J.
 Cell 37, 403-408, 1984
 A:Title: A homologous protein-coding sequence in Drosophila homeotic genes and its conse
 A:Reference number: A90847; MUID:84205674
 A:Accession: A03318
 A:Molecule type: DNA
 A:Residues: 'I'LEPT', 296-362, 'D' <MCG>
 A:Cross-references: GB:K01948; NID:gl56931; PIDN:AAA28373.1; PID:gl56934

R:Regulski, M.; Harding, K.; Kostriken, R.; Karch, F.; Levine, M.; McGinnis, W.
 Cell 43, 71-80, 1985
 A:Title: Homeo box genes of the Antennapedia and Bithorax complexes of Drosophila.
 A:Reference number: A90874; MUID:86079516
 A:Accession: C24780
 A:Molecule type: DNA
 A:Residues: 297-299, 'E' 301-357 <REG>
 A:Cross-references: GB:M12009; NID:gl56939; PIDN:AAA79241.1; PID:gl56940
 A:Note: the authors translated the codon GAA for residue 300 as Gly and TAC for resid
 R:Bermingham Jr., J.R.; Scott, M.P.
 EMBO J. 7, 3211-3222, 1988
 A:Title: Developmentally regulated alternative splicing of transcripts from the Dros
 A:Reference number: S02593; MUID:89030617
 C:Contents: annotation; alternative splicing
 C:Comment: This homeotic protein controls development of cells in the mesothorax segm
 C:Genetics:
 A:Gene: FlyBase:Antp
 A:Cross-references: FlyBase:FBgn00000095
 A:Map position: 3R47.8; 84B1-2
 A:Introns: 207/3; 220/3; 296/1
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regul
 F:298-354/Domain: homeobox homology <HOX>

Query Match 40.8%; Score 51; DB 2; Length 378;
 Best Local Similarity 45.0%; Pred. No. 15;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 4 MVKEQKGKGGAPPKDLMY 23
 Db 230 MYQQQSGVPPVPGAPPQGMH 249

RESULT 5

I54432
 MHC class II histocompatibility antigen DQ1-beta chain precursor - human
 N:Alternate names: cell surface glycoprotein DQ1; HLA-DQB1
 C:Species: Homo sapiens (man)
 C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 05-May-2000
 C:Accession: I54432; I67725; I68723; I59623
 R:Tsukamoto, K.; Yasunami, M.; Kimura, A.; Inoko, H.; Ando, A.; Hirose, T.; Inayama,
 Immunogenetics 25, 343-346, 1987
 A:Title: DQ1 beta gene from HLA-DR2-Dw12 consists of six exons and expresses multipl
 A:Reference number: I54432; MUID:87192945
 A:Accession: I54432
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <TSU>
 A:Cross-references: GB:M16276; NID:gl88397; PIDN:AAA59823.1; PID:g307272
 R:Yasunami, M.
 Fukuoka Igaku Zasshi 79, 153-167, 1988
 A:Title: [Structural analysis of human major histocompatibility complex class II gene
 A:Reference number: I53630; MUID:88226367
 A:Accession: I67725
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 6-269 <FUK>
 A:Cross-references: GB:M57649; NID:gl87852; PIDN:AAA63217.1; PID:gl87853
 R:Lee, B.S.; Bell, J.I.; Rust, N.A.; McDevitt, H.O.
 Immunogenetics 26, 85-91, 1987
 A:Title: Structural and functional variability among DQ beta alleles of DR2 subtypes.
 A:Reference number: I54440; MUID:87278366
 A:Accession: I68723
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 33-83, P', 85-122 <LEB>
 A:Cross-references: GB:M17204; NID:gl87906; PIDN:AAA59698.1; PID:gl87907
 R:Singal, D.P.; Qiu, X.; Sood, S.K.
 Tissue Antigens 40, 104-107, 1992
 A:Title: Molecular analysis of novel HLA-DR2.DQ1 haplotypes in Asian Indians.
 A:Reference number: I59623; MUID:93031783
 A:Accession: I59623

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 45-83, P', 85-112 <SIN>
A:Cross-references: GB:M86740; NID:g188221; PIDN:AAA59778.1; PID:g188222
C:Genetics:
A:Gene: GDB:HLA-DQB1; HLA-DW12
A:Cross-references: GDB:120517; OMIM:142857
A:Map position: 6p21.3-6p21.3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein
F:142-207/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 50; DB 2; Length 269;
Best Local Similarity 34.8%; Pred. No. 14;
Matches 8; Conservative 7; Mismatches 0;

QY 1 LDTMVKEQKGKGGGAPPKDLMY 23
| : : : : | | | | : :
Db 247 LGLTIQRQSKGPGQPPAGLLH 269

RESULT 6
D32880
hypothetical protein (pulB 3' region) - Klebsiella pneumoniae (fragment)
C:Species: Klebsiella pneumoniae
C:Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 30-Sep-1993
C:Accession: D32880
R:D'Entert, C.; Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
A:Title: Klebsiella pneumoniae pulB gene encodes an outer membrane lipoprotein required
A:Reference number: A32880; MUID:89291709
A:Accession: D32880
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <DEN>
A:Cross-references: GB:M29097
C:Superfamily: penicillin-binding protein 1B

Query Match 39.2%; Score 49; DB 2; Length 142;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 2; Conservative 2; Mismatches 0; Gaps 0;

QY 8 QKXGKGGGAPPK 19
: : : : : | : : : :
Db 49 RKXGKGGGKPPR 60

RESULT 7
B84351
pseudouridylylate synthase I [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 24-May-2001
C:Accession: B84351
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: B84160; MUID:20504483
A:Accession: B84351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <STO>
A:Cross-references: GB:AE004437; NID:g10581435; PIDN:AAG20174.1; GSPDB:GN00138
C:Genetics:
A:Gene: trua
C:Superfamily: tRNA-pseudouridine synthase I

Query Match 39.2%; Score 49; DB 2; Length 266;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GKXGKGGGAPPKDLM 22

Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGGAPPKD 20
: : : : : | | | | : :
Db 197 IDTVLGDEPVGAGPGVPPAD 216

RESULT 8
A36358
T-cell acute lymphocytic leukemia 1 protein - human
C:Species: Homo sapiens (man)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Nov-2000
C:Accession: A36358; A34519; S55280; I38254; S12374
R:Aplan, P.D.; Begley, C.G.; Bertness, V.; Nussmeier, M.; Ezquerro, A.; Colligan, J.; Mol. Cell. Biol. 10, 6426-6435, 1990
A:Title: The SCL gene is formed from a transcriptionally complex locus.
A:Reference number: A36358; MUID:91061750
A:Accession: A36358
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-331 <APL>
A:Cross-references: GB:M61108; NID:g469058; PIDN:AAA36600.1; PID:g337970
R:Begin, C.G.; Aplan, P.D.; Denning, S.M.; Haynes, B.F.; Waldmann, T.A.; Kirsch, I.R. Proc. Natl. Acad. Sci. U.S.A. 86, 10128-10132, 1989
A:Title: The gene SCL is expressed during early hematopoiesis and encodes a different
A:Reference number: A34519; MUID:90099309
A:Accession: A34519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 118-331 <BEG>
A:Cross-references: GB:M29038; NID:g337958; PIDN:AAA36598.1; PID:g337959
R:Bernard, O.; Lecoindre, N.; Jonveaux, P.; Souyri, M.; Mauchauffe, M.; Berger, R.; La Oncogene 6, 1477-1488, 1991
A:Title: Two site-specific deletions and t(1;14) translocation restricted to human T-
A:Reference number: S55280; MUID:91360285
A:Accession: S55280
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-292, '294-331 <BER>
A:Cross-references: EMBL:S53245; NID:g234755; PIDN:AAB19683.1; PID:g234756
R:Chen, Q.; Tang, C.Y.; Tsan, J.T.; Xia, Y.; Ragab, A.H.; Peiper, S.C.; Carroll, A.; J. Exp. Med. 172, 1403-1408, 1990
A:Title: Coding sequences of the tal-1 gene are disrupted by chromosome translocation
A:Reference number: I38253; MUID:91037802
A:Accession: I38254
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 106-148 <RES>
A:Cross-references: EMBL:X58622; NID:g36685; PIDN:CAA41477.1; PID:g36686
R:Chen, Q.; Cheng, J.T.; Tsai, L.H.; Schneider, N.; Buchanan, G.; Carroll, A.; Crist, EMBO J. 9, 415-424, 1990
A:Title: The tal gene undergoes chromosome translocation in T cell leukemia and poten
A:Reference number: S12374; MUID:90151616
A:Accession: S12374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'R', 157-331 <CHE>
A:Cross-references: EMBL:X51990
C:Genetics:
A:Gene: GDB:TAL1; SCL; TCL5
A:Cross-references: GDB:120759; OMIM:187040
A:Map position: lp32-lp32
A:Introns: 180/3
C:Superfamily: lyl-1 protein
C:Keywords: DNA binding; transcription regulation

Query Match 39.2%; Score 49; DB 2; Length 331;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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A:Accession: T42070
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-598 <OGA>
A:Cross-references: EMBL:AB016932; PIDN:BAA32455.1
C:Genetics:
A:Gene: pkad

Query Match 37.6%; Score 47; DB 2; Length 598;
Best Local Similarity 72.7%; Pred. No. 84;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 GKGGGAPPKD 20
| | | | | | | | | |
DB 433 GKGGGGVPAD 443

RESULT 14
T49456
hypothetical protein B14D6.80 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49456
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Partmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49456
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-739 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.80
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.80
A:Map position: 6

Query Match 37.6%; Score 47; DB 2; Length 739;
Best Local Similarity 61.5%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

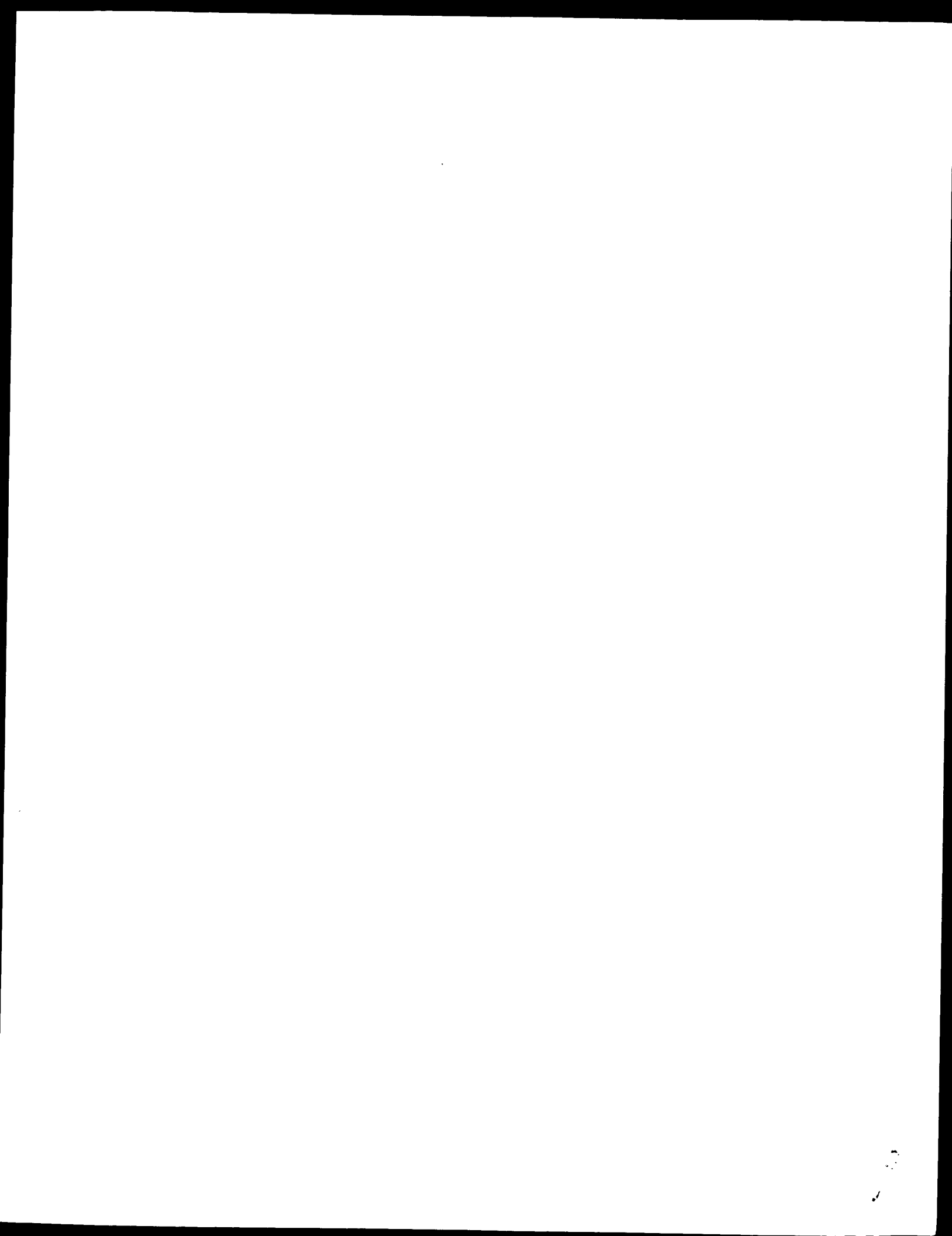
QY 6 KEQKGKGGGAPP 18
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DB 217 REQKGKGPASTP 229

RESULT 15
AH2515
hypothetical protein alr7304 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC7120
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AH2515
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2515
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4936 <KUR>
A:Cross-references: GB:BA000020; PIDN:BA078388.1; PID:gl7135842; GSPDB:GN00180
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7304
A:Genome: plasmid

Query Match 37.6%; Score 47; DB 2; Length 4936;
Best Local Similarity 40.0%; Pred. No. 6.9e+02;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMYKEQKGKGGAPPKD 20
: | | | | | | | | | |
DB 2312 VDDGIEQNGRDPNNPDPKD 2331

Search completed: September 4, 2002, 16:47:30
Job time: 366 sec



us-09-821-726-2.rspt

Thu Sep 5 11:23:36 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:01:31 : Search time 124.34 Seconds
(without alignments)
32.000 Million cell updates/sec

Title: US-09-821-726-2
Perfect score: 125
Sequence: 1 LDMWKEQKGGPGGAPPKDLMY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	47.2	1677	11 070373	070373 mus musculus
2	54	43.2	1194	5 09W485	Q9W485 drosophila
3	54	43.2	1284	5 0960F1	Q960F1 drosophila
4	51.5	41.2	681	4 09UP10	Q9UP10 homo sapien
5	51.5	41.2	1308	4 060307	Q60307 homo sapien
6	51	40.8	153	17 057795	O57795 pyrococcus
7	51	40.8	297	5 095526	Q95526 drosophila
8	50	40.0	237	7 030097	Q30097 homo sapien
9	50	40.0	237	7 030098	Q30098 homo sapien
10	50	40.0	264	7 029970	Q29970 homo sapien
11	50	40.0	269	7 030155	Q30155 homo sapien
12	50	40.0	611	5 09N893	Q9N893 plasmodium
13	49	39.2	191	3 074299	O74299 schizophtyll
14	49	39.2	266	17 09HNP6	Q9HNP6 halobacteri
15	49	39.2	331	4 Q16509	Q16509 homo sapien
16	49	39.2	333	4 Q9NY94	Q9NY94 homo sapien

Q931f5 streptomyce
Q9v58 drosophila
Q9vry3 drosophila
Q931j1 streptomyce
Q9vel7 drosophila
Q9rkpl streptomyce
Q9fwd2 oryza sativ
Q9figu0 arabidopsi
Q9nps8 homo sapien
Q92kj2 rhizobium m
Q9tx29 strongyloce
Q83032 streptomyce
Q91010 streptomyce
Q9c215 neurospora
Q9by10 homo sapien
Q95k63 macaca fasc
Q9p2f5 homo sapien
Q9w093 drosophila
Q70576 mus musculu
P91282 caenorhabdi
O31405 bacillus su
Q94ha9 oryza sativ
Q9h713 homo sapien
O18468 heliothsis v
Q00625 chironomus
Q9h7q8 homo sapien
Q9h7i6 homo sapien
Q69856 streptomyce
Q9h7q7 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT: 1677 AA.
ID 070373			
AC 070373;			
DT 01-AUG-1998 (TREMBLrel. 07, Created)			
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE XIN.			
GN XIN.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=HEART MUSCLE;			
RC PubMed=9159189;			
RA Wang D.-Z., Hu X., Lin J.L.-C., Kitten G.T., Solursh M., Lin J.J.-C.;			
RT "Differential display of mRNAs from the atrioventricular region of			
RT developing chicken hearts at stages 15 and 21.;"			
RL Front. Biosci. 1:al-a15(1996).			
RN [2]			
RP SEQUENCE FROM N.A.			
RC TISSUE=HEART MUSCLE;			
RC MEDLINE=99146891; PubMed=10021346;			
RA Wang D.-Z., Reiter R.S., Lin J.L.-C., Wang Q., Williams H.S.,			
RA Krob S.L., Schultzeiss T.M., Evans S., Lin J.J.-C.;			
RT "Requiem of a novel gene Xln, in cardiac morphogenesis.;"			
RL Development 126:1281-1294(1999).			
DR EMBL; AF051945; AAC06023.1; -			
DR MGD; MG1:1333878; Xln.			
DR MGD; MG1:1333878; Xln.			
SQ SEQUENCE 1677 AA; 182085 MW; A201CFC9A710C7FF CRC64;			

Query Match 47.2%; Score 59; DB 11; Length 1677;
Best Local Similarity 64.3%; Pred. No. 3.2;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 6 KEQKGGPGGAPPK 19

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db      571 EEEEGKGGGPPPE 584
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RESULT	2
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AC	PRT; 1194 AA.
TC	
JT	Q9W485;
CT	
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TT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
OT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE	CG3125 PROTEIN.
FE	
NS	CG3125.
SN	Drosophila melanogaster (Fruit fly).
VS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC	Ephydroidea; Drosophilidae; Drosophila.
NCBI	TXID=7727.
X	

SEQUENCE FROM N.A.
STRAIN-BERKELEY.
ADAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gallie R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A A Wan K.H., Doyle C., Baxter E.G., Helt G., Andrews-Pfannkoch C., Baldwin D.,
A A Brill J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A A Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A A Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A A Burks K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
A A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A A de Paulo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A A Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
A A Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.P., Glasser K.,
A A Glodak A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
A A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A A Kimmel B.E., Kodira C.D., Kraft A., Li J., Li Z., Liang Y., Lin X.,
A A Lasto P., Lei Y., Levitsky A.A., Li J., Li Z., Kennison J.A., Ketchum K.A.,
A A Markulov G., Milshina N.V., Mobarry C., McLeod M.P., McPherson D.,
A A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A A Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
A A Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A A Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,
A A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A A Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
A A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A A "The genome sequence of *Drosophila melanogaster*,"
A A Science 287:2185-2195 (2000).
A A EMBL; AE003435; AAF46073.1.
A A FlyBase; FBgn029797; CG3125.
A A SEQUENCE 1194 34 15

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Best Local Similarity 64.3%; Pred. No. 13;
Matches          9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Thu Sep 5 11:23:36 2002

Query Match 41.2%; Score 51.5; DB 4; Length 681;
Best Local Similarity 54.2%; Pred. No. 18;
Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 1 LDTMPKFAFSSDEGVGPGGAPPK 19
155 LDTMPKFAFSSDEGVGPGGAPPK 178

RESULT 5
ID O60307 PRELIMINARY; PRT; 1308 AA.
AC O60307;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DT KIAA0561 PROTEIN (FRAGMENT).
GN KIAA0561.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:31-39(1998).
RN [2]
RP SEQUENCE OF 1-593 FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
RT pDE4C.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB011133; BAA25487.1; -;
DR EMBL; AC005793; AAC62830.1; -;
DR HSSP; P05132; 1CTP.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS01016; PDZ; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 1308 AA; 143004 MW; 9B3A23C528EF47A6 CRC64;

Query Match 41.2%; Score 51.5; DB 4; Length 1308;
Best Local Similarity 54.2%; Pred. No. 34;
Matches 13; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 1 LDTMPKFAFSSDEGVGPGGAPPK 19

Db 782 LDTMPKFAFSSDEGVGPGGAPPK 805

RESULT 6
ID O57795 PRELIMINARY; PRT; 153 AA.
AC O57795;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DT HYPOTHETICAL 17.0 KDA PROTEIN PH0068.
GN PH0068.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OC NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000001; BAA29137.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 16966 MW; 9063F41B6DA9255B CRC64;

Query Match 40.8%; Score 51; DB 17; Length 153;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDTMPKFAFSSDEGVGPGG 15
Db 121 LDTMPKFAFSSDEGVGPGG 135

RESULT 7
ID Q95S26 PRELIMINARY; PRT; 297 AA.
AC Q95S26;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LD33666P.
GN ANTP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., R.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060407; AAL25446.1; -;
SQ SEQUENCE 297 AA; 32845 MW; A88C5435ABD619B3 CRC64;

Query Match 40.8%; Score 51; DB 5; Length 297;
Best Local Similarity 45.0%; Pred. No. 9;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 MVKEQKGKGGPGGAPPKDLMY 23
 I : : I I I I I I I I : :
 Db 230 MYQOSGVPVPGAPPQGNMH 249

RESULT 8
 Q30097
 ID Q30097 PRELIMINARY; PRT; 237 AA.
 AC Q30097;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT).
 GN HLA-DQB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasunaga S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L40180; AAA92331.1; -;
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 27038 MW; 460B63ABCA7BC8EA CRC64;

Query Match 40.0%; Score 50; DB 7; Length 237;
 Best Local Similarity 34.8%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGPGGAPPKDLMY 23
 I : : I I I I I I I I : :
 Db 215 LGLIIRSRKGGPGGPPAGLLH 237

RESULT 9
 Q30098
 ID Q30098 PRELIMINARY; PRT; 237 AA.
 AC Q30098;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT).
 GN HLA-DQB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yasunaga S.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L40181; AAA92332.1; -;
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.

DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 237 AA; 27179 MW; 75C1B91440C0D5DF CRC64;

Query Match 40.0%; Score 50; DB 7; Length 237;
 Best Local Similarity 34.8%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGPGGAPPKDLMY 23
 I : : I I I I I I I I : :
 Db 215 LGLIIRSRKGGPGGPPAGLLH 237

RESULT 10
 Q29970
 ID Q29970 PRELIMINARY; PRT; 264 AA.
 AC Q29970;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN (FRAGMENT).
 GN HLA-DWI2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226367; PubMed=3371836;
 RA Yasunami M.;
 RT "Structural analysis of human major histocompatibility complex class II genes".
 RL Fukuoka Igaku Zasshi 79:153-167(1988).
 DR EMBL; M57649; AAA63217.1; -;
 DR HSSP; P13760; 2SEB.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 DR SMART; SM00407; IGcl; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 264 AA; 29871 MW; BB6A4A9054F3CB75 CRC64;

Query Match 40.0%; Score 50; DB 7; Length 264;
 Best Local Similarity 34.8%; Pred. No. 11;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGPGGAPPKDLMY 23
 I : : I I I I I I I I : :
 Db 242 LGLIIRSRKGGPGGPPAGLLH 264

RESULT 11
 Q30155
 ID Q30155 PRELIMINARY; PRT; 269 AA.
 AC Q30155;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HLA-DRB2 PROTEIN.
 GN HLA-DRB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

Thu Sep 5 11:23:36 2002

```

RP SEQUENCE FROM N.A.
RX MEDLINE=87192945; PubMed=3494674;
RA Tsukamoto K., Yasunuki M., Kimura A., Inoko H., Ando A., Hirose T.,
RA Inayama S., Sasazuki T.;
RT "DQW1 beta gene from HLA-DP2-Dw12 consists of six exons and expresses
RT multiple DQW1 beta polypeptides through alternative splicing.";
RL Immunogenetics 25:343-346(1987).
DR EMBL: M16276; AAA59823.1; -.
DR HSSP: P13760; 2SEP.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00969; MHC_II_beta; 1.
DR ProDom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IGc1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Glycoprotein; MHC II; Transmembrane.
KW SEQUENCE 269 AA; 30532 MW; 4FF81EC5AD92A6EA CRC64;

Query Match 40.0%; Score 50; DB 7; Length 269;
Best Local Similarity 34.8%; Pred. No. 12;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGCGAPPKDMY 23
DB 247 LGLIIRQSRKQGGPGPPAGLLH 269

RESULT 12
Q9N893 PRELIMINARY; PRT; 611 AA.
ID Q9N893
AC Q9N893;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE VIR12 PROTEIN.
GN VIR12.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliver K., Bowman S., Hall N., Quail M., Rajandream M.A., Harris D.,
RA del Portillo H.A., Lanzer M., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL360354; CAB96702.1; -.
SQ SEQUENCE 611 AA; 68442 MW; A642D1893D7DD8F4 CRC64;

Query Match 40.0%; Score 50; DB 5; Length 611;
Best Local Similarity 56.2%; Pred. No. 27;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 MVKEQKGKGGCGAPPK 19
DB 366 ITKEQKGVSPAGSPSK 381

RESULT 13
O74299 PRELIMINARY; PRT; 191 AA.
ID O74299
AC O74299;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORF15 PROTEIN PRECURSOR.
OS Schizophyllum commune [Bracket fungus].
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Stereales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=4-40 (CBS 340.81);
RA Lugones L.G.;
RL Thesis (1998), University of Groningen.
DR EMBL: AJ007543; CAA07544.1; -.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 191 AA; 19973 MW; 778518EF0D830179 CRC64;

Query Match 39.2%; Score 49; DB 3; Length 191;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 VKEQKGKGGCGAPPK 19
DB 90 IEELKGGKPGAGHPK 104

RESULT 14
Q9HNP6 PRELIMINARY; PRT; 266 AA.
ID Q9HNP6
AC Q9HNP6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PSEUDOURIDYLATE SYNTHASE I.
GN TRUA OR VNG2003G.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Shroqna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AE005094; AAG20174.1; -.
DR InterPro: IPR001406; PseudoU_synth_1.
DR Pfam: PF01416; PseudoU_synth_1; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 28863 MW; FD2D3373A9E98037 CRC64;

Query Match 39.2%; Score 49; DB 17; Length 266;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LDTMVKEQKGKGGCGAPPK 20
DB 197 IDTVLGDEPVGPGVPPAD 216

RESULT 15
Q16509 PRELIMINARY; PRT; 331 AA.
ID Q16509
AC Q16509;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TAL-1.
GN TAL-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91360285; PubMed=1886719;
 RA Bernard O., Lecoq N., Jonveaux P., Souyri M., Mauchauffe M.,
 RT Berger R., Larsen C.J., Mathieu-Mahul D.;
 RL "Two site-specific deletions and t(1;14) translocation restricted to
 human T-cell acute leukemias disrupt the 5' part of the tal-1 gene.";
 DR Oncogene 6:1477-1488(1991).
 DR EMBL; S53245; AAB19683.1; -;
 DR InterPro; IPR001092; HLH_dim.
 DR Pfam; PF00010; HLH; 1.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN 1.
 SQ SEQUENCE 331 AA; 34284 MW; 58D0E31589DBB396 CRC64;

Query Match 39.2%; Score 49; DB 4; Length 331;
 Best Local Similarity 69.2%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 10 KGKGGGAPPKDL 22
 Db 269 GGGGGGAPPDDL 281
 | | | | | | | | | |
 | | | | | | | | | |

Search completed: September 4, 2002, 17:01:33
 Job time: 1154 sec

Thu Sep 5 11:23:43 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:06 : Search time 34.18 Seconds
(without alignments)
21.523 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90
Sequence: 1 KKEVMPISQSLDALVKEKK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	94.4	199	1 C11P_HUMAN	Q9ns71 homo sapien
2	62	68.9	184	1 C11P_MOUSE	Q9cr36 mus musculu
3	43	47.8	633	1 TOPL_THEMA	P46799 thermotoga
4	43	47.8	734	1 METE_THEMA	Q9x112 thermotoga
5	42.5	47.2	715	1 ERF2_CANAL	O13354 candida alb
6	42.5	47.2	203	1 NAHD_PSEPU	Q51948 pseudomonas
7	42.5	46.7	212	1 NAHD_PSESP	O52462 pseudomonas
8	41	45.6	292	1 SPAN_SHIFL	Q9uww2 methanococc
9	41	45.6	334	1 RL3_METVA	O22263 arabidopsis
10	41	45.6	361	1 PDA6_ARATH	P12063 neurospora
11	41	45.6	669	1 SYRM_NEUCR	O84783 chlamydia t
12	41	45.6	753	1 PRIA_CHLTR	P47235 campylobact
13	41	45.6	862	1 GYRA_CAMFE	O29406 archaeoglob
14	40.5	45.0	451	1 GLYA_ARCFU	P32908 saccharomyc
15	40.5	45.0	1225	1 SMC1_YEAST	P36263 mycoplasma
16	40	44.4	162	1 RL10_MYCGE	Q9dc71 mus musculu
17	40	44.4	258	1 RT15_MOUSE	P44870 haemophilus
18	40	44.4	390	1 LPXB_HAEIN	O30513 acinetobact
19	40	44.4	414	1 FTSY_HAEIN	P07868 bacillus su
20	40	44.4	466	1 BENK_ACICA	P48564 saccharomyc
21	40	44.4	482	1 GRAA_BACSU	P08158 emericaella
22	40	44.4	524	1 YN35_YEAST	O67708 aquifex aeo
23	40	44.4	548	1 ANDS_EMENI	Q9hj84 thermoplas
24	40	44.4	663	1 UVRB_AQUAE	P25651 saccharomyc
25	39	43.3	175	1 GRPE_THEAC	Q41643 volvox carl
26	39	43.3	190	1 YCX6_YEAST	P16486 clover yell
27	39	43.3	202	1 PSBQ_VOLCA	O56418 aquifex aeo
28	39	43.3	212	1 COAT_CYMW	Q9d9w0 mus musculu
29	39	43.3	259	1 Y227_AQUAE	P53586 arabidopsis
30	39	43.3	342	1 C256_MOUSE	P07600 bacillus su
31	39	43.3	347	1 SUCA_ARATH	P52288 kluyveromyc
32	39	43.3	400	1 TRPB_BACSU	
33	39	43.3	543	1 MIG1_KLUMA	

34	39	43.3	657	1 HUTH_HUMAN	P42357 homo sapien
35	39	43.3	771	1 KYO0_YEAST	Q02208 saccharomyc
36	39	43.3	1176	1 YOR8_YEAST	Q08236 saccharomyc
37	38	42.2	121	1 Y429_PYRAB	Q9v108 pyrococcus
38	38	42.2	147	1 RS12_SULSO	P39573 sulfolobus
39	38	42.2	152	1 IL2_ORCOR	O97513 orcinus orc
40	38	42.2	152	1 LUXS_HELPJ	O92mw8 helicobacte
41	38	42.2	155	1 LUXS_HELPJ	O24931 helicobacte
42	38	42.2	230	1 DCTR_BACHD	Q9k998 bacillus ha
43	38	42.2	252	1 DHSB_SCHPO	P21911 schizosacch
44	38	42.2	275	1 YMA9_CAEEL	P34454 caenorhabdi
45	38	42.2	280	1 Y466_HAEIN	P44000 haemophilus

ALIGNMENTS

RESULT 1					
C11P_HUMAN					
ID	C11P_HUMAN	STANDARD;	PRT;	199 AA.	
AC	Q9NS71;				
DT	01-MAR-2002 (Rel. 41, Created)				
DT	01-MAR-2002 (Rel. 41, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	CALL protein.				
GN	CALL				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Stomach;				
RA	MEDLINE=20296773; PubMed=10835488;				
RA	Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;				
RT	"Isolation of two novel genes, down-regulated in gastric cancer.";				
RL	Jpn. J. Cancer Res. 91:459-463(2000).				
CC	-I- TISSUE SPECIFICITY: Expressed in stomach. No expression is				
CC	detected in cancer tissue or gastric cancer cell lines.				
CC	-----				
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CC	-----				
DR	EMBL; AB039886; BAA92433.1; -				
DR	MIM; 606402; -				
SQ	SEQUENCE 199 AA; 21999 MW; C099B8B9A1338D7A CRC64;				

Query Match 94.4%; Score 85; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEKK 19
IIIIIIIIIIIIIIIIIIII

DB 102 KEVMPISQSLDALVKEKK 119

RESULT 2

C11P_MOUSE					
ID	C11P_MOUSE	STANDARD;	PRT;	184 AA.	
AC	Q9CR36; Q9D7K7; Q9CTZ5;				
DT	01-MAR-2002 (Rel. 41, Created)				
DT	01-MAR-2002 (Rel. 41, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	CALL protein homolog.				
GN	CALL				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUP=Stomach, and Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 CC EMBL; AK008990; BAB26010.1;
 CC EMBL; AK008622; BAB25784.1;
 CC EMBL; AK008641; BAB25801.1;
 CC EMBL; AK008647; BAB25805.1;
 CC EMBL; AK008722; BAB25856.1;
 CC EMBL; AK008745; BAB25872.1;
 CC EMBL; AK008933; BAB25975.1;
 CC EMBL; AK008956; BAB25988.1;
 CC EMBL; AK009145; BAB26103.1;
 CC EMBL; AK019050; BAB31525.1;
 CC CONFLICT 113 113 P -> L (IN REF. 1; BAB26103).
 FT SEQUENCE 184 AA; 201134 MW; 288982F0404FFA8B CRC64;
 CC -----
 CC Query Match 68.9%; Score 62; DB 1; Length 184;
 CC Best Local Similarity 61.1%; Pred. No. 0.0037;
 CC Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KDAMPQLDLDTWVEQK 105
 I: |||: ||: |||: |
 K: |||: ||: |||: |
 RESULT 3
 ID TOPI_THEME STANDARD; PRT; 633 AA.
 AC P46799;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
 DE (Untwisting enzyme) (Swivelase).
 GN TOPA OR TM0258.
 OS Thermotoga maritima
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=96138548; PubMed=8547314;
 RA Bouthier de la Tour C., Kaltoum H., Portemer C., Confalonieri F.,
 RA Huber R., Duquet M.;
 RT "Cloning and sequencing of the gene coding for topoisomerase I from
 RT the extremely thermophilic eubacterium, *Thermotoga maritima*.";
 RL Biochim. Biophys. Acta 1264:279-283(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermotoga maritima*.";
 RL Nature 399:323-329(1999).
 CC -----
 CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
 CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
 CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
 CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
 CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
 CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U27841; AAA68949.1;
 CC EMBL; AE001708; AAD35346.1;
 CC HSSP; P06612; IECL.
 CC TIGR; TM0258;
 CC InterPro; IPR003601; DNATopI_ATP_bind.
 CC InterPro; IPR003602; DNATopI_DNA_bind.
 CC InterPro; IPR000380; Pro_topoisomerase.
 CC InterPro; IPR002936; Toprim.
 CC Pfam; PF01131; Topoisom_bac; 1.
 CC Pfam; PF01751; Toprim; 1.
 CC PRINTS; PR00417; PRTPISMRASEI.
 CC SMART; SM00437; TOPIAC; 1.
 CC SMART; SM00436; TOPIBC; 1.
 CC SMART; SM00493; TOPRIM; 1.
 CC PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Isomerase; Topoisomerase; DNA-binding; zinc-finger; Metal-binding;
 KW Complete proteome.
 FT ZN_FING 559 580 C4-TYPE.
 FT ACT_SITE 288 288 DNA CLEAVAGE (BY SIMILARITY).
 SQ SEQUENCE 633 AA; 72694 MW; F7262A044060CE9 CRC64;
 CC -----
 CC Query Match 47.8%; Score 43; DB 1; Length 633;
 CC Best Local Similarity 52.9%; Pred. No. 19;
 CC Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 3 EVMPISQSLDALVKEKK 19
 Db 216 ETLKEIQSIDLVVEEK 232
 I: |||: ||: |||: |
 K: |||: ||: |||: |
 RESULT 4
 ID TOPI_THEME
 AC P46799;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
 DE (Untwisting enzyme) (Swivelase).
 GN TOPA OR TM0258.
 OS Thermotoga maritima
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.

GN SUP35.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=2005E;
RC Resende C.G., Ferreira P.C., Tuite M.F., Duarte J.B.;
RA Submitted (Aug-1997) to the EMBL/GenBank/DDBJ databases.
RL
CC -|- FUNCTION: INVOLVED IN TRANSLATION TERMINATION. STIMULATES THE
CC -|- ACTIVITY OF ERF1. BINDS GUANINE NUCLEOTIDES.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -|- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC ERF3 SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF020554; AAB82541.1; -
CC DR HSSP; P02990; 1FTU.
CC DR InterPro; IPR000795; GTP_EFTU.
CC DR InterPro; IPR004161; GTP_EFTU_D2.
CC DR InterPro; IPR004160; GTP_EFTU_D3.
CC DR Pfam; PF00009; GTP_EFTU; 1.
CC DR Pfam; PF03144; GTP_EFTU_D2; 1.
CC DR Pfam; PF03143; GTP_EFTU_D3; 1.
CC DR PROSITE; PS00301; EFATOR.GTP; 1.
CC DR Protein biosynthesis; Repeat; phosphorylation; Gtp-binding.
CC KW DOMAIN 5 128 SEVERAL SORT OF REPEATS.
CC FT DOMAIN 129 285 CHARGED.
CC FT SIMILAR 286 715 TO ELONGATION FACTORS EF-1.
CC FT NP_BIND 299 306 GTP (BY SIMILARITY).
CC FT NP_BIND 376 380 GTP (BY SIMILARITY).
CC FT NP_BIND 438 441 GTP (BY SIMILARITY).
CC FT MOD_RES 373 373 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 715 AA; 79074 MW; 740964B9561C49B3 CRC64;

Query Match 47.2%; Score 42.5; DB 1; Length 715;
Best Local Similarity 45.8%; Pred. No. 27;
Matches 11; Conservative 4; Mismatches 4; Indels 5; Gaps 1;
QY 1 KKEVMP-----SIQSLDALVKEKK 19
||| 1 : : : ||||| : :
DB 252 KKESTPVSNSASVATADALVKQGE 275

RESULT 6
NAHD_PSEPU STANDARD; PRT; 203 AA.
ID NAHD_PSEPU
AC Q51948;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 2-hydroxychromene-2-carboxylate isomerase (HCCA isomerase).
GN NAHD.
OS Pseudomonas putida.
OG Plasmid NAH7.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
CC
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=G7 / ATCC 17485;
CC MEDLINE=95095951; PubMed=8002605;
CC Eaton R.W.;
CC *Organization and evolution of naphthalene catabolic pathways;
CC
CC -----
Query Match 47.8%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 EYMPSTQSLDALVKEKK 19
||| : : : || : :
DB 713 EYIPSLRNVALAKEMR 729

RESULT 5
ERF2_CANAL STANDARD; PRT; 715 AA.
ID ERF2_CANAL
AC Q1354;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (Translational release factor 3) (ERF3) (ERF-3).

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EMBL; AE001784; AAD36360.1; -
TIGR; TM1286; -
InterPro; IPR002629; Methionine_synth.
Pfam; PF01717; Methionine_synth; 1.
Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
Complete proteome. ZINC (BY SIMILARITY).
METAL 618 618 ZINC (BY SIMILARITY).
METAL 620 620 ZINC (BY SIMILARITY).
METAL 704 704 ZINC (BY SIMILARITY).
SEQUENCE 734 AA; 85570 MW; 34B19187480D443B CRC64;

Query Match 47.1%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 EYMPSTQSLDALVKEKK 19
||| : : : || : :
DB 713 EYIPSLRNVALAKEMR 729

RESULT 5
ERF2_CANAL STANDARD; PRT; 715 AA.
ID ERF2_CANAL
AC Q1354;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (Translational release factor 3) (ERF3) (ERF-3).

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EMBL; AE001784; AAD36360.1; -
TIGR; TM1286; -
InterPro; IPR002629; Methionine_synth.
Pfam; PF01717; Methionine_synth; 1.
Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
Complete proteome. ZINC (BY SIMILARITY).
METAL 618 618 ZINC (BY SIMILARITY).
METAL 620 620 ZINC (BY SIMILARITY).
METAL 704 704 ZINC (BY SIMILARITY).
SEQUENCE 734 AA; 85570 MW; 34B19187480D443B CRC64;

Query Match 47.1%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 EYMPSTQSLDALVKEKK 19
||| : : : || : :
DB 713 EYIPSLRNVALAKEMR 729

RESULT 5
ERF2_CANAL STANDARD; PRT; 715 AA.
ID ERF2_CANAL
AC Q1354;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (Translational release factor 3) (ERF3) (ERF-3).

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EMBL; AE001784; AAD36360.1; -
TIGR; TM1286; -
InterPro; IPR002629; Methionine_synth.
Pfam; PF01717; Methionine_synth; 1.
Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
Complete proteome. ZINC (BY SIMILARITY).
METAL 618 618 ZINC (BY SIMILARITY).
METAL 620 620 ZINC (BY SIMILARITY).
METAL 704 704 ZINC (BY SIMILARITY).
SEQUENCE 734 AA; 85570 MW; 34B19187480D443B CRC64;

Query Match 47.1%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 EYMPSTQSLDALVKEKK 19
||| : : : || : :
DB 713 EYIPSLRNVALAKEMR 729

RESULT 5
ERF2_CANAL STANDARD; PRT; 715 AA.
ID ERF2_CANAL
AC Q1354;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Eukaryotic peptide chain release factor GTP-binding subunit (ERF2)
DE (Translational release factor 3) (ERF3) (ERF-3).

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EMBL; AE001784; AAD36360.1; -
TIGR; TM1286; -
InterPro; IPR002629; Methionine_synth.
Pfam; PF01717; Methionine_synth; 1.
Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
Complete proteome. ZINC (BY SIMILARITY).
METAL 618 618 ZINC (BY SIMILARITY).
METAL 620 620 ZINC (BY SIMILARITY).
METAL 704 704 ZINC (BY SIMILARITY).
SEQUENCE 734 AA; 85570 MW; 34B19187480D443B CRC64;

Query Match 47.1%; Score 43; DB 1; Length 734;
Best Local Similarity 47.1%; Pred. No. 23;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 3 EYMPSTQSLDALVKEKK 19
||| : : : || : :
DB 713 EYIPSLRNVALAKEMR 729

RESULT 5
ERF2_CANAL STANDARD; PRT;

sequence of the DNA encoding 2-hydroxychromene-2-carboxylate isomerase and trans-o-hydroxybenzylidenepyrivate hydratase-aldolase from the NAH7 plasmid.";
 J. Bacteriol. 176:7757-7762(1994).
 [2]
 CHARACTERIZATION
 STRAIN-G7 / ATCC 17485;
 MEDLINE=93077433; PubMed=1447127;
 Eaton R.W., Chapman P.J.;
 "Bacterial metabolism of naphthalene: construction and use of recombinant bacteria to study ring cleavage of 1,2-dihydroxynaphthalene and subsequent reactions.";
 J. Bacteriol. 174:7542-7554(1992).
 CC -!- FUNCTION: CATALYZES THE ISOMERIZATION OF 2-HYDROXYCHROMENE-2-CARBOXYLATE (HCCA) TO TRANS-O-HYDROXYBENZYLIDENEPYRIVATE (THBPA).
 CC THE OPTIMUM PH FOR THE ENZYME IS 10. THE REACTION IS REVERSIBLE.
 CC -!- COFACTOR: GLUTATHIONE SEEMS TO STABILIZE THE ENZYME, WHICH LOSES ACTIVITY RAPIDLY IN THE ABSENCE OF THIS COMPOUND.
 CC -!- PATHWAY: UPPER NAPHTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPHTHALENE TO SALICYLATE.
 CC -----
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 CC -----
 CC EMBL; U09057; AAA6G358.1; .
 CC InterPro; IPR004287; HCCA_isomerase.
 CC Pfam; PF03046; HCCA_isomerase; 1.
 CC Isomerase; Plasmid; Aromatic hydrocarbons catabolism.
 CC SEQUENCE 203 AA; 23061 MW; E84B56F21C604945 CRC64;
 CC -----
 CC Query Match 46.7%; Score 42; DB 1; Length 203;
 CC Best Local Similarity 53.3%; Pred. No. 8.6;
 CC Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 4 VMPSTQSLDALVKEK 18
 CC : | : | | | | | | | |
 CC Db 118 IAPDLESIPALVSEK 132
 CC : | : | | | | | | | |
 CC -----
 CC RESULT 7
 CC NAHD_PSESP
 CC ID NAHD_PSESP STANDARD; PRT; 212 AA.
 CC AC Q52462;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE 2-hydroxychromene-2-carboxylate isomerase (HCCA isomerase).
 CC GN DOXJ.
 CC OS Pseudomonas sp. (strain C18).
 CC OG Plasmid.
 CC OC Bacteria; Proteobacteria.
 CC OX NCBI_TaxID=306;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=94042852; PubMed=8226631;
 CC RA Denome S.A., Stanley D.C., Olson E.S., Young K.D.;
 CC RT "Metabolism of dibenzothioephene and naphthalene in pseudomonas strains: complete DNA sequence of an upper naphthalene catabolic pathway.";
 CC RL J. Bacteriol. 175:6890-6901(1993).
 CC -!- FUNCTION: CATALYZES THE ISOMERIZATION OF 2-HYDROXYCHROMENE-2-CARBOXYLATE (HCCA) TO TRANS-O-HYDROXYBENZYLIDENEPYRIVATE (THBPA).
 CC THE OPTIMUM PH FOR THE ENZYME IS 10. THE REACTION IS REVERSIBLE.
 CC -!- PATHWAY: UPPER NAPHTHALENE CATABOLIC PATHWAY WHICH INVOLVES CONVERSION OF NAPHTHALENE TO SALICYLATE, AND CATABOLISM OF DIBENZOTHIOEPHENE (DBT) AND PHENANTHRENE. CONVERTS PHENANTHRENE TO 1-HYDROXY-2-NAPHTHOIC ACID AND THE METABOLISM OF DBT IS LIMITED TO

OXIDATION OF THE AROMATIC RING.
 -!- MISCELLANEOUS: DOXH AND DOXJ ENCODE DIFFERENT ENZYMES THAT MAY HAVE INTERCHANGEABLE FUNCTIONS.
 CC -----
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 CC -----
 CC EMBL; M60405; AAA16133.2; ALT_SEQ.
 CC InterPro; IPR004287; HCCA_isomerase.
 CC Pfam; PF03046; HCCA_isomerase; 1.
 CC Isomerase; Plasmid; Aromatic hydrocarbons catabolism.
 CC SEQUENCE 212 AA; 24039 MW; 5EF96A619913DB4F CRC64;
 CC -----
 CC Query Match 46.7%; Score 42; DB 1; Length 212;
 CC Best Local Similarity 53.3%; Pred. No. 9;
 CC Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 4 VMPSTQSLDALVKEK 18
 CC : | : | | | | | | | |
 CC Db 131 IAPDLESIPALVSEK 145
 CC : | : | | | | | | | |
 CC -----
 CC RESULT 8
 CC SPAN_SHIFL
 CC ID SPAN_SHIFL STANDARD; PRT; 292 AA.
 CC AC P35532;
 CC DT 01-JUN-1994 (Rel. 29, Created)
 CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
 CC DT 13-JUL-1999 (Rel. 38, Last annotation update)
 CC DE Surface presentation of antigens protein span (Spa32 protein).
 CC GN SPAN OR SPA32.
 CC OS Shigella flexneri, and
 CC OG Plasmid 210 kb invasion pWR100, and plasmid 230 kb pMYSH6000.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Shigella.
 CC OX NCBI_TaxID=623, 624;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=S.flexneri; STRAIN=M90T; PLASMID=210 kb invasion pWR100;
 CC RX MEDLINE=92193289; PubMed=1312536;
 CC RA Venkatesan M.M., Buysse J.M., Oaks E.V.;
 CC RT "Surface presentation of Shigella flexneri invasion plasmid antigens requires the products of the spa locus.";
 CC RL J. Bacteriol. 174:1990-2001(1992).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=S.flexneri; STRAIN=2A; PLASMID=230 kb pMYSH6000;
 CC RX MEDLINE=93224456; PubMed=8385666;
 CC RA Sasaki C., Komatsu K., Tobe T., Suzuki T., Yoshikawa M.;
 CC RT "Eight genes in region 5 that form an operon are essential for invasion of epithelial cells by Shigella flexneri 2a.";
 CC RL J. Bacteriol. 175:2334-2346(1993).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=S.sonnei; STRAIN=HW383;
 CC RA Arakawa E., Kato J.I., Ito K.I., Watanabe H.;
 CC RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC RN [4]
 CC RP DISULFIDE BOND, AND MUTAGENESIS.
 CC RC SPECIES=S.flexneri;
 CC RX MEDLINE=95281569; PubMed=7761426;
 CC RA Watarai M., Tobe T., Yoshikawa M., Sasaki C.;
 CC RT "Disulfide oxidoreductase activity of Shigella flexneri is required for release of Ipa proteins and invasion of epithelial cells.";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 92:4927-4931(1995).
 CC -!- FUNCTION: REQUIRED FOR SURFACE PRESENTATION OF INVASION PLASMID


```

Db      266  VESLDALVKE 275
:::|||||
RESULT  11
SYMM_NEUCR
ID      SYM_NEUCR      STANDARD;      PRT;      669 AA..
AC      P12063;
DT      01-OCT-1989 (Rel. 12, Created)

```

DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Tyrosyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.1)
 DE (Tyrosine--tRNA ligase) (TVRRS).
 GN CVT-18.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87273496; PubMed=3607872;
 RA Akins R.A., Lambowitz A.M.;
 RT "A protein required for splicing group I introns in Neurospora
 RT mitochondria is mitochondrial tyrosyl-tRNA synthetase or a derivative
 RT thereof.";
 RL Cell 50:331-345(1987).
 RN [2]
 RP REVISIONS.
 RA Lambowitz A.M.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTIONS.
 RX MEDLINE=90352708; PubMed=2143700;
 RA Cherniack A.D., Garriga G., Kittle J.D. Jr., Akins R.A.,
 RA Lambowitz A.M.;
 RT "Function of Neurospora mitochondrial tyrosyl-tRNA synthetase in RNA
 RT splicing requires an idiosyncratic domain not found in other
 RT synthetases.";
 RL Cell 62:745-755(1990).
 CC -1- FUNCTION: HAS BOTH A AMINOACYL-TRNA SYNTHETASE ACTIVITY AND IS
 CC INVOLVED IN THE SPLICING OF GROUP I INTRONS. IT ACTS IN INTRON
 CC SPLICING BY STABILIZING THE CATALYTICALLY ACTIVE STRUCTURE OF THE
 CC INTRON.
 CC -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
 CC diphosphate + L-tyrosyl-tRNA(Tyr).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; M17118; AAA33620.1; -
 DR PIR; A27158; SYNCYT.
 DR HSSP; P00952; 2TSI.
 DR InterPro; IPR002305; trna-synt_lb.
 DR InterPro; IPR001412; trna-synt_I.
 DR InterPro; IPR002307; trna-synt_tyr.
 DR Pfam; PF00579; trna-synt_lb; 1.
 DR PRINTS; PR01040; TRNASYNTHYR.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
 DR KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Mitochondrion; transit peptide; mRNA processing.
 FT TRANSIT 1 32 MITOCHONDRION.
 FT CHAIN 33 669 TYROSYL-TRNA SYNTHETASE.
 FT SITE 104 113 "HIGH" REGION.
 FT SITE 324 328 "KMSKS" REGION.
 FT BINDING 327 327 ATP (BY SIMILARITY).
 FT DOMAIN 33 75 INVOLVED IN SPLICING (PROBABLE).
 FT MUTAGEN 127 127 G->E: SPLICING AND AMINOACYLATION
 FT DEFECTS (MUTANTS C-18-1 AND C-18-2).
 SQ SEQUENCE 669 AA; 75422 MW; DD136CAC9AD1BEB5 CRC64;
 Query Match 45.6%; Score 41; DB 1; Length 669;
 Best Local Similarity 33.3%; Pred. No. 44;
 Matches 6; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

OY 1 KKEVMPSTQSLDALVKEK 18
 |:::|:::|:::|:::|:::|
 DB 631 KQEMIASVKTIDGMDEK 648

RESULT 12
 PRIA_CHLTR STANDARD; PRT; 753 AA.
 AC 084783;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Primosomal protein N' (Replication factor Y).
 GN PRIA OR Cn778.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D/OW-3/CX;
 RX MEDLINE=99000809; PubMed=97841136;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 CC -1- FUNCTION: RECOGNIZES A SPECIFIC HAIRPIN SEQUENCE ON PHIX SSDNA.
 CC THIS STRUCTURE IS THEN RECOGNIZED AND BOUND BY PROTEINS PRIA AND
 CC PRIC. FORMATION OF THE PRIMOSOME PROCEEDS WITH THE SUBSEQUENT
 CC ACTIONS OF DNAB, DNAC, DNAT AND PRIMASE. PRIA THEN FUNCTIONS AS A
 CC HELICASE WITHIN THE PRIMOSOME (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. PRIA SUBFAMILY.

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 CC or send an email to license@isb-sib.ch)
 CC -----
 DR EMBL; AE001350; AAC68373.1; -
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW DNA replication; DNA-binding; ATP-binding; Helicase; Primosome;
 KW Zinc-finger; Complete proteome.
 FT NP_BIND 241 248 ATP (POTENTIAL).
 FT SITE 337 340 DEEH BOX.
 FT ZN_FING 458 470 C4-TYPE (POTENTIAL).
 FT ZN_FING 485 501 C4-TYPE (POTENTIAL).
 SQ SEQUENCE 753 AA; 84831 MW; C91861B4385C5E35 CRC64;

Query Match 45.6%; Score 41; DB 1; Length 753;
 Best Local Similarity 61.1%; Pred. No. 50;
 Matches 11; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

OY 1 KKEVMPSTQSLDALVKEK 18
 |:::|:::|:::|:::|:::|
 DB 172 KTEV--SAKTLDALVKOK 187

RESULT 13
 GYRA_CAMEE STANDARD; PRT; 862 AA.
 ID GYRA_CAMEE
 AC P47235;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

Thu Sep 5 11:23:43 2002

us-09-821-726-5-rsp

```

DE DNA gyrase subunit A (EC 5.99.1.3).
GN GYRA.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=196;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97209069; PubMed=9056011;
RX Taylor D.E., Chau A.S.;
RA "Cloning and nucleotide sequence of the gyrA gene from Campylobacter
RT fetus subsp. fetus ATCC 27374 and characterization of ciprofloxacin-
RT resistant laboratory and clinical isolates.";
RL Antimicrob. Agents Chemother. 41:665-671(1997).
CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: MADE UP OF TWO CHAINS, THE A CHAIN IS RESPONSIBLE FOR DNA
CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
CC ENZYME FORMS AN A2B2 TETRAMER.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U25640; AAA67068.1; -
CC HSP; P09097; IAB4.
CC InterPro: IPR002205; DNA_topoisomIV.
CC SMART: SM00521; DNA_topoisomIV; 1.
CC SMART: SM00434; TOP4c; 1.
CC Topoisomerase; Isomerase; ATP-binding; Antibiotic resistance.
CC ACT_SITE 126 126 DNA_CLEAVAGE (BY SIMILARITY).
CC SEQUENCE 862 AA; 95820 MW; E450D81809A10C35 CRC64;
CC -----
DR EMBL; U25640; AAA67068.1; -
DR HSP; P09097; IAB4.
DR InterPro: IPR002205; DNA_topoisomIV.
DR SMART: SM00521; DNA_topoisomIV; 1.
DR SMART: SM00434; TOP4c; 1.
DR Topoisomerase; Isomerase; ATP-binding; Antibiotic resistance.
DR ACT_SITE 126 126 DNA_CLEAVAGE (BY SIMILARITY).
DR SEQUENCE 862 AA; 95820 MW; E450D81809A10C35 CRC64;
DR -----
Query Match 45.6%; Score 41; DB 1; Length 862;
Best Local Similarity 41.2%; Pred. No. 58;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
OY 2 KEVMPSTQSLDALVKEK 18
DB 447 KEILEIEKLDLAKSE 463
|||||:|:|:|:|:|
SMCL_YEAST
ID SMCL_YEAST STANDARD; PRT; 451 AA.
AC Q29406;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)
DE (SHMT).
GN GLYA OR AF0852.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA

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RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., Mckenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glöde A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RA "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -!- FUNCTION: INTERCONVERSION OF SERINE AND GLYCINE.
CC -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + glycine +
CC H(2)O = tetrahydrofolate + L-serine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- PATHWAY: KEY ENZYME IN THE BIOSYNTHESIS OF PURINES, LIPIDS,
CC HORMONES AND OTHER COMPONENTS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SHMT FAMILY.
CC -----
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CC -----
CC EMBL; A5001045; AAB90386.1; -
CC HSP; P07511; 1CJ0.
CC TIGR; AF0852; -.
CC InterPro: IPR001085; SHMT.
CC Pfam; PF00464; SHMT; 1.
CC PROSITE; PS00096; SHMT; 1.
CC Transferrase; Pyridoxal phosphate; One-carbon metabolism;
KW BINDING 252 252 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 451 AA; 50411 MW; 5329CA21149FEF58 CRC64;
SQ
Query Match 45.0%; Score 40.5; DB 1; Length 451;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 10; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
OY 1 KKEVMPSTQSLDALVKEK 19
DB 397 KEEMRAIAEIMDAAIKEK 416
|||||:|:|:|:|:|
SMCL_YEAST
ID SMCL_YEAST STANDARD; PRT; 1225 AA.
AC P32908;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Chromosome segregation protein SMCL (DA-box protein SMCL).
DE SMCL OR CHL10 OR YFL008W.
GN Saccharomyces cerevisiae (Baker's yeast).
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94103320; PubMed=8276886;
RA Strunnikov A.V., Iarionov V.L., Koshland D.;
RA "SMCL: an essential yeast gene encoding a putative head-rod-tail
RT protein is required for nuclear division and defines a new ubiquitous
RL protein family.";
RL J. Cell Biol. 123:1635-1648(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;

```

RX MEDLINE=95400292; PubMed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.,
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:261-268(1995).
CC -!- FUNCTION: INVOLVED IN CHROMOSOME SEGREGATION IN MITOSIS. COULD BE
CC PART OF A CHROMOSOME CONDENSATION MOTOR.
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER WITH SMC2 OR OLIGOMERS.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
CC FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY.
CC -----
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CC -----
DR EMBL; L00602; AAA16595.1; -;
DR EMBL; D50617; BAA09230.1; -;
DR EMBL; D31600; BAA06496.1; -;
DR PIR; A49464; A49464.
DR PIR; S41804; S41804.
DR SGD; S0001886; SMC1.
DR InterPro; IPR001687; ATP_GTP_A.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02483; SMC_C; 1.
DR Pfam; PF02463; SMC_N; 1.
KW Mitosis; ATP-binding; Coiled coil; Nuclear protein.
FT NP_BIND 33 40
FT DOMAIN 173 489
FT DOMAIN 679 1063
FT DOMAIN 1057 1061
FT DOMAIN 1137 1164
FT MUTAGEN 173 173
FT MUTAGEN 458 458
SQ SEQUENCE 1225 AA; 141279 MW; B504017AA0ECCA8C CRC64;

Query Match 45.0%; Score 40.5; DB 1; Length 1225;
Best Local Similarity 36.7%; Pred. No. le+02; 5; Indels 11; Gaps 1;
Matches 11; Conservative 3; Mismatches 5;
QY 1 KKEVMSIOSL-----DALVKEKK 19
Db 753 KEIQPKITELKKKLDLLENTKDLNVLKEKE 782
:||:| | | | |
| | | | |

Search completed: September 4, 2002, 17:05:07
Job time: 1133 sec

sw protein - protein search, using sw model

Run on: September 4, 2002, 17:04:23 ; Search time 166.13 Seconds
(without alignments)
28 128 Million cell updates/sec

```

US-09-821-726-5
Title:
perfect score: 90
Sequence: 1 KKEVMSIQSLDALVREKK 19
Scoring table:
BLOSUM62
Gap 10 0 . Gapext 0.5

```

Searched: 763338 seqs, 245939087 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

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Database : Pending_Patents_AA_New.*
1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, N is the number of results of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	85	94.4	185	5	US-09-091-150-211	Sequence 211, App
2	85	94.4	185	5	US-09-720-533-49	Sequence 49, Appl
3	85	94.4	185	6	US-10-119-480-148	Sequence 148, App
4	85	94.4	185	6	US-10-216-159A-148	Sequence 148, App
5	85	94.4	185	6	US-10-216-162-148	Sequence 148, App
6	85	94.4	185	6	US-10-216-163-148	Sequence 148, App
7	85	94.4	185	6	US-10-216-164-148	Sequence 148, App
8	85	94.4	185	6	US-10-216-165-148	Sequence 148, App
9	85	94.4	185	6	US-10-216-166-148	Sequence 148, App
10	85	94.4	185	6	US-10-216-167-148	Sequence 148, App
11	85	94.4	185	6	US-10-216-168-148	Sequence 148, App
12	85	94.4	185	6	US-10-216-169-148	Sequence 148, App
13	85	94.4	185	6	US-10-218-849-148	Sequence 148, App
14	85	94.4	185	6	US-10-218-930-148	Sequence 148, App
15	85	94.4	185	6	US-10-219-003-148	Sequence 148, App
16	85	94.4	185	6	US-10-218-612-148	Sequence 148, App
17	85	94.4	185	6	US-10-219-003-148	Sequence 148, App
18	85	94.4	185	6	US-10-218-956-148	Sequence 148, App
19	85	94.4	185	6	US-10-219-010-148	Sequence 148, App
20	85	94.4	185	6	US-10-218-765-148	Sequence 148, App
21	85	94.4	185	6	US-10-218-784-148	Sequence 148, App
22	85	94.4	185	6	US-10-219-061-148	Sequence 148, App
23	85	94.4	185	6	US-10-219-062-148	Sequence 148, App
24	85	94.4	185	6	US-10-219-063-148	Sequence 148, App
25	85	94.4	185	6	US-10-219-064-148	Sequence 148, App
26	85	94.4	185	6	US-10-219-065-148	Sequence 148, App
27	85	94.4	185	6	US-10-219-066-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-991-150-211

```

Sequence 211, Application US/0999911150
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Tr
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730P1C48
CURRENT APPLICATION NUMBER: US/09/99911150
CURRENT FILING DATE: 2001-11-16
Prior Application removed - See File
NUMBER OF SEQ ID NOS: 532
SEQ ID NO 211
LENGTH: 185
TYPE: PRT
ORGANISM: Homo sapiens
ns-09-991-150-211

```

0. 10 0000 95. DR 5. Length 185;

	Query Match	Score 87, Bkgs.	Gaps 0;
	Best Local Similarity	Pred. No. 3.6e-06;	Mismatches 0; Indels 0;
	Conservative	Matches 18;	Gaps 0;

2 KEVMP SIQSLDALVKEK 19

88 KEVMP SIOS DALVKEK 105

RESULT 2
US-09-720-533-49
; Sequence 49, Application US/09720533
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: GORGONE, Gina A.
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AKERBLUM, Ingrid E.
; APPLICANT: AU-FOUNG, Janice
; APPLICANT: YUE, Henry
; APPLICANT: PATTERSON, Chandra
; APPLICANT: REDDY, Roopa
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PP-0541 PCT
; CURRENT APPLICATION NUMBER: US/09720,533
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte Clone No: 2593853
US-09-720-533-49

Query Match 94.4%; Score 85; DB 5; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 3
US-10-119-480-148
; Sequence 148, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-119-480-148

Query Match 94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 4
US-10-216-159A-148
; Sequence 148, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105
RESULT 5
US-10-216-162-148
; Sequence 148, Application US/10216162
; GENERAL INFORMATION:

us-09-821-726-5.rapn

Thu Sep 5 11:23:42 2002

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC2
; CURRENT APPLICATION NUMBER: US/10/216,162
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match          94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKKK 19
   |||||
Db 88 KEVMPISQSLDALVKKK 105

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC5
; CURRENT APPLICATION NUMBER: US/10/216,164
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

Query Match          94.4%; Score 85; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKKK 19
   |||||
Db 88 KEVMPISQSLDALVKKK 105

RESULT 6
US-10-216-163-148
; Sequence 148, Application US/10216163
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163

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; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-164-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 8
 US-10-216-165-148
 ; Sequence 148, Application US/10216165
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C7
 ; CURRENT APPLICATION NUMBER: US/10/216,165
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-165-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 10
 US-10-216-167-148
 ; Sequence 148, Application US/10216167
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 9
 US-10-216-166-148
 ; Sequence 148, Application US/10216166
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C9
 ; CURRENT APPLICATION NUMBER: US/10/216,166
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-216-166-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEVMPISQSLDALVKEKK 19
 Db 88 KEVMPISQSLDALVKEKK 105

RESULT 10
 US-10-216-167-148
 ; Sequence 148, Application US/10216167
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc

QY 2 KEVMPSIQSLDALVKEK 19
 |||||
 db 88 KEVMPSIQSLDALVKEK 105

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RESULT 11
US-10-216-168-148
; Sequence 148, Application US/10216168
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSFERRED
; TITLE OF INVENTION: ACIDS ENCODING
; FILE REFERENCE: P3530P1C10
; CURRENT APPLICATION NUMBER: US/10/216168
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480

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RESULT 13
 US-10-218-849-148
 ; Sequence 148, Application US/10218849
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC11
 ; CURRENT APPLICATION NUMBER: US/10/218,849
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-849-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19
 |||||

Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 14
 US-10-218-930-148
 ; Sequence 148, Application US/10218930
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC13
 ; CURRENT APPLICATION NUMBER: US/10/218,930
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-218-930-148

Query Match 94.4%; Score 85; DB 6; Length 185;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPSTQSLDALVKEKK 19
 |||||

Db 88 KEVMPSTQSLDALVKEKK 105

RESULT 15
 US-10-219-003-148
 ; Sequence 148, Application US/10219003
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; CURRENT FILING DATE: 2002-08-12
 ; Prior Application Number: 10/119,480
 ; Prior Filing Date: 2002-04-09
 ; Prior Application Number: 60/059113
 ; Prior Filing Date: 1997-09-17
 ; Prior Application Number: 60/062287
 ; Prior Filing Date: 1997-10-17
 ; Prior Application Number: 60/063549
 ; Prior Filing Date: 1997-10-28
 ; Prior Application Number: 60/064103
 ; Prior Filing Date: 1997-10-31
 ; Prior Application Number: 60/069873
 ; Prior Filing Date: 1997-12-17
 ; Prior Application Number: 60/078910
 ; Prior Filing Date: 1998-03-20
 ; Prior Application Number: 60/079294
 ; Prior Filing Date: 1998-03-25
 ; Prior Application Number: 60/079656
 ; Prior Filing Date: 1998-03-26
 ; Prior Application Number: 60/079728
 ; Prior Filing Date: 1998-03-27
 ; Prior Application Number: 60/081819
 ; Prior Filing Date: 1998-04-15
 ; Prior Application Number: 60/081955
 ; Prior Filing Date: 1998-04-15
 ; Prior Application Number: 60/082804
 ; Prior Filing Date: 1998-04-22
 ; Prior Application Number: 60/084441
 ; Prior Filing Date: 1998-05-06
 ; Prior Application Number: 60/085323
 ; Prior Filing Date: 1998-05-13
 ; Prior Application Number: 60/085579
 ; Prior Filing Date: 1998-05-15
 ; Prior Application Number: 60/086392
 ; Prior Filing Date: 1998-05-22
 ; Prior Application Number: 60/089532
 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089538
 ; Prior Filing Date: 1998-06-17
 ; Prior Application Number: 60/089905
 ; Prior Filing Date: 1998-06-18
 ; Prior Application Number: 60/090472
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090557
 ; Prior Filing Date: 1998-06-24
 ; Prior Application Number: 60/090691
 ; Prior Filing Date: 1998-06-25
 ; Prior Application Number: 60/090695
 ; Prior Filing Date: 1998-06-25

PRIOR APPLICATION NUMBER: 60/091982	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/095302	
PRIOR FILING DATE: 1998-08-04	
PRIOR APPLICATION NUMBER: 60/095318	
PRIOR FILING DATE: 1998-08-04	
PRIOR APPLICATION NUMBER: 60/095916	
PRIOR FILING DATE: 1998-08-10	
PRIOR APPLICATION NUMBER: 60/096146	
PRIOR FILING DATE: 1998-08-11	
PRIOR APPLICATION NUMBER: 60/096791	
PRIOR FILING DATE: 1998-08-17	
PRIOR APPLICATION NUMBER: 60/097986	
PRIOR FILING DATE: 1998-08-26	
PRIOR APPLICATION NUMBER: 60/098544	
PRIOR FILING DATE: 1998-08-31	
PRIOR APPLICATION NUMBER: 60/099596	
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PRIOR APPLICATION NUMBER: 60/099598	
PRIOR FILING DATE: 1998-09-09	
PRIOR APPLICATION NUMBER: 60/099803	
PRIOR FILING DATE: 1998-09-10	
PRIOR APPLICATION NUMBER: 60/099811	
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PRIOR APPLICATION NUMBER: 60/099812	
PRIOR FILING DATE: 1998-09-10	
PRIOR APPLICATION NUMBER: 60/099816	
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PRIOR FILING DATE: 1998-09-15	
PRIOR APPLICATION NUMBER: 60/100627	
PRIOR FILING DATE: 1998-09-16	
PRIOR APPLICATION NUMBER: 60/100848	
PRIOR FILING DATE: 1998-09-18	
PRIOR APPLICATION NUMBER: 60/100919	
PRIOR FILING DATE: 1998-09-17	
PRIOR APPLICATION NUMBER: 60/101477	
PRIOR FILING DATE: 1998-09-23	
PRIOR APPLICATION NUMBER: 60/101738	
PRIOR FILING DATE: 1998-09-24	
PRIOR APPLICATION NUMBER: 60/101741	
PRIOR FILING DATE: 1998-09-24	
PRIOR APPLICATION NUMBER: 60/101786	
PRIOR FILING DATE: 1998-09-25	
PRIOR APPLICATION NUMBER: 60/101916	
PRIOR FILING DATE: 1998-09-24	
PRIOR APPLICATION NUMBER: 60/101922	
PRIOR FILING DATE: 1998-09-24	
PRIOR APPLICATION NUMBER: 60/106178	
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PRIOR APPLICATION NUMBER: 60/106464	
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PRIOR APPLICATION NUMBER: 60/106905	
PRIOR FILING DATE: 1998-11-03	
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PRIOR APPLICATION NUMBER: 60/113296	
PRIOR FILING DATE: 1998-12-22	
PRIOR APPLICATION NUMBER: 60/113605	
PRIOR FILING DATE: 1998-12-23	
PRIOR APPLICATION NUMBER: 60/113621	

QY

2 KEVMPSIQSILDALVKKEK 19
| | | | | | | | | | | | | | |
QB

88 KEVMPSIQSILDALVKKEK 105

Search completed: September 4, 2002, 17:04:23

Thu Sep 5 11:23:42 2002

Job time: 1154 sec

us-09-821-726-5.rapn

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:59:20 ; Search time 704.77 Seconds
(without alignments)
9.489 Million cell updates/sec

Title: US-09-821-726-5

Perfect score: 90

Sequence: 1 KKEVMPSTQSLDALVKEKK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
- 9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
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- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	19	22	US-09-821-726-5
2	90	100.0	42	22	US-09-821-726-6
3	90	100.0	185	22	US-09-821-726-13
4	85	94.4	150	13	US-08-906-708-24
5	85	94.4	182	20	US-09-684-524-212
6	85	94.4	182	24	US-10-050-704-212
7	85	94.4	185	1	PCT-US98-16318-18
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 13, Appl
					Sequence 24, Appl
					Sequence 212, App
					Sequence 218, Appl

8	85	94.4	185	15	US-09-130-189-18	Sequence 18, Appl
9	85	94.4	185	20	US-09-684-524-105	Sequence 105, App
10	85	94.4	185	21	US-09-709-238-211	Sequence 211, App
11	85	94.4	185	21	US-09-746-783-146	Sequence 146, App
12	85	94.4	185	23	US-09-941-992-211	Sequence 211, App
13	85	94.4	185	23	US-09-989-279-211	Sequence 211, App
14	85	94.4	185	23	US-09-989-293A-211	Sequence 211, App
15	85	94.4	185	23	US-09-989-721-211	Sequence 211, App
16	85	94.4	185	23	US-09-989-722-211	Sequence 211, App
17	85	94.4	185	23	US-09-989-723-211	Sequence 211, App
18	85	94.4	185	23	US-09-989-724-211	Sequence 211, App
19	85	94.4	185	23	US-09-989-725-211	Sequence 211, App
20	85	94.4	185	23	US-09-989-726-211	Sequence 211, App
21	85	94.4	185	23	US-09-989-727-211	Sequence 211, App
22	85	94.4	185	23	US-09-989-728-211	Sequence 211, App
23	85	94.4	185	23	US-09-989-729A-211	Sequence 211, App
24	85	94.4	185	23	US-09-989-730-211	Sequence 211, App
25	85	94.4	185	23	US-09-989-731-211	Sequence 211, App
26	85	94.4	185	23	US-09-989-732-211	Sequence 211, App
27	85	94.4	185	23	US-09-989-734-211	Sequence 211, App
28	85	94.4	185	23	US-09-989-735-211	Sequence 211, App
29	85	94.4	185	23	US-09-989-862-211	Sequence 211, App
30	85	94.4	185	23	US-09-990-427-211	Sequence 211, App
31	85	94.4	185	23	US-09-990-436-211	Sequence 211, App
32	85	94.4	185	23	US-09-990-437-211	Sequence 211, App
33	85	94.4	185	23	US-09-990-438-211	Sequence 211, App
34	85	94.4	185	23	US-09-990-439-211	Sequence 211, App
35	85	94.4	185	23	US-09-990-440-211	Sequence 211, App
36	85	94.4	185	23	US-09-990-441-211	Sequence 211, App
37	85	94.4	185	23	US-09-990-442-211	Sequence 211, App
38	85	94.4	185	23	US-09-990-443-211	Sequence 211, App
39	85	94.4	185	23	US-09-990-444-211	Sequence 211, App
40	85	94.4	185	23	US-09-990-456-211	Sequence 211, App
41	85	94.4	185	23	US-09-990-562-211	Sequence 211, App
42	85	94.4	185	23	US-09-990-711-211	Sequence 211, App
43	85	94.4	185	23	US-09-990-726-211	Sequence 211, App
44	85	94.4	185	23	US-09-991-073-211	Sequence 211, App
45	85	94.4	185	23	US-09-991-157-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-821-726-5
; Sequence 5, Application US/09821726
; GENERAL INFORMATION:
; APPLICANT: MARTIN, TERENCE E.
; APPLICANT: TOBACK, F. GARY
; APPLICANT: POWELL, C. THOMAS
; APPLICANT: AGARWAL, KAN
; TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
; FILE REFERENCE: 21459/90913
; CURRENT APPLICATION NUMBER: US/09/821,726
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-821-726-5

Query Match 100.0%; Score 90; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKEVMPSTQSLDALVKEKK 19
Db 1 KKEVMPSTQSLDALVKEKK 19

Query Match	94.4%	Score 85;	DB 20;	Length 182;
Best Local Similarity	100.0%	Pred. No. 1.7e-05;		
Matches	18;	Conservative	0;	Mismatches 0; Indels
QY	2	KEVMPISQSLDALVKEKK	19	
Db	88	KEVMPISQSLDALVKEKK	105	

RESULT 8

US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 94.4%; Score 85; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 9

US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 94.4%; Score 85; DB 20; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 10
US-09-709-238-211
; Sequence 211, Application US/09709238
; GENERAL INFORMATION:

RESULT 6

US-10-050-704-212
; Sequence 212, Application US/10050704
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/10/050,704
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 09/684,524
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 212
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-704-212

Query Match 94.4%; Score 85; DB 24; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 7

PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 94.4%; Score 85; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

APPLICANT: Baker, Kevin
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Yuan, Jian
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2730R1C1
CURRENT APPLICATION NUMBER: US/09/709,238
PRIORITY FILING DATE: 2000-11-08
PRIORITY APPLICATION NUMBER: PCT/US99/12252
PRIORITY FILING DATE: 1999-06-02
PRIORITY APPLICATION NUMBER: US 60/087,607
PRIORITY FILING DATE: 1998-06-02
PRIORITY APPLICATION NUMBER: US 60/087,609
PRIORITY FILING DATE: 1998-06-02
PRIORITY APPLICATION NUMBER: US 60/087,759
PRIORITY FILING DATE: 1998-06-03
PRIORITY APPLICATION NUMBER: US 60/087,827
PRIORITY FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: US 60/088,021
PRIORITY FILING DATE: 1998-06-04
PRIORITY APPLICATION NUMBER: US 60/088,025
PRIORITY FILING DATE: 1998-06-04
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PRIORITY FILING DATE: 1998-06-04
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PRIORITY FILING DATE: 1998-06-04
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PRIORITY FILING DATE: 1998-06-05
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PRIORITY FILING DATE: 1998-06-05
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PRIORITY FILING DATE: 1998-06-05
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PRIORITY APPLICATION NUMBER: US 60/090,429
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PRIORITY FILING DATE: 1998-06-23
PRIORITY APPLICATION NUMBER: US 60/090,444
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,445
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,461
PRIORITY FILING DATE: 1998-06-24
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PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,535
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,538
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,540
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,557
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: US 60/090,676
PRIORITY FILING DATE: 1998-06-25


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; PRIOR APPLICATION NUMBER: US 60/090,678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,862
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,863
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/091,358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,486
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,646
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,673
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/091,982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/092,182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

Query Match 94.4%; Score 85; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 11
US-09-746-783-146
; Sequence 146, Application US/09746783
; GENERAL INFORMATION:
; APPLICANT: McCoy, Kenneth
; LaVallie, Edward R.
; Racie, Lisa A.
; Treacy, Maurice
; Spaulding, Vikki
; Agostino, Michael J.

; PRIOR APPLICATION NUMBER: US 60/090,678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,688
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,862
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/090,863
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 60/091,358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: US 60/091,478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,646
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,673
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/091,982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/092,182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

Query Match 94.4%; Score 85; DB 21; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKEKK 19
Db 88 KEVMPISQSLDALVKEKK 105

RESULT 12
US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; Baker, Kevin P.
; Botstein, David
; Desnoyers, Luc
; Eaton, Dan L.
; Ferrara, Napoleone
; Fong, Sherman
; Gerber, Hanspeter
; Gerritsen, Mary E.
; Goddard, Audrey
; Godowski, Paul J.
; Grimaldi, J. Christopher
; Gurney, Austin L.
; Kljavin, Ivar J.
; Napier, Mary A.
; Pan, James
; Paoni, Nicholas F.
; Roy, Margaret Ann
; Stewart, Timothy A.
; Tumas, Daniel
; Watanabe, Colin K.
; Williams, P. Mickey

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; ENCODING THEM
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,783
; FILING DATE: 21-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Milasincic, Debra J.
; REGISTRATION NUMBER: 46,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 146:
; US-09-746-783-146
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730Plc1
CURRENT APPLICATION NUMBER: US/09/941,992
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690

; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
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; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25

; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;
Best Local Similarity: 100.0%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKKK 19

|||||

Db 88 KEVMPISQSLDALVKKK 105

RESULT 14

US-09-989-293A-211
; Sequence 211, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

[illegible]

;
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 94.4%; Score 85; DB 23; Length 185;

Best Local Similarity 100.0%; Pred.No. 1.7e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVMPISQSLDALVKKK 19

|||||

Db 88 KEVMPISQSLDALVKKK 105

RESULT 15

US-09-989-721-211

; Sequence 211, Application US/09989721

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P27301C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599

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: PRIORITY APPLICATION NUMBER: 60/091633
: PRIORITY FILING DATE: 1998-07-02
: PRIORITY APPLICATION NUMBER: 60/091978
: PRIORITY FILING DATE: 1998-07-07
: PRIORITY APPLICATION NUMBER: 60/091982
: PRIORITY FILING DATE: 1998-07-07
: PRIORITY APPLICATION NUMBER: 60/092182
: PRIORITY FILING DATE: 1998-07-09
: PRIORITY APPLICATION NUMBER: 60/092472

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Query Match	94.4%;	Score 85;	DB 23;	Length 185;
Best Local Similarity	100.0%;	Pred. No. 1.7e-05;		
Matches 18:	Conservative 0;	Mismatches 0;	Indels	

Qy 2 KEVPSIQSLDALVKEK 19
 |||||
 db 88 KEVPSIQSLDALVKEK 105

Search completed: September 4, 2002, 16:59:20
Job time: 1041 sec

QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 QY 181 DTVEN 185
 Db 181 DTVEN 185

RESULT 2

US-09-720-533-49
 ; Sequence 49, Application US/09720533
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE PHARMACEUTICALS, INC.
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: GORGONE, Gina A.
 ; APPLICANT: CORLEY, Neil C.
 ; APPLICANT: GUEGLER, Karl J.
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: AKERBLOM, Ingrid E.
 ; APPLICANT: AU-YOUNG, Janice
 ; APPLICANT: YUE, Henry
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: REDDY, Roopa
 ; APPLICANT: HILLMAN, Jennifer L.
 ; APPLICANT: BANDMAN, Olga
 ; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
 ; FILE REFERENCE: PF-0541 PCT
 ; CURRENT APPLICATION NUMBER: US/09/720,533
 ; CURRENT FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
 ; PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
 ; NUMBER OF SEQ ID NOS: 268
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 49
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte Clone No: 2593853
 US-09-720-533-49

Query Match 99.0%; Score 984; DB 5; Length 185;
 Best Local Similarity 98.9%; Pred. No. 1.6e-95;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
 Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
 QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 QY 181 DTVEN 185
 Db 181 DTVEN 185

RESULT 3

US-10-119-480-148

; Sequence 148, Application US/10119480
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C1
 ; CURRENT APPLICATION NUMBER: US/10/119,480
 ; CURRENT FILING DATE: 2002-04-09
 ; NUMBER OF SEQ ID NOS: 246
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 148
 ; LENGTH: 185
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-119-480-148

Query Match 99.0%; Score 984; DB 6; Length 185;
 Best Local Similarity 98.9%; Pred. No. 1.6e-95;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
 Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
 QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
 QY 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 Db 121 YSNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQASLFFYSGTCTYTSVLWIVDISFCG 180
 QY 181 DTVEN 185
 Db 181 DTVEN 185

RESULT 4

US-10-216-159A-148
 ; Sequence 148, Application US/10216159A
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530P1C6
 ; CURRENT APPLICATION NUMBER: US/10/216,159A
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60

Qy 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKGGPPPKGLM 120

Qy 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180

Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 6
US-10-216-163-148
Sequence 148, Application US/10216163
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Victoria
APPLICANT: Smith, Victor
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C3
CURRENT APPLICATION NUMBER: US/10/216,163
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 148
LENGTH: 185
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-159A-148

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60

Qy 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKGGPPPKGLM 120

Qy 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180

Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 5
US-10-216-162-148
Sequence 148, Application US/10216162
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Victoria
APPLICANT: Smith, Victor
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C2
CURRENT APPLICATION NUMBER: US/10/216,162
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-12-17

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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGQGSVSVNNEHNVANDNNGWDSW 60
   |||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGQGSVSVNNEHNVANDNNGWDSW 60
   |||||
QY 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKELKQGGPPPKGLM 120
   |||||
Db 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKELKQGGPPPKGLM 120
   |||||
QY 121 YSVNPNKVDLDSKFGKNTIANMCRGIPITYMAEMOEASLFFYSGTCYTTSLVLIWIDISFCG 180
   |||||
Db 121 YSVNPNKVDLDSKFGKNTIANMCRGIPITYMAEMOEASLFFYSGTCYTTSLVLIWIDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 7
US-10-216-164-148
; Sequence 148, Application US/10216164
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C5
; CURRENT APPLICATION NUMBER: US/10/216,164
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
```

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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-164-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGQGSVSVNNEHNVANDNNGWDSW 60
   |||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNNDNAGSGQGSVSVNNEHNVANDNNGWDSW 60
   |||||
QY 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKELKQGGPPPKGLM 120
   |||||
Db 61 NSIWDYGNCGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKELKQGGPPPKGLM 120
   |||||
QY 121 YSVNPNKVDLDSKFGKNTIANMCRGIPITYMAEMOEASLFFYSGTCYTTSLVLIWIDISFCG 180
   |||||
Db 121 YSVNPNKVDLDSKFGKNTIANMCRGIPITYMAEMOEASLFFYSGTCYTTSLVLIWIDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 8
US-10-216-165-148
; Sequence 148, Application US/10216165
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C7
; CURRENT APPLICATION NUMBER: US/10/216,165
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
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; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-166-148

Query Match      99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSYNNEHNVANVDNNNGWDSW 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSYNNEHNVANVDNNNGWDSW 60

QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSCTCTTSLVLIWIVDISFCG 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSCTCTTSLVLIWIVDISFCG 180

QY 181 DTVEN 185
    |||||
Db 181 DTVEN 185

RESULT 10
US-10-216-167-148
; Sequence 148, Application US/10216167
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C4
; CURRENT APPLICATION NUMBER: US/10/216,167
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185

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; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-148

Query Match      99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSYNNEHNVANVDNNNGWDSW 60
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKFTIVFAGLLGVFLAPALANYINVDNDNNAGSGQSVSYNNEHNVANVDNNNGWDSW 60

QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSCTCTTSLVLIWIVDISFCG 180
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPITYMAEEMQEAASLFFYSCTCTTSLVLIWIVDISFCG 180

QY 181 DTVEN 185
    |||||
Db 181 DTVEN 185

RESULT 9
US-10-216-166-148
; Sequence 148, Application US/10216166
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C9
; CURRENT APPLICATION NUMBER: US/10/216,166
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-168-148

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[illegible]

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; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-930-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDDNNNGWDSW 60
QY 61 NSIWDYGNNGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
Db 61 NSIWDYGNNGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 15
US-10-219-003-148
; Sequence 148, Application US/10219003
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22

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RESULT 13
US-10-218-849-148
; Sequence 148, Application US/10218849
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-148

Query Match          99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQGQSVSVNNEHNVANVDDNNNGWDSW 60
QY 61 NSIWDYGNNGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
Db 61 NSIWDYGNNGFAATRLFOKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 14
US-10-218-930-148
; Sequence 148, Application US/10218930
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC13
; CURRENT APPLICATION NUMBER: US/10/218,930
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 148

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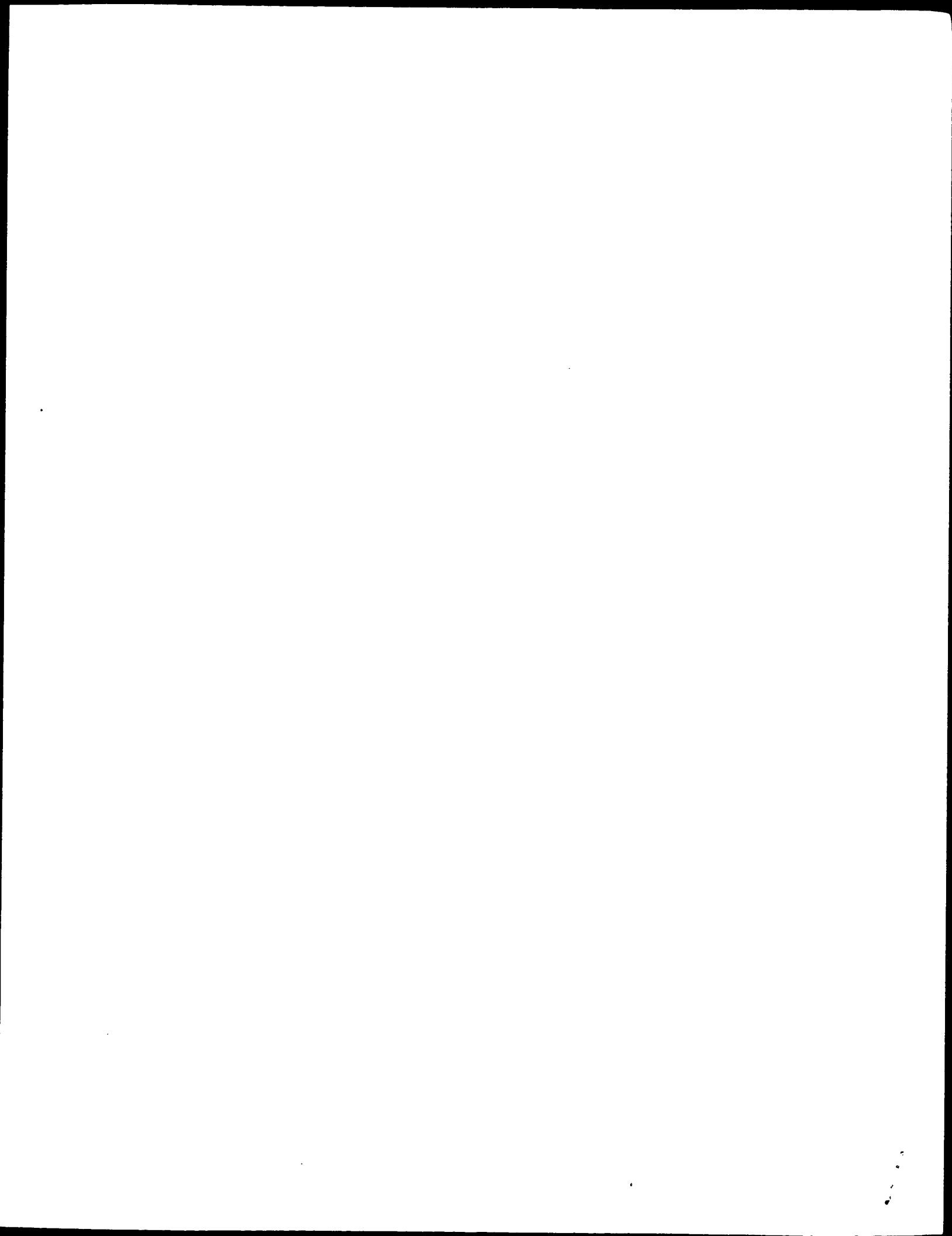
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;	PRIOR FILING DATE:	1998-10-29
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;	PRIOR FILING DATE:	1998-10-30
;	PRIOR APPLICATION NUMBER:	60/106905
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;	PRIOR APPLICATION NUMBER:	60/112422
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;	PRIOR APPLICATION NUMBER:	60/113296
;	PRIOR FILING DATE:	1998-12-22
;	PRIOR APPLICATION NUMBER:	60/113605
;	PRIOR FILING DATE:	1998-12-23
;	PRIOR APPLICATION NUMBER:	60/113621
;	PRIOR FILING DATE:	1998-12-23
;	PRIOR APPLICATION NUMBER:	60/115558
;	PRIOR FILING DATE:	1999-01-12
;	PRIOR APPLICATION NUMBER:	60/115565
;	PRIOR FILING DATE:	1999-01-12
;	PRIOR APPLICATION NUMBER:	60/115733
;	PRIOR FILING DATE:	1999-01-12
;	PRIOR APPLICATION NUMBER:	60/119549
;	PRIOR FILING DATE:	1999-02-10
;	PRIOR APPLICATION NUMBER:	60/123618
;	PRIOR FILING DATE:	1999-03-10
;	PRIOR APPLICATION NUMBER:	60/125259
;	PRIOR FILING DATE:	1999-03-19
;	PRIOR APPLICATION NUMBER:	60/125775
;	PRIOR FILING DATE:	1999-03-23
;	PRIOR APPLICATION NUMBER:	60/126773
;	PRIOR FILING DATE:	1999-03-29
;	PRIOR APPLICATION NUMBER:	60/127887
;	PRIOR FILING DATE:	1999-04-05
;	PRIOR APPLICATION NUMBER:	60/130232
;	PRIOR FILING DATE:	1999-04-21
;	PRIOR APPLICATION NUMBER:	60/131022
;	PRIOR FILING DATE:	1999-04-26
;	PRIOR APPLICATION NUMBER:	60/131270
;	PRIOR FILING DATE:	1999-04-27
;	PRIOR APPLICATION NUMBER:	60/131291
;	PRIOR FILING DATE:	1999-04-27
;	PRIOR APPLICATION NUMBER:	60/131445
;	PRIOR FILING DATE:	1999-04-28
;	PRIOR APPLICATION NUMBER:	60/134287
;	PRIOR FILING DATE:	1999-05-14
;	PRIOR APPLICATION NUMBER:	60/140650
;	PRIOR FILING DATE:	1999-06-22
;	PRIOR APPLICATION NUMBER:	60/140723
;	PRIOR FILING DATE:	1999-06-22
;	PRIOR APPLICATION NUMBER:	60/141037
;	PRIOR FILING DATE:	1999-06-23
;	PRIOR APPLICATION NUMBER:	60/144758
;	PRIOR FILING DATE:	1999-07-20
;	PRIOR APPLICATION NUMBER:	60/145698
;	PRIOR FILING DATE:	1999-07-26
;	PRIOR APPLICATION NUMBER:	60/146222
;	PRIOR FILING DATE:	1999-07-28
;	PRIOR APPLICATION NUMBER:	60/146963
;	PRIOR FILING DATE:	1999-08-03
;	PRIOR APPLICATION NUMBER:	60/149320
;	PRIOR FILING DATE:	1999-08-17
;	PRIOR APPLICATION NUMBER:	60/149638
;	PRIOR FILING DATE:	1999-08-17
;	PRIOR APPLICATION NUMBER:	60/151733
;	PRIOR FILING DATE:	1999-08-31

; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match 99.0%; Score 984; DB 6; Length 185;
Best Local Similarity 98.9%; Pred. No. 1.6e-95;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGQQSVSVNNEHNVANVDNNNGWDSW	60
Db	1	MKFTIVFAGLLGVFLAPALANYNINVDNNAGSGQQSVSVNNEHNVANVDNNNGWDSW	60
QY	61	NSIWDYGNCGFAATRLFOKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM	120
Db	61	NSIWDYGNCGFAATRLFOKKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKGGPPKGLM	120
QY	121	YSVNPKNVDLKSFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG	180
Db	121	YSVNPKNVDLKSFGKNIANMCRGIPTYMAEEMQEAFLFFYSGTCYTTSVLWIVDISFCG	180
QY	181	DTVEN 185	
Db	181	DTVEN 185	

Search completed: September 4, 2002, 17:04:24
Job time: 1155 sec



Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 2

PCT-US98-16318-18
; Sequence 18, Application PC/TUS9816318
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: PCT/US98/16318
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-16318-18

Query Match 99.0%; Score 984; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

Query Match 99.0%; Score 984; DB 1; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 3

US-09-130-189-18
; Sequence 18, Application US/09130189
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.

; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: G16051A
; CURRENT APPLICATION NUMBER: US/09/130,189
; CURRENT FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-130-189-18

Query Match 99.0%; Score 984; DB 15; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 4

US-09-684-524-105
; Sequence 105, Application US/09684524
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 62 Human Secreted Proteins
; FILE REFERENCE: P2039P1
; CURRENT APPLICATION NUMBER: US/09/684,524
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08979
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,693
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/130,991
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-684-524-105

Query Match 99.0%; Score 984; DB 20; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNAGSGQGSVSVNNEHNVANVDNNNGWDSW 60
QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Db 121 YSVNPNKVDLDSKFGKNIANMCRGIPTVMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180

Db 121 YSNPNKVDLSKFGKNIAMCKGIPETYMAEEMQENSLFFYSGTCYTTSVLWIVDSFCG 180

OY 181 DTVEN 185

|||||

Db 181 DTVEN 185

RESULT 5

US-09-709-238-211

; Sequence 211, Application US/09709238

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Chen, Jian

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Collin K.

; APPLICANT: Wood, William I.

; APPLICANT: Yuan, Jean

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same

; FILE REFERENCE: P2730R1C1

; CURRENT APPLICATION NUMBER: US/09/709,238

; CURRENT FILING DATE: 2000-11-08

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: 1999-06-02

; PRIOR APPLICATION NUMBER: US 60/087,607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,609

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: US 60/087,759

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: US 60/087,827

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,021

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,025

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,028

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,029

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,030

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,033

; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: US 60/088,326

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,167

; PRIOR FILING DATE: 1988-06-05

; PRIOR APPLICATION NUMBER: US 60/088,202

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,212

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,217

; PRIOR FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: US 60/088,655

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: US 60/088,722

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,730

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,734

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,738

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,740

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,741

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,742

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,810

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,810

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,811

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,824

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,825

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,826

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: US 60/088,858

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,861

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,863

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/088,876

; PRIOR FILING DATE: 1998-06-11

; PRIOR APPLICATION NUMBER: US 60/089,090

; PRIOR FILING DATE: 1998-06-12

; PRIOR APPLICATION NUMBER: US 60/089,105

; PRIOR FILING DATE: 1998-06-12

; PRIOR APPLICATION NUMBER: US 60/089,440

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,512

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,514

; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: US 60/089,532

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,538

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,598

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,599

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,600

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,653

; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: US 60/089,801

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,907

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,908

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: US 60/089,947

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/089,948

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/089,952

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 60/090,246

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,252

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,254

; PRIOR FILING DATE: 1998-06-22

; PRIOR APPLICATION NUMBER: US 60/090,355

; PRIOR FILING DATE: 1998-06-23

; PRIOR APPLICATION NUMBER: US 60/090,429

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,431

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,435

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,349

; PRIOR FILING DATE: 1998-06-23

; PRIOR APPLICATION NUMBER: US 60/090,444

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,445

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,461

; PRIOR FILING DATE: 1998-06-24

; PRIOR APPLICATION NUMBER: US 60/090,472

PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 60/090,676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,688
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,862
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/090,863
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 60/091,358
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,486
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: US 60/091,626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,628
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,646
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,673
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/091,978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/091,982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: US 60/092,182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/092,472
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/093,339
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30

Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTTIFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
|||||
Db 1 MKFTTIFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60
|||||
QY 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

Db 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
QY 121 YSVNPNKVDLSKFGKNIANMCRGIPTTYMAEEMQEASLFFYSGTCYTTSVLWTVDISFCG 180
|||||
Db 121 YSVNPNKVDLSKFGKNIANMCRGIPTTYMAEEMQEASLFFYSGTCYTTSVLWTVDISFCG 180
QY 181 DTVEN 185
|||||
Db 181 DTVEN 185

RESULT 6

US-09-746-783-146
Sequence 146, Application US/09746783

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

NUMBER OF SEQUENCES: 231

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/746,783

FILING DATE: 21-Dec-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Milasincic, Debra J.

REGISTRATION NUMBER: 46,931

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 146:

US-09-746-783-146

Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTTIFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60

Db 1 MKFTTIFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANVDNNGWDSW 60

QY 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

Db 61 NSIWDYNGGFAATRLFOKKTCTIVHKMKVMPISQSLDALVKEKKLOGKGGPPPKGLM 120

QY 121 YSVNPKVDDLSKFGKNIANCMRGIPITYMAEEMOEASLFFYSYGTCTTTSVLWIVDISFCG 180
DB 121 YSVNPKVDDLSKFGKNIANCMRGIPITYMAEEMOEASLFFYSYGTCTTTSVLWIVDISFCG 180
QY 181 DTVEN 185
DB 181 DTVEN 185

RESULT 7

US-09-941-992-211
; Sequence 211, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhenli
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941.992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025

; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-19

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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;

Best Local Similarity 98.9%; Pred. No. 5.8e-102;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYINVDNNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
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DB 1 MKFTIVFAGLLGVFLAPALANYINVDNNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
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|||||
Db 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPSTQSLDALYKCKLQKGGPGPPKGLM 120
|||||
QY 121 YSVNPNKVDDLSKFGKNTIANMCRGIPTTYMAEQEASLFFYSGTCYTTSVLWIVDISECG 180
|||||
Db 121 YSVNPNKVDDLSKFGKNTIANMCRGIPTTYMAEQEASLFFYSGTCYTTSVLWIVDISECG 180
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QY 181 DTVEN 185
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Db 181 DTVEN 185
|||||
RESULT 8
US-09-989-279-211
; Sequence 211, Application US/09989279
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-06-02

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23	PRIOR APPLICATION NUMBER: 60/088212
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PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09	PRIOR APPLICATION NUMBER: 60/092472
PRIOR FILING DATE: 1998-07-09	PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;

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Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db 61 NSIWDYNGFAATRLFOKKTCTIVHKMKKEVMPSTQSLDALVKEKKLQKGGPPPKGLM 120
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QY 181 DTVEN 185
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Db 181 DTVEN 185
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RESULT 9
US-09-989-293A-211
; Sequence 211, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182

;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNNAGSGQGSVSVNNEHNVANVDNNGWDSW 60
|||||
DB 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNNAGSGQGSVSVNNEHNVANVDNNGWDSW 60
|||||
QY 61 NSIWDYGNCFATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLQCKGPGGPPKGLM 120
|||||
DB 61 NSIWDYGNCFATRLFKKTCIVHKMKKEVMPSTQSLDALVKEKKLQCKGPGGPPKGLM 120
|||||
QY 121 YSVNPNKVDDLSKFGKNIANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDIFSCG 180
|||||
DB 121 YSVNPNKVDDLSKFGKNIANMCRGIPTYMAEEMQESLFFYSGTCYTTSVLWIVDIFSCG 180
|||||
QY 181 DTVEN 185
|||||
DB 181 DTVEN 185
|||||

RESULT 10
US-09-989-721-211
;; Sequence 211, Application US/09989721
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC55
;; CURRENT APPLICATION NUMBER: US/09/989,721
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28


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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match          99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKETIVFAGLLGVFLAPALANYINVDNNNAGSQSQSVSNVNNHHNVANVDNNGWDSW 60
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Db 1 MKETIVFAGLLGVFLAPALANYINVDNNNAGSQSQSVSNVNNHHNVANVDNNGWDSW 60
   |||||
QY 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
Db 61 NSIWDYNGNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKKLOGKGGPPPKGLM 120
   |||||
QY 121 YSNPNKVDLDSKFGKNTANMCRGIPTYMAEDMQEASLFFYSGTCTYTSVLWIVDISFCG 180
   |||||
Db 121 YSNPNKVDLDSKFGKNTANMCRGIPTYMAEDMQEASLFFYSGTCTYTSVLWIVDISFCG 180
   |||||
QY 181 DTVEN 185
   |||||
Db 181 DTVEN 185

RESULT 11
US-09-989-722-211
; Sequence 211, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
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; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/089440
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; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-06-19
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; PRIOR APPLICATION NUMBER: 60/090254
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; PRIOR APPLICATION NUMBER: 60/090349
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; PRIOR APPLICATION NUMBER: 60/090429
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; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/090542
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; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKFTIVFAGLLGVFLAPALANYNIDVDDNNNAGSQGSVSVNNEHNVYVNDNNNGDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNINVDNNNAGSQGSVSVNNEHNVYVNDNNNGDSW 60

Qy 61 NSIWDYGNNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKPGGPPKGLM 120
Db 61 NSIWDYGNNGFAATRLFOKKTCTIVHKMKKEVMPISQSLDALVKEKLOGKPGGPPKGLM 120

Qy 121 YSVNPNKYVDDLSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSLVLIWIDISFCG 180
Db 121 YSVNPNKYVDDLSKFGKNIANMCRGIPTYMAEEMQEAASLFFYSGTCYTTSLVLIWIDISFCG 180

Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 12

US-09-989-723-211
; Sequence 211, Application US/099899723
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12

3	PRIOR APPLICATION NUMBER: 60/065311
4	PRIOR FILING DATE: 1997-11-13
5	PRIOR APPLICATION NUMBER: 60/066770
6	PRIOR FILING DATE: 1997-11-24
7	PRIOR APPLICATION NUMBER: 60/075945
8	PRIOR FILING DATE: 1998-02-25
9	PRIOR APPLICATION NUMBER: 60/078910
10	PRIOR FILING DATE: 1998-03-20
11	PRIOR APPLICATION NUMBER: 60/083322
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13	PRIOR APPLICATION NUMBER: 60/084600
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25	PRIOR APPLICATION NUMBER: 60/088021
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55	PRIOR APPLICATION NUMBER: 60/088742
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;	PRIOR APPLICATION NUMBER:	60/090444	
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;	PRIOR APPLICATION NUMBER:	60/090445	
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;	PRIOR APPLICATION NUMBER:	60/090472	
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;	PRIOR FILING DATE:	1998-06-25	
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;	PRIOR APPLICATION NUMBER:	60/091360	
;	PRIOR FILING DATE:	1998-07-01	

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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match          99.0%; Score 984; DB 23; Length 185;
Best Local Similarity 98.9%; Pred. No. 5.8e-102;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60
Db 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSGQSVSVNNEHNVANVDNNNGWDSW 60

QY 61 NSIWDYNGFAATRLFOKKTICIVHKMKKEVMPYSIQSLDALVKEKKLQGGPGGPPKGLM 120
Db 61 NSIWDYNGFAATRLFOKKTICIVHKMKKEVMPYSIQSLDALVKEKKLQGGPGGPPKGLM 120

QY 121 YSNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQASLFYSGTCYTTSLVLIWIVDSFG 180
Db 121 YSNPNKVDLSKFGKNIANMCRGIPTIYMAEEMQASLFYSGTCYTTSLVLIWIVDSFG 180

QY 181 DTVEN 185
Db 181 DTVEN 185

RESULT 13
US-09-989-724-211
; SEQUENCE 211, Application US/09989724
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC67
; CURRENT APPLICATION NUMBER: US/09/989,724
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 99.0%; Score 984; DB 23; Length 185;

Best Local Similarity 98.9%; Pred. No. 5.8e-102;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 121 YSVNPNKVDLKSFGKNIANCMRGIPITYMAEEMOEASLFFYSGTCYTTSVLWIVDISFCG 180
Qy 181 DTVEN 185
Db 181 DTVEN 185

RESULT 15

US-09-989-726-211

;; Sequence 211, Application US/09989726

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
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;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC60
;; CURRENT APPLICATION NUMBER: US/09/989,726
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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Best Local Similarity 98.9%; Pred. No. 5.8e-102;
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Search completed: September 4, 2002, 16:59:21
Job time: 1042 sec

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PR	07-JUL-1998;	98US-0091778.
PR	07-JUL-1998;	98US-0091978.
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PR	09-JUL-1998;	98US-0092182.
PR	10-JUL-1998;	98US-0092472.
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PR	10-AUG-1998;	98US-0096012.
PR	11-AUG-1998;	98US-0096143.
PR	11-AUG-1998;	98US-0096329.
PR	12-AUG-1998;	98US-0096339.
PR	17-AUG-1998;	98US-0096757.

[illegible]

(GETH) GENENTECH INC.

Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK; Wood WI, Yuan J;

WPI; 2000-072883/06.

NIH, 2000-07-2003/
N-PSDB; AAZ65023.

Membrane-bound proteins and related nucleotide sequences

claim 12; Fig 139; 822pp; English.

The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.

AA	Sequence	185 AA:
SQ		

Query Match 64.5%; Score 640; DB 21; Length 185;
Best Local Similarity 63.8%; Pred. No. 1.7e-60;

Best local similarity 93.8%, Fied. NO: 1.7E-60;
Matches 118; Conservative 24; Mismatches 39;
Indels 4; Gaps 3;

[illegible]

CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein of the invention.
 XX
 SQ Sequence 184 AA;

Query Match 16.2%; Score 161; DB 22; Length 184;
 Best Local Similarity 26.6%; Pred. No. 4.1e-09;
 Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;

QY 1 MKLTMFVVGILGLLAAPGAYTV-NI---NGDGNVDGSGQOSVSIINGVHNVANIDNNNG 56
 Db 1 mkilvafvlvtifglsghyevfnliispsngnv----qetvtdidnektainihag 56
 QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTMVKQKGGPGGAPPKD 116
 Db 57 scssttfdykhgyiasrvlsrracfilkmdhqnplnlqwyiyekqa-----ld 108
 QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTVVAEETPGNPPLYSKKCYT 165
 Db 109 nmfsskytwvkynpleslikdvdfllgspiekckhiplkygevvventhn-vgaggcak 167
 QY 166 ADILWILRMSFC 177
 Db 168 agllgilgisic 179

RESULT 12
 AAE04233
 ID AAE04233 standard; Protein; 184 AA.
 AC AAE04233;
 XX
 DT 09-AUG-2001 (first entry)
 XX
 DE Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:88.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive; chromosome 2;
 KW binding partner identification.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= signal_peptide
 FT 21..184
 FT /note= "Mature secreted protein"
 XX
 PN WO200136432-A2.
 XX
 XX 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-US31162.
 XX
 PR 19-NOV-1999; 99US-0166415.
 PR 30-JUN-2000; 2000US-0215136.
 XX

PA
 XX
 PI Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 XX
 DR WPI; 2001-343793/36.
 DR N-PSDB; AAD08523.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 11: Page 463-464; 509pp; English.
 XX
 CC AAD08488-AAD08529 represent cDNAs corresponding to 18 human secreted
 CC protein genes, and AAE04199-AAE04239 represent the proteins they encode.
 CC AAE04240-AAE04297 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 18 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin ageing due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein of the invention.
 XX
 SQ Sequence 184 AA;

Query Match 16.2%; Score 161; DB 22; Length 184;
 Best Local Similarity 26.6%; Pred. No. 4.1e-09;
 Matches 51; Conservative 45; Mismatches 68; Indels 28; Gaps 8;

QY 1 MKLTMFVVGILGLLAAPGAYTV-NI---NGDGNVDGSGQOSVSIINGVHNVANIDNNNG 56
 Db 1 mkilvafvlvtifglsghyevfnliispsngnv----qetvtdidnektainihag 56
 QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTMVKQKGGPGGAPPKD 116
 Db 57 scssttfdykhgyiasrvlsrracfilkmdhqnplnlqwyiyekqa-----ld 108
 QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTVVAEETPGNPPLYSKKCYT 165
 Db 109 nmfsskytwvkynpleslikdvdfllgspiekckhiplkygevvventhn-vgaggcak 167
 QY 166 ADILWILRMSFC 177
 Db 168 agllgilgisic 179

RESULT 13
 AAY66690
 ID AAY66690 standard; protein; 184 AA.
 XX
 AC AAY66690;
 XX
 DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO813.
XX DE
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX OS
XX OS Homo sapiens.
PN WO9963088-A2.
XX PD
XX PD 09-DEC-1999.
XX PF 02-JUN-1999; 99WO-US12252.
XX PF
XX PF 02-JUN-1998; 98US-0087607.
XX PF 02-JUN-1998; 98US-0087609.
XX PF 02-JUN-1998; 98US-0087759.
XX PF 03-JUN-1998; 98US-0087827.
XX PF 04-JUN-1998; 98US-0088021.
XX PF 04-JUN-1998; 98US-0088025.
XX PF 04-JUN-1998; 98US-0088028.
XX PF 04-JUN-1998; 98US-0088029.
XX PF 04-JUN-1998; 98US-0088030.
XX PF 04-JUN-1998; 98US-0088033.
XX PF 04-JUN-1998; 98US-0088326.
XX PF 05-JUN-1998; 98US-0088167.
XX PF 05-JUN-1998; 98US-0088202.
XX PF 05-JUN-1998; 98US-0088212.
XX PF 05-JUN-1998; 98US-0088217.
XX PF 09-JUN-1998; 98US-0088655.
XX PF 10-JUN-1998; 98US-0088722.
XX PF 10-JUN-1998; 98US-0088730.
XX PF 10-JUN-1998; 98US-0088734.
XX PF 10-JUN-1998; 98US-0088738.
XX PF 10-JUN-1998; 98US-0088740.
XX PF 10-JUN-1998; 98US-0088741.
XX PF 10-JUN-1998; 98US-0088742.
XX PF 10-JUN-1998; 98US-0088810.
XX PF 10-JUN-1998; 98US-0088811.
XX PF 10-JUN-1998; 98US-0088824.
XX PF 10-JUN-1998; 98US-0088825.
XX PF 11-JUN-1998; 98US-0088826.
XX PF 11-JUN-1998; 98US-0088858.
XX PF 11-JUN-1998; 98US-0088861.
XX PF 11-JUN-1998; 98US-0088863.
XX PF 11-JUN-1998; 98US-0088876.
XX PF 12-JUN-1998; 98US-0089090.
XX PF 12-JUN-1998; 98US-0089105.
XX PF 16-JUN-1998; 98US-0089440.
XX PF 16-JUN-1998; 98US-0089512.
XX PF 16-JUN-1998; 98US-0089514.
XX PF 17-JUN-1998; 98US-0089532.
XX PF 17-JUN-1998; 98US-0089538.
XX PF 17-JUN-1998; 98US-0089538.
XX PF 17-JUN-1998; 98US-0089599.
XX PF 17-JUN-1998; 98US-0089599.
XX PF 17-JUN-1998; 98US-0089653.
XX PF 18-JUN-1998; 98US-0089601.
XX PF 18-JUN-1998; 98US-0089907.
XX PF 18-JUN-1998; 98US-0089908.
XX PF 19-JUN-1998; 98US-0089947.
XX PF 19-JUN-1998; 98US-0089948.
XX PF 19-JUN-1998; 98US-0089952.
XX PF 22-JUN-1998; 98US-0090246.
XX PF 22-JUN-1998; 98US-0090252.
XX PF 22-JUN-1998; 98US-0090254.
XX PF 23-JUN-1998; 98US-0090349.
XX PF 23-JUN-1998; 98US-0090355.
XX PF 24-JUN-1998; 98US-0090429.
XX PF 24-JUN-1998; 98US-0090431.
XX PF 24-JUN-1998; 98US-0090435.
XX PF 24-JUN-1998; 98US-0090444.
XX PF 24-JUN-1998; 98US-0090445.
XX PF 24-JUN-1998; 98US-0090445.
XX PF 24-JUN-1998; 98US-0090461.
XX PF 24-JUN-1998; 98US-0090472.
XX PF 24-JUN-1998; 98US-0090535.
XX PF 24-JUN-1998; 98US-0090538.
XX PF 24-JUN-1998; 98US-0090540.
XX PF 24-JUN-1998; 98US-0090557.
XX PF 25-JUN-1998; 98US-0090676.
XX PF 25-JUN-1998; 98US-0090678.
XX PF 25-JUN-1998; 98US-0090688.
XX PF 25-JUN-1998; 98US-0090690.
XX PF 25-JUN-1998; 98US-0090691.
XX PF 25-JUN-1998; 98US-0090694.
XX PF 25-JUN-1998; 98US-0090695.
XX PF 25-JUN-1998; 98US-0090696.
XX PF 26-JUN-1998; 98US-0090862.
XX PF 26-JUN-1998; 98US-0090863.
XX PF 01-JUL-1998; 98US-0091358.
XX PF 01-JUL-1998; 98US-0091360.
XX PF 01-JUL-1998; 98US-0091544.
XX PF 02-JUL-1998; 98US-0091478.
XX PF 02-JUL-1998; 98US-0091486.
XX PF 02-JUL-1998; 98US-0091519.
XX PF 02-JUL-1998; 98US-0091626.
XX PF 02-JUL-1998; 98US-0091628.
XX PF 02-JUL-1998; 98US-0091633.
XX PF 02-JUL-1998; 98US-0091646.
XX PF 02-JUL-1998; 98US-0091673.
XX PF 07-JUL-1998; 98US-0091978.
XX PF 07-JUL-1998; 98US-0091982.
XX PF 09-JUL-1998; 98US-0092182.
XX PF 10-JUL-1998; 98US-0092472.
XX PF 20-JUL-1998; 98US-0093339.
XX PF 30-JUL-1998; 98US-0094651.
XX PF 04-AUG-1998; 98US-0095285.
XX PF 04-AUG-1998; 98US-0095301.
XX PF 04-AUG-1998; 98US-0095302.
XX PF 04-AUG-1998; 98US-0095318.
XX PF 04-AUG-1998; 98US-0095321.
XX PF 04-AUG-1998; 98US-0095325.
XX PF 04-AUG-1998; 98US-0095916.
XX PF 10-AUG-1998; 98US-0095929.
XX PF 10-AUG-1998; 98US-0096012.
XX PF 11-AUG-1998; 98US-0096143.
XX PF 12-AUG-1998; 98US-0096146.
XX PF 12-AUG-1998; 98US-0096329.
XX PF 17-AUG-1998; 98US-0096757.
XX PF 17-AUG-1998; 98US-0096766.
XX PF 17-AUG-1998; 98US-0096768.
XX PF 17-AUG-1998; 98US-0096773.
XX PF 17-AUG-1998; 98US-0096791.
XX PF 17-AUG-1998; 98US-0096867.
XX PF 17-AUG-1998; 98US-0096891.
XX PF 17-AUG-1998; 98US-0096894.
XX PF 17-AUG-1998; 98US-0096895.
XX PF 17-AUG-1998; 98US-0096897.
XX PF 18-AUG-1998; 98US-0096949.
XX PF 18-AUG-1998; 98US-0096950.
XX PF 18-AUG-1998; 98US-0096959.
XX PF 18-AUG-1998; 98US-0096960.
XX PF 18-AUG-1998; 98US-0097022.
XX PF 19-AUG-1998; 98US-0097141.
XX PF 20-AUG-1998; 98US-0097218.
XX PF 24-AUG-1998; 98US-0097661.
XX PF 26-AUG-1998; 98US-0097951.
XX PF 26-AUG-1998; 98US-0097952.
XX PF 26-AUG-1998; 98US-0097954.
XX PF 26-AUG-1998; 98US-0097955.
XX PF 26-AUG-1998; 98US-0097971.
XX PF 26-AUG-1998; 98US-0097974.
XX PF 26-AUG-1998; 98US-0097978.
XX PF 26-AUG-1998; 98US-0097979.
XX PF 26-AUG-1998; 98US-0097986.

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PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI: 2000-072883/06.
DR N-PSDB; AAB65029.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX
XX Claim 12; Fig 149; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
XX Sequence 184 AA;
XX
XX
XX Query Match 16.1%; Score 160; DB 21; Length 184;
XX Best Local Similarity 26.0%; Pred. No. 5.3e-09;
XX Matches 50; Conservative 46; Mismatches 68; Indels 28; Gaps 8;
XX
QY 1 MKLTFMVVGLLGLLAAPGFAYTV-NI---NGNDGNVDSGQQSVSINGVHNVANIDNNNG 56
DB 1 mklilvafvlvltifgshgyevfniispsnngnv----getvtdnektaihviahg 56
QY 57 WDSWNSLWDYENSFAATFLSKKSCIVHRMKNDAKPSLODLDTMVKBQKCKGPGGAPPKD 116
DB 57 scsattifdykhgyiaarvlsrracflkmdhqnippnlqwyiekga-----ld 108
QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTYVAEIPGNQPLYSKCYT 165
DB 109 nmfsnktytwkynpleslikdvdfllgspiekckhpiykgevvventhn-vgaggcak 167
QY 166 ADILWILRMSPC 177
DB 168 agllgilgisic 179
XX
XX RESULT 14
XX AAB65213
XX ID AAB65213 standard; Protein; 184 AA.
XX AC
XX AAB65213;
XX
XX 02-APR-2001 (first entry)
XX
XX Human PRO813 (UNQ465) protein sequence SEQ ID NO:221.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic;
XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX
XX Homo sapiens.
XX
XX WO200073454-A1.
XX

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XX
XX 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 17-AUG-1999; 99US-0149396.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 08-OCT-1999; 99US-0158663.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CU, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI: 2001-032160/04.
XX N-PSDB; AAF44175.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX bioactive molecules such as toxins, radiolabels or antibodies, to
XX specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 149; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX can be used for targeted delivery of bioactive molecules, such as
XX toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA
XX and DNA. They may also be used to produce transgenic animals which are
XX used to develop and screen therapeutically useful reagents. The PRO
XX nucleotide and protein sequence can be used for tissue typing and in
XX treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX sequences given in the exemplification of the present invention.
XX
XX Sequence 184 AA;
XX

```

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Query Match 16.1%; Score 160; DB 22; Length 184;
Best Local Similarity 26.0%; Pred. No. 5.3e-09;
Matches 50; Conservative 46; Mismatches 68; Indels 28; Gaps 8;
QY 1 MKLTFMVVGLLGLLAAPGFAYTV-NI---NGNDGNVDSGQQSVSINGVHNVANIDNNNG 56
DB 1 mklilvafvlvltifgshgyevfniispsnngnv----getvtdnektaihviahg 56

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```
QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTVMVKEQKGGPGGAPPKD 116
Db 57 scssttfdykhgylasrvlsrracfilkmhqnippnlmqlwyiyekqa-----ld 108
QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTVVAEEIPGNQPLYSKKCYT 165
Db 109 mfnfsknytwtwkympleslikdvflilgspieklckhpiykgevvventhn-vgaggcak 167
QY 166 ADILWILRMSFC 177
Db 168 agllgilglsic 179

RESULT 15
AAU29238
ID AAU29238 standard; Protein; 176 AA.
XX
AC AAU29238;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #215.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000US-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
```

```
PR 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000WO-US34956.
XX (GETH ) GENENTECH INC.
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-602746/68.
DR N-PSDB; AAS46139.
XX
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -
XX Claim 11; Fig 430; 774pp; English.
PS
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 176 AA;
```

Query Match 15.6%; Score 155; DB 22; Length 176;

Best Local Similarity 27.1%; Pred. No. 1.7e-08;

Matches 52; Conservative 43; Mismatches 61; Indels 36; Gaps 9;

QY 1 MKLTMFVVGLLGLLAAPGFAYTV-NI---NGNDGNVDGSGQGSVINGVHVNVANIDNNNG 56

Db 1 mvlitfigiqshg-----yevfnlspnngnv---qetvtdidnektaiwnihag 48

QY 57 WDSWNSLWDYENSFAATRLFSKSCIVHRMKNKDAMPSLQDLDTVMVKEQKGGPGGAPPKD 116

Db 49 scssttfdykhgylasrvlsrracfilkmhqnippnlmqlwyiyekqa-----ld 100

QY 117 LMYS-----VNP--TRVEDLNTF--GPKIAGMCRGIPTVVAEEIPGNQPLYSKKCYT 165

Db 101 mfnfsknytwtwkympleslikdvflilgspieklckhpiykgevvventhn-vgaggcak 159

QY 166 ADILWILRMSFC 177

Db 160 agllgilglsic 171

Search completed: September 4, 2002, 16:45:06

Job time: 382 sec

CHM1_BOVIN
ID CHM1_BOVIN STANDARD; PRT; 335 AA.
AC P17404: P23590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chondromodulin-I precursor (CHM-I) (Small cartilage-derived glycoprotein) (SCGP) [Contains: Chondrosurfactant protein (CH-SP)].
GN CHM1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 215-241 AND 297-317.
RP [2]
RX TISSUE=Fetal epiphyseal cartilage;
RX MEDLINE=9122210; PubMed=1709014;
RA Hiraki Y., Tanaka H., Inoue H., Kondo J., Kamizono A., Suzuki F.;
RT "Molecular cloning of a new class of cartilage-specific matrix, chondromodulin-I, which stimulates growth of cultured chondrocytes.";
RL Biochem. Biophys. Res. Commun. 175:971-977(1991).
RN [3]
RP [2]
RX SEQUENCE OF 215-335, VARIANT MET-221, AND GLYCOSYLATION.
RC TISSUE=Nasal cartilage;
RX MEDLINE=90277643; PubMed=2351661;
RA Neame P.J., Treep J.T., Young C.N.;
RT "An 18-kDa glycoprotein from bovine nasal cartilage. Isolation and primary structure of small, cartilage-derived glycoprotein.";
RL J. Biol. Chem. 265:9628-9633(1990).
RN [3]
RP [2]
RA Neame P.J., Treep J.T., Young C.N.;
RL J. Biol. Chem. 265:22056-22056(1990).
RN [4]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21316541; PubMed=11323410;
RA Azizan A., Holaday N., Neame P.J.;
RT "Post-translational processing of bovine chondromodulin-I.";
RL J. Biol. Chem. 276:23632-23638(2001).
RN [5]
RP REVIEW.
RX MEDLINE=20367654; PubMed=10912526;
RA Hiraki Y., Shukunani C.;
RT "Chondromodulin-I as a novel cartilage-specific growth-modulating factor.";
RL [4]
CC -!- FUNCTION: Bifunctional growth regulator that stimulates the growth of cultured chondrocytes in the presence of basic fibroblast growth factor (FGF) but inhibits the growth of cultured vascular endothelial cells. May contribute to the rapid growth of cartilage and vascular invasion prior to the replacement of cartilage by bone during endochondral bone development.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the interterritorial matrix of cartilage.
CC -!- TISSUE SPECIFICITY: Nasal and articular cartilage, and fetal epiphysis.
CC -!- PTM: After cleavage, the post-translationally modified CHM-I is secreted as a glycoprotein.
CC -!- PTM: Two other smaller nonglycosylated chondromodulin forms (9 kDa and 7kDa) are found either in developing articular cartilage or in chondrocytes. The 9 kDa form could be processed by an extracellular matrix-associated protease as a metalloproteinase and the 7 kDa form could be processed intracellularly.
CC -!- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
CC
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CC EMBL; M65081; AAA30445.1; -
DR PIR: J0569; J0569.
DR PIR: A33138; A33138.
DR InterPro: IPR001729; Pulm_surfact_AP.
DR SMART: SM00019; SF_P; 1.
KW Cartilage; Glycoprotein; Transmembrane;
KW Cleavage on pair of basic residues.
FT CHAIN 1 210 CHONDROSURFACTANT PROTEIN (POTENTIAL).
FT PROPEP 211 214 POTENTIAL.
FT CHAIN 215 335 CHONDROMODULIN-I.
FT TRANSMEM 45 65 POTENTIAL.
FT DISULFID 283 287 POTENTIAL.
FT DISULFID 284 324 POTENTIAL.
FT CARBOHYD 223 223 O-LINKED.
FT CARBOHYD 236 236 O-LINKED (GALNAC: .).
FT CARBOHYD 244 244 N-LINKED (GLCNAC: .).
FT VARIANT 221 221 V -> M.
FT CONFLICT 223 224 TT -> NE (IN REF. 2).
FT CONFLICT 256 256 P -> PD (IN REF. 2).
SQ SEQUENCE 335 AA; 37164 MW; 6D72CA8740448441 CRC64;
Query Match 8.6%; Score 85.5; DB 1; Length 335;
Best Local Similarity 22.3%; Pred. NO. 0.71;
Matches 39; Conservative 29; Mismatches 70; Indels 37; Gaps 7;
QY 7 VVCLGLLAAPGF-----AYTVNNG--NDGNVDSGGQSVSGVINGVHNVANIDN 53
DB 52 VLLLLGAIGAFYFWKSDNHHIYNVHTMSINKLOGD-----SMEIDAGNNLETFKM 103
QY 54 NNGWDSWNSLWDSYENFAATRLFSKSCVHRNMKNKDAMPSLQDDLTWYK-----BQCK- 107
DB 104 GCAEEAVEVNDPFGITGIRFAGGKCYKKAQVKARIP---EVGTMTKQSSSELEGI 160
QY 108 GPGCAPKDLMSVNTFRVEDLNTFGPKIAGMCRGIPITYVAEEIPGNOPLYSKK 162
DB 161 MPVKEENSLIIVAGDQPVKDNSFLSSKVLLECGDLPIFWL-----KPIYPKE 208
RESULT 7
EFBL_HUMAN STANDARD; PRT; 346 AA.
AC P98172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2) (LERK-2) (ELK ligand) (ELK-L).
GN EFN1 OR EPLG2 OR LERK2 OR EFL-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349923; PubMed=8070404;
RA Beckmann M.P., Cerretti D.P., Baum P., Vandenbos T., James L., Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E., Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
RT "Molecular characterization of a family of ligands for eph-related tyrosine kinase receptors";
RL EMBO J. 13:3757-3762(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Davis S., Gale N.W., Aldrich T.H., Maisonnier P.C., Lhotak V., Pawson T., Goldfarb M., Vancopoulos G.D.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U., Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,

AC Q921F6: O9CXU5; STANDARD: PRT; 334 AA.
ID 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chondromodulin-I precursor (ChM-I) (Leukocyte cell-derived chemotaxin
1) [Contains: Chondrosurfactant protein (Ch-SP)].
GN CHM1 OR LECT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP HIRAKI Y., SHUKUNAMI C., INOUE H., SUZUKI F.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Bifunctional growth regulator that stimulates the growth
of cultured chondrocytes in the presence of basic fibroblast
growth factor (FGF) but inhibits the growth of cultured vascular
endothelial cells. May contribute to the rapid growth of cartilage by
and vascular invasion prior to the replacement of cartilage by
bone during endochondral bone development (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and secreted. Accumulated in the
inter-territorial matrix of cartilage (By similarity).
CC -!- PTM: After cleavage, the post-translationally modified ChM-I is
secreted as a glycoprotein (By similarity).
CC -!- SIMILARITY: BELONGS TO THE CHONDROMODULIN-I FAMILY.
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CC EMBL; U43509; AAD00027.1; .
DR EMBL; AK013975; BAB29095.1; .
DR MGD; MGI:1341171; LECT1.
KW Cartilage; Glycoprotein; Transmembrane;
KW Cleavage on pair of basic residues.
FT CHAIN 1 210 CHONDROSURFACTANT PROTEIN
FT (BY SIMILARITY).
FT PROPEP 211 214
FT CHAIN 215 334 CHONDROMODULIN-I (BY SIMILARITY).
FT TRANSMEM 46 66 POTENTIAL
FT CARBOHYD 243 243 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 108 109 AK -> RE (IN REF. 2).
FT CONFLICT 163 163 V -> A (IN REF. 2).

FT CONFLICT 207 207 K -> KANFA (IN REF. 2).
SQ SEQUENCE 334 AA; 37252 MW; DAFDEC43C7D745D6 CRC64;
Query Match 8.5%; Score 84.5; DB 1; Length 334;
Best Local Similarity 20.8%; Pred. No. 0.89;
Matches 31; Conservative 29; Mismatches 64; Indels 25; Gaps 5;
QY 21 YTVNNG--NGNVDSGQSVISNGVHNVANIDNNWDSWNSLWDYENSAFATRLFSK 78
DB 78 YMSYNGKLQD-----SMEIDAVNNLETFKMGSCAKAEIEVDFKNGITGIRFAGG 129
QY 79 KSCIVHRMKNKDAMPDLSQDLDTVMVKEQKQKPGGAPP-----KDLMSVNPTRVEDLNTFG 133
DB 130 EKCYIKAOVKARIP--EVGVTQKQISELEKIMPVNYESNLIWVAVDQPVKDSFSL 186
QY 134 PKIAGMCRGIPYVAEEIPGPNOLYSKK 162
DB 187 SKILELCGLDPIFWL-----KPMYPKE 208
RESULT 10
HYSA_PROAC STANDARD: PRT; 752 AA.
AC Q59634;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hyaluronate lyase precursor (EC 4.2.2.1) (Hyaluronidase) (HYase).
OS Propionibacterium acnes.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Propionibacterineae; Propionibacteriaceae;
OC Propionibacterium.
OX NCBI_TaxID=1747;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=97270208; PubMed=9115089;
RA Steiner B.M., Romero-Stelner S., Cruce D., George R.;
RT "Cloning and sequencing of the hyaluronate lyase gene from
Propionibacterium acnes."
RL Can. J. Microbiol. 43:315-321(1997).
CC -!- CATALYTIC ACTIVITY: Hyaluronate = N 3-(4-deoxy-beta-D-gluc-4-
enuronosyl)-N-acetyl-D-glucosamine.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: CELL-ASSOCIATED.
CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC EMBL; U15927; AAA51650.1; .
DR InterPro; IPR003159; Lyase_8.
DR InterPro; IPR004103; Lyase_8_C.
DR Pfam; PF02278; Lyase_8; 1.
DR Pfam; PF02884; Lyase_8_C; 1.
KW Lyase; Signal.
FT SIGNAL 1 32
FT CHAIN 33 752 HYALURONATE LYASE.
SQ SEQUENCE 752 AA; 81910 MW; 60D5DCAA691C41A4 CRC64;
Query Match 8.5%; Score 84; DB 1; Length 752;
Best Local Similarity 24.18; Pred. No. 2.7;
Matches 33; Conservative 18; Mismatches 62; Indels 24; Gaps 6;
QY 15 AAGPAYTVNNGNDGNGVDSGQSVISNGVHNVANIDNNWDSWNSLWDYENSAFATR 74
DB 119 ATPGSSY-----HKDPEI-----LSACIEGLRDFCLRLYNPQDEYGNWMDWED--GASR 166

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EMBL: AF045017; AAC24209.1; -.
 EMBL: L10406; AAA03159.1; -.
 EMBL: X71939; CAA50741.1; -.
 HSSP: Q63245; 2HFH.
 TRANSFAC: T02426; -.
 MGD: MGI:1347466; Foxcl.
 InterPro: IPR001766; Fork_head.
 Pfam: PF00250; Fork_head.1.
 PRINTS: PR00053; FORKHEAD.
 SMART: SM00339; FH; 1.
 PROSITE: PS00657; FORK_HEAD.1; 1.
 PROSITE: PS00658; FORK_HEAD.2; 1.
 PROSITE: PS00659; FORK_HEAD.3; 1.
 DNA-binding; Nuclear protein; Transcription regulation.
 KW DOMAIN 28 33 POLY-ALA.
 FT DNA_BIND 77 168 FORK-HEAD.
 FT DOMAIN 169 173 POLY-ARG.
 FT DOMAIN 194 197 POLY-PRO.
 FT DOMAIN 264 274 POLY-SER.
 FT DOMAIN 375 386 POLY-GLY.
 FT DOMAIN 444 451 POLY-SER.
 FT DOMAIN 453 456 POLY-GLY.
 FT DOMAIN 486 496 POLY-ALA.
 FT CONFLICT 180 187 VKDKEKG -> KKEITFIG (IN REF. 3).
 SQ SEQUENCE 553 AA; 56953 MW; 3CDD12F69CA4F217 CRC64;

Query Match 8.2%; Score 81; DB 1; Length 553;
 Best Local Similarity 19.8%; Pred. No. 3.6;
 Matches 38; Conservative 21; Mismatches 61; Indels 72; Gaps 9;

QY 14 LAAPGFAYTVNINGDNGVDGSGQSVSINGVHVA-----NIDNNGW----- 57
 Db 76 MVKPPYSIALIT---MAIONAPDKKITLNGIYQFIMDRFPFFYEDNKGQNSIRHLSL 132
 QY 58 -----DSWNSLWDYENS--FAATRLFSKSCIVHRMKNKDM 91
 Db 133 NECFVKVPRDDKKPKGSGYWTLPDPSYNN---FENGSLRRRRRFRKKDAVKDKKEKGRU 189
 QY 92 PSLODLTWMYKEQKGGPGAPKDLMSV-----NPTRVEDLNTFGPKIAGMCRGIPTY 146
 Db 190 ----HLQEPPPPQAGROPAPAPPEQAEGSAPPQPPPVRIQDIKTEN-----GTC----- 235
 QY 147 VAEIIPGNPL 158
 Db 236 -----PSPQPL 242

RESULT 13
 KDGL_ARATH
 ID KDGL_ARATH STANDARD; PRT; 728 AA.
 AC Q39017; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diacylglycerol kinase 1 (EC 2.7.1.107) (Diglyceride kinase 1)
 DE (DGL 1) (DAG kinase 1).
 GN DGL1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=96189276; PubMed=8605313;
 RA Katagiri T., Mizoguchi T., Shinozuchi K.

"Molecular cloning of a cDNA encoding diacylglycerol kinase (DGK) in Arabidopsis thaliana".
 Plant Mol. Biol. 30:647-653(1996).
 CC -|- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-diacylglycerol 3-phosphate.
 CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -|- TISSUE SPECIFICITY: DETECTED IN ROOTS, SHOOTS, AND LEAVES.
 CC -|- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE FAMILY.
 CC -|- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAINS.
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EMBL: D63787; BAA09856.1; -.
 InterPro: IPR000756; DAGKa.
 InterPro: IPR001206; DAGKc.
 InterPro: IPR002219; DAG_PE-bind.
 Pfam: PF00609; DAGKa; 1.
 Pfam: PF00781; DAGKc; 1.
 ProDom: PD002939; DAGKa; 1.
 SMART: SM00109; Cl; 2.
 SMART: SM00045; DAGKa; 1.
 SMART: SM00046; DAGKc; 1.
 PROSITE: PS00479; DAG_PE_BIND_DOM.1; FALSE_NEG.
 PROSITE: PS00081; DAG_PE_BIND_DOM.2; 2.
 KW Transferase; Kinase; Phorbol-ester binding; Transmembrane; Repeat.
 FT TRANSFER 27 48 POTENTIAL.
 FT DOMAIN 95 137 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 169 212 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 359 490 CATALYTIC (POTENTIAL).
 FT DOMAIN 507 664 CATALYTIC (POTENTIAL).
 SQ SEQUENCE 728 AA; 79970 MW; 78E4FD2252B76DA8 CRC64;

Query Match 8.1%; Score 80.5; DB 1; Length 728;
 Best Local Similarity 24.1%; Pred. No. 5.7;
 Matches 34; Conservative 27; Mismatches 57; Indels 23; Gaps 7;

QY 27 GNDG-NVDGSGQSV-----SINGVH-----NVANIDNNNGDSWNSLWDYENSFAATR 74
 Db 275 GNSGNCDESTESTADTGTPTNGAHAVLENSISVHNGSSNGSDSNGKLEKPPSVKRTG 334
 QY 75 LFSKXSCIVHRMKNKDAMPSLODLT-----MVKEQKGGPGGAPKDLMSVNPTRVE 127
 Db 335 SFGQKE--YHALRSKLYELADLPDARPLLVFINKKSGAQRGSLRORLHLNLPQVVF 392
 QY 128 DLNTP-GPKIA-GMCRGIPTY 146
 Db 393 ELSSVQGPVEVGLFLFRKVPHF 413

RESULT 14
 F263_RAT
 ID F263_RAT STANDARD; PRT; 555 AA.
 AC O35552; O35553; O35554; O35555; O35556; O35557; O9QWQ6; O9QWQ6;
 AC O35096;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (6PF-2-K/Fru-2,6-P2ASE brain-type isozyme) (R6ZK) [Includes: 6-phosphofructo-2-kinase (EC 2.7.1.105); Fructose-2,6-bisphosphatase (EC 3.1.3.46)].
 GN PFKFB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=97345796; PubMed=9202288;
RA Watanabe F., Sakai A., Furuya E.;
RT "Novel isoforms of rat brain fructose 6-phosphate 2-kinase/fructose
splicing.";
RL J. Neurochem. 69:1-9(1997).
[2]
SEQUENCE OF 61-369 FROM N.A.
RP STRAIN=WISTAR; TISSUE=Placenta;
RA Sakakibara R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SYNTHESIS AND DEGRADATION OF FRUCTOSE 2,6-BISPHOSPHATE.
CC -!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
fructose 2,6-bisphosphate.
CC -!- CATALYTIC ACTIVITY: D-fructose 2,6-bisphosphate + H(2)O = D-
fructose 6-phosphate + phosphate.
CC -!- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1/RB2K1 (SHOWN HERE), 2/RB2K2,
3/RB2K3, 4/RB2K4, 5/RB2K5, 6/RB2K6, 7/RB2K7 AND 8/RB2K8; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
PHOSPHOGLYCERATE MUTASE FAMILY.

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DR EMBL; D87240; BAA21749.1; -
DR EMBL; D87241; BAA21750.1; -
DR EMBL; D87242; BAA21751.1; -
DR EMBL; D87243; BAA21752.1; -
DR EMBL; D87244; BAA21753.1; -
DR EMBL; D87245; BAA21754.1; -
DR EMBL; D87246; BAA21755.1; -
DR EMBL; D87247; BAA21756.1; -
DR EMBL; AB006710; BAA22048.1; -
DR HSP; P07953; 1FBI.
DR InterPro; IPR000546; 6PF2K.
DR InterPro; IPR003094; 6PF2K_kin.
DR InterPro; IPR001345; 6PF2K.
DR Pfam; PF01591; 6PF2K; 1.
DR Pfam; PF00300; PGAM; 1.
DR PRINTS; P000991; 6PF2KTNASE.
DR ProDom; PD002665; 6PF2K; 1.
DR PROSITE; PS00175; PG_MUTASE; 1.
KW Multifunctional enzyme; Transferase; Kinase; Hydrolase; ATP-binding;
KW Phosphorylation; Multigene family; Alternative splicing.
FT DOMAIN 1 245 6-PHOSPHOFRUCTO-2-KINASE.
FT DOMAIN 246 555 FRUCTOSE-2,6-BISPHOSPHATASE.
FT NP_BIND 42 49 ATP (BY SIMILARITY).
FT BINDING 99 99 TO FRU-6-P (BY SIMILARITY).
FT BINDING 190 190 TO FRU-6-P (BY SIMILARITY).
FT ACT_SITE 125 125 POTENTIAL.
FT ACT_SITE 155 155 POTENTIAL.
FT ACT_SITE 254 254 FORMS THE PHOSPHOTIDINE INTERMEDIATE.
FT ACT_SITE 323 323 POTENTIAL.
FT ACT_SITE 388 388 PROTON DONOR (BY SIMILARITY).
FT VARSPPLIC 448 476 MISSING (IN ISOFORM 4, ISOFORM 5, ISOFORM
6 AND ISOFORM 8).
FT VARSPPLIC 543 555 RTVCHIFSPSP -> T (IN ISOFORM 2 AND
ISOFORM 5).
FT VARSPPLIC 535 555 PLIGRACLRVTVCHIFSPSP -> NMRSPRGAESSQKH
(IN ISOFORM 3 AND ISOFORM 6).
FT VARSPPLIC 543 555 MISSING (IN ISOFORM 7 AND ISOFORM 8).
FT CONFLICT 185 195 D -> H (IN REF. 2).
FT CONFLICT 367 367 V -> L (IN REF. 2).

SQ SEQUENCE 555 AA; 63675 MW; 45B2D090B44FCD8D CRC64;
Query Match 8.1%; Score 80; DB 1; Length 555;
Best Local Similarity 24.8%; Pred. No. 4.5;
Matches 26; Conservative 17; Mismatches 42; Indels 20; Gaps 4;
QY 79 KSCIVHRMKNKDM-----PSLQDLDTM-----VKEQKKGKGGAPPKDL---MYS 120
Db 437 ESVSTHRESEAVKIQHFASVVRPSYITELDFLSVESAKODAKKGNPLMRNRNVTPLAS 496
QY 121 VNPTRVEDLNTFGPKIAGMCRGIPTVVAEIPG--PNQPLYSKCC 163
Db 497 PETTKPRINSFEHVASTSAALPSCLPPEVPTQLPQQLGKAC 541
RESULT 15
EFB2_MOUSE STANDARD; PRT; 336 AA.
AC P52800;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN EFN2 OR EPLG5 OR LERK5 OR HTKL OR ELF2 OR EPL5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96145238; PubMed=8559144;
RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Fletcher R.A.;
RT "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
kinases.";
RL Mol. Immunol. 32:1197-1205(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CB57B1/6J X SJL/J;
RX MEDLINE=95199254; PubMed=7534404;
RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA Gillett N., Matthews W.;
RT "Molecular cloning of a ligand for the EPH-related receptor protein-
tyrosine kinase Htk";
RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RX MEDLINE=95379837; PubMed=7651410;
RA Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT "ELF-2, a new member of the EPH ligand family, is segmentally
expressed in mouse embryos in the region of the hindbrain and newly
forming somites.";
RL Mol. Cell. Biol. 15:4921-4929(1995).
RN [4]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
in the mouse spinal cord: a possible role in constraining the
orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN CONSTRAINING THE ORIENTATION OF
LONGITUDINALLY PROJECTING AXONS.
CC -!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASE EPHB4.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON LATERAL FLOOR
SPECIFICALLY ON COMMISSURAL AXON SEGMENTS THAT HAVE PASSED THROUGH
THE FLOOR PLATE. EXPRESSED IN CELLS OF THE RETINAL GANGLION CELL
LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISC.

Query Match	8.0%;	Score 79;	DB 1;	Length 336;
Best Local Similarity	24.6%;	Pred. No. 3;		
Matches 34;	Conservative 21;	Mismatches 47;	Indels 36;	Gaps 9;

49	ANIDNNNCWSNLSDYENSFAATRLFS--KKSCIV-----	HRMVK 88
	::: :::: :: :: :::: :: :::: :: ::::	
209	SSTDGNSAGHSGNNLLGSE-----VALFAGIASGCIIFIVIIITVLVLLKYRRHRKHS	263
	::: :::: :: :: :::: :: :::: :: ::::	
89	DAMPSLDLODTWYKEGKGPGGAPKDLMYSNPTRVEDLNTFGP---KIAGMCRGPT	145
	::: :::: :: :: :::: :: :::: :: ::::	
264	POHTITLSTLATPRGGNGNSESDEV---IILPRTAD-SVFCPHYEKYSG-DYGHVP	318
	::: :::: :: :: :::: :: :::: :: ::::	
146	YVAEEIFGPNQP--LYSK	161
	::: :: :: :: :::: :: :::: :: ::::	
319	YIVOEMP-POSANIYK	335
	::: :: :: :: :::: :: :::: :: ::::	

Search completed: September 4, 2002, 17:05:10
Job time: 1136 sec

Page 11

dsr.91

XX DT 11-MAY-2000 (first entry)

XX DE Human signal peptide containing protein HSPP-49 SEQ ID NO:49.

XX KW Human: signal peptide-containing protein; HSPP; diagnosis; cancer;

XX KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

XX KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;

XX KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

XX KW reproductive disorder; developmental disorder; arteriosclerosis;

XX KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

XX KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

XX KW Parkinson's disease; Huntington's diseases; ovulatory defect;

XX KW muscular dystrophy.

XX OS Homo sapiens.

XX PN WO200000610-A2.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14484.

XX PR 26-JUN-1998; 98US-0090762.

XX PR 31-JUL-1998; 98US-0094983.

XX PR 01-OCT-1998; 98US-0102686.

XX PR 11-DEC-1998; 98US-0112129.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

XX PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

XX PI Bandman O;

XX DR WPI; 2000-160673/14.

XX DR N-PSDB; AA298157.

XX PT New human signal peptide-containing proteins useful in treatment,

XX PT prevention and diagnosis of e.g. cancer, inflammation and

XX PT cardiovascular disease -

XX PS Claim 1; Page 193-194; 327pp; English.

XX AA AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

XX CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have

XX CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,

XX CC neuroprotective, cardiovascular and antiasthmatic activities, and can

XX CC be used in gene therapy. HSPPs can be used to treat or prevent disorders

XX CC associated with decreased activity or function of HSPP. Antagonists of

XX CC HSPP are used to treat or prevent disorders associated with increased

XX CC activity or function of HSPP. Such diseases include cell proliferation

XX CC (including cancer), inflammation, cardiovascular, neurological,

XX CC reproductive or developmental disorders, (e.g. arteriosclerosis,

XX CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

XX CC asthma, Crohn's disease, microbial or other infections, congestive or

XX CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's

XX CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP

XX CC nucleic acids can be used for the recombinant production of HSPP, for

XX CC detecting HSPP in standard hybridisation and amplification assays (for

XX CC diagnosis and monitoring), in gene therapy, as antisense,

XX CC triplex-forming or ribozyme therapeutics, for detecting related sequences

XX CC or genetic variations, and for chromosomal mapping. HSPP are also used to

XX CC raise specific antibodies (Ab) and to screen for agonists and

XX CC antagonists (potential therapeutic agents). Ab are used to diagnose, or

XX CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic

XX CC antagonists, in competitive drug screens, and for purification of HSPP

XX CC from natural sources.

XX CC Sequence 185 AA;

Query Match 99.0%; Score 984; DB 21; Length 185;

Best Local Similarity 98.9%; Pred. No. 2.6e-93;

Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSCQSQSVSYNNEHVANVDNNNGWDSW 60

DB 1 mkftivfagllgvflapalanyndvddnnagsgqsgsvsnnehnvanvndnnngwds 60

QY 61 NSIWDYNGGFAATRLFOKKTICIVHKMKKEVMPISQSLDALVKREKKLOGKGGPPPKGLM 120

DB 61 nsiwdynggfaatrifqkttcivhkmkempsiqsladalvkeklqgkpgpppgkglm 120

QY 121 YSNPNKVDLDSKFGKNIANMCRGIPITYMAEQEASLFFYSGTCYTTSTVLWIVDISFCG 180

DB 121 ysnpnkvdldskfkgknianmcrgiptymaeenqeasllfysgtcyttstvlwivdisfcg 180

QY 181 DTVEN 185

DB 181 dtven 185

RESULT 4

AY66686

ID AAY66686 standard; protein; 185 AA.

XX AC AAY66686;

XX DT 05-APR-2000 (first entry)

XX DE Membrane-bound protein PRO1005.

XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

XX KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX PN WO9963088-A2.

XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99WO-US12252.

XX PR 02-JUN-1998; 98US-0087607.

XX PR 02-JUN-1998; 98US-0087609.

XX PR 02-JUN-1998; 98US-0087759.

XX PR 03-JUN-1998; 98US-0087827.

XX PR 04-JUN-1998; 98US-0088021.

XX PR 04-JUN-1998; 98US-0088025.

XX PR 04-JUN-1998; 98US-0088028.

XX PR 04-JUN-1998; 98US-0088029.

XX PR 04-JUN-1998; 98US-0088030.

XX PR 04-JUN-1998; 98US-0088033.

XX PR 04-JUN-1998; 98US-0088326.

XX PR 05-JUN-1998; 98US-0088167.

XX PR 05-JUN-1998; 98US-0088202.

XX PR 05-JUN-1998; 98US-0088212.

XX PR 05-JUN-1998; 98US-0088217.

XX PR 09-JUN-1998; 98US-0088655.

XX PR 10-JUN-1998; 98US-0088722.

XX PR 10-JUN-1998; 98US-0088730.

XX PR 10-JUN-1998; 98US-0088734.

XX PR 10-JUN-1998; 98US-0088738.

XX PR 10-JUN-1998; 98US-0088740.

XX PR 10-JUN-1998; 98US-0088741.

XX PR 10-JUN-1998; 98US-0088742.

XX PR 10-JUN-1998; 98US-0088810.

XX PR 10-JUN-1998; 98US-0088811.

XX PR 10-JUN-1998; 98US-0088824.

XX PR 10-JUN-1998; 98US-0088825.

XX PR 10-JUN-1998; 98US-0088826.

XX PR 11-JUN-1998; 98US-0088858.

XX PR 11-JUN-1998; 98US-0088861.

XX PR 11-JUN-1998; 98US-0088863.

XX PR 11-JUN-1998; 98US-0088876.

XX PR 12-JUN-1998; 98US-0089090.

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PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
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PR 18-JUN-1998; 98US-0089907.
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PR 19-JUN-1998; 98US-0089952.
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PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
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PR 24-JUN-1998; 98US-0090540.
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PR 25-JUN-1998; 98US-0090688.
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PR 25-JUN-1998; 98US-0090694.
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PR 25-JUN-1998; 98US-0090696.
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PR 26-JUN-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
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PR 02-JUL-1998; 98US-0091478.
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PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096013.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.

PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
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PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
XX N-PSDB; AA265023.
XX
XX Membrane-bound proteins and related nucleotide sequences -
XX
XX claim 12; Fig 139; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
XX Sequence 185 AA;

Query Match 99.0%; Score 984; DB 21; Length 185;
Best Local Similarity 98.9%; Pred. No. 2.6e-93;
Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKFTIVFAGLLGVFLAPALANYNDVNDNNAGSQQSQSVSVNHNHNVNDNNNGWSW 60
Db 1 mkftivfagllgvflapalanynvndnnnagsgqqsqsvsvnnhnvndnnngwds 60
QY 61 NSIWDYNGFGAATRLFKKTCIVHMKKEVMPISQSLALVKEKKLQKGGPGPPKGLM 120
Db 61 nsiwdyngfgaatrifkktciivhmkkevmvpsiqsldalvkekklqkgpgppkglm 120

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QY 121 YSNPNKVDLSKFGKNIAMCRGIPTYMAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysnpnkvddlskfgkniamcrgiptymaemqaslffysgtctttsvlwivdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 5
 ID AAB65209 standard; Protein; 185 AA.
 AC AAB65209;
 XX
 XX 02-APR-2001 (first entry)
 XX
 DE Human PRO1005 (UNC489) protein sequence SEQ ID NO:211.
 XX
 XX Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 XX 07-DEC-2000.
 XX
 XX 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.
 DR N-PSDB; AAF44169.
 XX
 XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 139; 935pp; English.
 XX

CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 185 AA;
 Query Match 99.0%; Score 984; DB 22; Length 185;
 Best Local Similarity 98.9%; Pred. No. 2.6e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTIVFAGLLGVFLAPALANYINDVDDNNNAGSQGSVSNVNEHHVANYVNDNNNGWDSW 60
 DB 1 mkftivfagllgvflapalanyinvddnnnagsgqgsvsnvnehhvanyvndnnngwdsw 60
 QY 61 NSIWDYGNCFATRLFOKKTCIVHKMKKEVMPISIGSLDALVKEKKLOGKPGPPKGLM 120
 DB 61 nsiwdyngngfaatrlfokktcivhkmkkevmpisigsldalvkekklqgkpgppkglm 120
 QY 121 YSNPNKVDLSKFGKNIAMCRGIPTYMAEEMQASLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysnpnkvddlskfgkniamcrgiptymaemqaslffysgtctttsvlwivdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 6
 ID AAB50957 standard; Protein; 185 AA.
 AC AAB50957;
 XX
 XX 21-MAR-2001 (first entry)
 XX
 DE Human PRO1005 protein.
 XX
 KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
 KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
 OS Homo sapiens.
 XX
 PN WO200073348-A2.
 XX
 XX 07-DEC-2000.
 XX
 XX 30-MAY-2000; 2000WO-US14941.
 PF
 XX 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-0140650.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.

PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-0187202.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
 PI Shelton DL, Smith V, Watanabe CK, Wood WI;
 XX
 DR WPI; 2001-016509/02.
 DR N-PSDB; AAC91559.
 XX
 XX Twenty eight nucleic acids encoding PRO polypeptides which are useful
 PT for treating various tumors, e.g. breast cancer, and other
 PT inflammatory, angiogenic and immunological disorders -
 XX
 PS Claim 31; Fig 14; 188pp; English.
 XX
 CC The present sequence is one of twenty eight novel PRO polypeptides. The
 CC PRO polypeptides and their agonists, including antibodies, peptides, and
 CC small molecule agonists, may be used to treat various tumours, e.g.,
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
 CC central nervous system cancer, melanoma or leukaemia. They are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
 CC blastocoeleic disorders, and inflammatory, angiogenic and immunological
 CC disorders.
 XX
 SQ Sequence 185 AA;
 Query Match 99.0%; Score 984; DB 22; Length 185;
 Best Local Similarity 98.9%; Pred. No. 2.6e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQSVSVNNEHNVANVDNNNGWDSW 60
 DB 1 mkftivfagllgvflapalanyninvddnnagsgqsvsvnnhnnvannvnnngwds 60
 QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLGKGGPPPKGLM 120
 DB 61 nsiwdynggfaatrllfkgttcivhkmknevmpsigsldalvkekklgkpgppkglm 120
 QY 121 YSVNPNKVDLKSFGKNANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysvnpnkvdldksfgknlanmcrgiptymaeemqeasiffysgtcyyttsvlwiwdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 7
 AAB38329
 ID AAB38329 standard; Protein; 186 AA.
 XX
 AC AAB38329;
 XX
 DT 31-JAN-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene 9 clone HNSAD53.
 XX
 KW Immunosuppressive; antiarthritic; antirheumatic; antiproliferative;
 KW cytosstatic; cardiant; vasotropic; cerebroprotective; neuroprotective;
 KW nootropic; antibacterial; virucide; fungicide; ophthalmological; human;

KW vulnery: gene therapy; infection; secreted protein.
 XX Homo sapiens.
 XX
 PN W0200061623-A1.
 XX 19-OCT-2000.
 XX
 XX 06-APR-2000; 2000WO-US08979.
 XX
 XX 09-APR-1999; 99US-0128693.
 PR 26-APR-1999; 99US-0130991.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Ni J, Komatsoulis GA, Rosen CA, Soppet DR, Shi Y;
 PI Lafleur DW, Olsen HS, Ebner R, Florence KA, Moore PA, Birse CE;
 PI Young PE;
 XX
 XX WPI; 2000-647418/62.
 DR
 XX New nucleic acid molecules encoding 62 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX
 XX Claim 11; Page 598; 716pp; English.
 XX
 CC Sequences AAB38321-B38396 represent the amino acid sequences of 62
 CC human secreted proteins encoded by the genes AAC69512-C69587. The genes
 CC and proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from
 CC a range of human tissues disclosed in the specification. The nucleic
 CC acids, proteins, antibodies and (ant)agonists are useful in the
 CC diagnosis, treatment and prevention of: (a) autoimmune diseases e.g.
 CC rheumatoid arthritis; (b) hyperproliferative disorders e.g. neoplasms
 CC of the breast or liver; (c) cardiovascular disorders e.g. cardiac
 CC arrest; (d) cerebrovascular disorders e.g. cerebral ischemia; (e)
 CC angiogenesis; (f) nervous system disorders e.g. Alzheimer's disease; (g)
 CC infections caused by bacteria, viruses and fungi; and (h) ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis.
 XX
 SQ Sequence 186 AA;
 Query Match 99.0%; Score 984; DB 21; Length 186;
 Best Local Similarity 98.9%; Pred. No. 2.7e-93;
 Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFTIVFAGLLGVFLAPALANYNDVDDNNAGSQSVSVNNEHNVANVDNNNGWDSW 60
 DB 1 mkftivfagllgvflapalanyninvddnnagsgqsvsvnnhnnvannvnnngwds 60
 QY 61 NSIWDYNGGFAATRLFKKTCIVHKMKKEVMPISQSLDALVKEKKLGKGGPPPKGLM 120
 DB 61 nsiwdynggfaatrllfkgttcivhkmknevmpsigsldalvkekklgkpgppkglm 120
 QY 121 YSVNPNKVDLKSFGKNANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCG 180
 DB 121 ysvnpnkvdldksfgknlanmcrgiptymaeemqeasiffysgtcyyttsvlwiwdisfcg 180
 QY 181 DTVEN 185
 DB 181 dtven 185
 RESULT 8
 AAW69974
 ID AAW69974 standard; Protein; 194 AA.
 XX

AC	AAW69974;	AC	AA76591;
XX		XX	
DT	16-NOV-1998 (first entry)	DT	10-APR-2000 (first entry)
XX		XX	
DE	Cancer associated protein.	DE	Human ovarian tumor EST fragment encoded protein 87.
XX		XX	
KW	Cancer; PCR; Northern blotting; ribonuclease protection assay;	KW	Expressed sequence tag; EST; human; ovarian tumor; anticancer;
KW	diagnosis; metastatic cancer.	KW	gene therapy; treatment.
XX		XX	
OS	Synthetic.	OS	Homo sapiens.
XX		XX	
PN	WO9837187-A1.	PN	DE19817557-A1.
XX		XX	
PD	27-AUG-1998.	PD	21-OCT-1999.
XX		XX	
PF	18-FEB-1998; 98WO-JP00667.	PF	09-APR-1998; 98DE-1017557.
XX		XX	
PR	21-FEB-1997; 97JP-0052508.	PR	09-APR-1998; 98DE-1017557.
XX		XX	
PA	(TAKI) TAKARA SHUZO CO LTD.	PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.
XX		XX	
PI	Asada K, Hino F, Kato I, Mukai H, Yoshikawa Y;	PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pillarsky C, Dahl E;
XX		XX	
DR	WPI; 1998-467552/40.	DR	WPI; 1999-591920/51.
XX		DR	N-PSDB; AA777487.
XX		XX	
PT	Detection of cancer cells in tissue samples - by changes in mRNA	PT	New nucleic acid sequences expressed in ovarian, and some other, cancer
PT	expression compared to normal tissue of specific cancer-associated	PT	tissues, and derived polypeptides, for treatment of ovarian cancer and
PT	gene sequences	PT	identification of therapeutic agents -
XX		XX	
PS	Claim 14; Page 64-65; 92pp; Japanese.	PS	Claim 25; Page 279; 310pp; German.
XX		XX	
CC	The cancer associated proteins AAW69974-W69976 where used in the method	CC	This invention describes novel nucleic acid (cDNA) sequences (A) which
CC	of the invention to detect cancer cells in tissue samples or biological	CC	have anticancer activity and are highly expressed in ovarian tumor
CC	fluids. They are detected by monitoring the change in mRNA expression	CC	tissue (and some also in testis and breast cancer tissue). The products
CC	as compared to normal tissue of one or more cancer-associated genes	CC	of the invention can be used for gene therapy. (A) are used (i) for
CC	whose cDNA stringently hybridises to cancer associated gene nucleic acid	CC	recombinant expression of polypeptides (B) and (ii) to isolate complete
CC	fragments. The change in expression may be an increase or a decrease	CC	genes. (B) are used (i) to identify agents suitable for treatment of
CC	compared to normal tissue. The mRNA expression may be determined by	CC	ovarian cancer; (ii) directly for treating this form of cancer
CC	PCR, Northern blotting or ribonuclease protection assay, or by	CC	(including expression from gene therapy vectors) and (iii) for generation
CC	determining the change in the amount of protein encoded by the gene(s) as	CC	specific antibodies. (A) are identified by assembling ESTs (expressed
CC	compared to normal tissue, for example by using a labelled antibody	CC	sequence tags) from a particular tissue type before comparison of
CC	recognising the protein. Detection of cancer cells for cancer diagnosis,	CC	expression patterns. This allows a significantly longer fragment of the
CC	including detection of metastatic cancer cells in tissues other than the	CC	gene to be revealed, so should reduce the number of failures associated
CC	primary tumour site.	CC	with the fact that ESTs from different libraries may represent different
XX		CC	parts of the same unknown gene, distorting the estimated frequency of
XX		CC	occurrence in a particular tissue. AA76505-Y76638 represent protein
XX		CC	fragments encoded by the human ovarian tumor cDNA library derived EST
XX		CC	fragments represented in AA77450-Z77572.
SQ	Sequence 194 AA;	SQ	Sequence 194 AA;
	Query Match 99.0%; Score 984; DB 19; Length 194;		Query Match 99.0%; Score 984; DB 20; Length 194;
	Best Local Similarity 98.9%; Pred. No. 2.8e-93;		Best Local Similarity 98.9%; Pred. No. 2.8e-93;
	Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		Matches 183; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	1 MKFTTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANDNNNGWDSW 60	QY	1 MKFTTIVFAGLLGVFLAPALANYNDVNDNNAGSQSQSVSVNNEHNVANDNNNGWDSW 60
DB	10 mkfttivrfaatrlfqqkktcihvkmmkevmpsigsldalvkekklqgkpgppkgglm 69	DB	10 mkfttivrfaatrlfqqkktcihvkmmkevmpsigsldalvkekklqgkpgppkgglm 69
QY	61 NSIWDYNGGFAATRLFQKKTCTIVHKKKEVMPSTOSLDALVKEKKLQCGPGPPPKGLM 120	QY	61 NSIWDYNGGFAATRLFQKKTCTIVHKKKEVMPSTOSLDALVKEKKLQCGPGPPPKGLM 120
DB	70 nsiwdynggfaatrlfqqkktcihvkmmkevmpsigsldalvkekklqgkpgppkgglm 129	DB	70 nsiwdynggfaatrlfqqkktcihvkmmkevmpsigsldalvkekklqgkpgppkgglm 129
QY	121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMQEAISFFYSYTCYTTSVLWIVDISFCG 180	QY	121 YSVNPNKVDLLSKFGKNIANMCRGIPTYMAEEMQEAISFFYSYTCYTTSVLWIVDISFCG 180
DB	130 ysvnpnkvdllskfgknianmcrgiptymaeemqeaiffysgcytttsvliwivdisfcg 189	DB	130 ysvnpnkvdllskfgknianmcrgiptymaeemqeaiffysgcytttsvliwivdisfcg 189
QY	181 DTVEN 185	QY	181 DTVEN 185
DB	190 dtven 194	DB	190 dtven 194
RESULT 9			
AA76591			
ID	AA76591 standard; Protein; 194 AA.		
XX			

RESULT 10
AA166690
ID AA166690 standard; protein; 184 AA.
XX
AC AA166690;
XX
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO813.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping.
XX
XX Homo sapiens.
XX
PN WO9963088-A2.
XX
XX
PD 09-DEC-1999.
XX
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087755.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096778.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096899.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.

Query Match	19.0%	Score 189;	DB 22;	Length 184;
Best Local Similarity	27.1%	Pred. No. 2.2e-11;		
Matches	52;	Conservative	40;	Mismatches 78; Indels 22; Gaps
Qy	1	MKFTIVFAGLLGVFLAPALANYNTDNDNNAGSGQGSVYNNEHNVANVDNNNGDSW	60	
Db	1	mkilvafvlvllfigiqshgyevfnliispsmgngvqetvtdnektainvnhagsscs	60	
Qy	61	NSTWDYNGFGAATRFQKKTCIVHMKKEVMPYSIQSLDALVREKKLOGKPGGPPKGLM	120	
Db	61	ttifdykghyiasrvlsrracfilkmdhqnippnlmlwyiekqaldn-----m	110	
Qy	121	YS-----VNPKNVDDLK-----FGKNIANMCRGIPTYMAEMOPASLFFYSGTCYTT	160	
Db	111	fsnkytwrkynplesiikldvdwflilgspilekchiplkyg-evventhnvgagcakag	160	
Qy	170	VLMVINDISFGD	181	
Db	170	llqilqisicad	181	

RESULT	12	
AAAM23556		
ID	AAAM23556 standard; Protein; 184 AA.	
XX		
XX	AAAM23556;	
XX		
DT	12-OCT-2001 (first entry)	
XX		
DE	Human EST encoded protein SEQ ID NO: 1081.	
XX		
KW	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;	
KW	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;	
KW	diagnostics; forensic test; gene mapping; genetic disorder;	
KW	biodiversity; gene therapy; nutrition.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200154477-A2.	
XX		
PD	02-AUG-2001.	
XX		
PF	25-JAN-2001; 2001WO-US02687.	
XX		
PR	25-JAN-2000; 2000US-0491404.	
PR	17-JUL-2000; 2000US-0617746.	
PR	03-AUG-2000; 2000US-0631451.	
PR	15-SEP-2000; 2000US-0663870.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;	
PI	Cao Y, Drmanac RA, Zhang J, Werhman I;	
XX		
XX	WPI; 2001-476164/51.	
DR	N-PSDB; AAH98215.	
XX		
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising	
PT	antibodies and research use -	
XX		
PS	Claim 20; Page 814-815; 1275pp; English.	

The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.

AA	
SQ	Sequence
	184 AA:

Query Match	18.9%;	Score 188;	DB 22;	Length 184;
Best Local Similarity	26.6%;	Pred. No. 2.8e-11;		
Matches	51;	Conservative 41;	Mismatches 78;	Indels 22; Gaps 4;
Qy	1	MKFTIVFAGLLGVFLAPALANYNDIVDDNNNAGSQGSVSVNNEHNVANYDNNNGWDSW	60	
		: : : : : : : : : : : : : : : : : : :		
Db	1	mkilvavflvltifgigshgyevfnllspnngnvgvctvtdnektalinihagsscs	60	
Qy	61	NSIWDYGNCFATRLFOKKTCIVHKMKKEVMPSTQSISDALYKEREKKGKPGGPPPKGLM	120	
		: : : : : : : : : : : : : : : : : : :		
Db	61	ttifdykhgyiasrvlsrtafcilkmhqnpinniqliwyiekqaldn-----m	110	
Qy	121	YS-----VNPKNVDLSK-----FGNIANNCRGITPYMAEEMQERSLFFYSTGCTVTTTS	169	
		: : : : : : : : : : : : : : : : : : :		
Db	111	fsskytwvknpyllesllkdvdfllgspiekickhiplkyg-evventhnvgaggcagak	169	
Qy	170	VLWIVDISFCGD	181	
		: : : :		
Db	170	llqllqisicad	181	
		: : : :		

RESULT	13	
AAE04211		
ID	AAE04211	standard; Protein; 184 AA.
XX	XX	
XX	AAE04211;	
XX		
09-AUG-2001	(first entry)	
DT		
XX		
DE	Human gene 14	encoded secreted protein HNSAA27, SEQ ID NO:66.
XX		
KW	Human;	secreted protein; proliferative disorder; cancer; tumour;
KW	foetal abnormality;	developmental abnormality; haematopoietic disorder;
KW	immune system disorder;	AIDS; autoimmune disease; rheumatoid arthritis;
KW	inflammation; allergy;	neurological disorder; Alzheimer's disease;
KW	Parkinson's disease;	cognitive disorder; schizophrenia; asthma;
KW	skin disorder;	psoriasis; sepsis; diabetes; atherosclerosis;
KW	cardiovascular disorder;	angiogenic disorder; kidney disorder;
KW	gastrointestinal disorder;	pregnancy-related disorder; gene therapy;
KW	endocrine disorder;	infection; wound healing; vulnerability;
KW	cell culture; chemotaxis;	food additive; chromosome 2;
KW	binding partner identification.	
KW		

OS	Homo sapiens.	
XX		
FX	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/label= signal_peptide
FT	Protein	21..184
FT		/note= "Mature secreted protein"
XX		
PN	WO200136432-A2.	

WO200136432-A2.

XX	25-MAY-2001.
XX	
XX	
PF	15-NOV-2000; 2000WO-US31162.
XX	
XX	
PR	19-NOV-1999; 99US-0166415.
PR	30-JUN-2000; 2000US-0215136.
XX	
XX	
PA	(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Komatsoulis GA, Baker KP, Young PE;
 WPI: 2001-343793/36.
 N-PSDE: AAD08501.

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

AAID08488-AAID08529 represent cDNAs corresponding to 18 human secreted protein genes, and AAEE04199-AAEE04239 represent the proteins they encode. AAEE04240-AAEE04297 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to culture, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

Sequence 184 AA;

```

Query Match      18.9%: Score 188; DB 22; Length 184;
Best Local Similarity 26.6%; Pred. No. 2.8e-11;
Matches 51; Conservative 41; Mismatches 78; Indels 22; Gaps 4;

Qy 1 MKETIVFAGLIGVFLAPALANYINDVNDNNAGSGOOSVNVNEHNVANVDNNNCWDSW 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 mkilvafvlvflfigiqshgyevfnlispnsgnvgvqetvidnektainihagscas 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 NSTWDYNGNGFAATRLFQKKTCIVHMKKEVWPSTQSDALVKKKKLQGGGPPPKGLUM 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 ttifdykhyiasrvlsrracfilkmdbhqnlpphnnlqwyiekqaldn-----m 110
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 YS-----VNPKNVDLSK-----FGKNIANMCRGIPTTYMAEQEASLFFYSQTCYTTS 169
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 fsksytwkynpieslikdvdvllqspieklckhpiylkg-evventhnvgaggcakag 169
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 170 VLWIVDISFCGD 181
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Db 170 llglldisicad 181
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RESULT 14

AAE04233
ID AAE04233 standard; Protein: 184 AA.

AA
AC
AAE04233;

09-AUG-2001 (first entry)

XX
DE Human gene 14 encoded secreted protein HNSAA27, SEQ ID NO:88.

Human; secreted protein; proliferative disorder; cancer; tumour;
foetal abnormality; developmental abnormality; hematopoietic disorder;
immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
inflammation; allergy; neurological disorder; Alzheimer's disease;
Parkinson's disease; cognitive disorder; schizophrenia; asthma;
skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
cardiovascular disorder; angioenic disorder; kidney disorder;
gastrointestinal disorder; pregnancy-related disorder; gene therapy;
endocrine disorder; infection; wound healing; vulvuary;

cell culture; chemotaxis; food additive; chromosome 2; binding partner identification.

Homo sapiens.

Key peptide	Location/Qualifiers
protein	1..20 /label= signal_peptide 21..184 /note= "Mature secreted protein"

WO200136432-A2.

25-MAY-2001.

15-NOV-2000: 2000WO-US31162.

19-NOV-1999: 99US-0166415.

30-JUN-2000; 2000US-0215136.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Baker KP, Young PE,

WPI; 2001-343793/36.

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used in preventing, treating or ameliorating a medical condition

protein genes, and AAEO4199-AAEO4239 represent the proteins they encode. AAEO4240-AAEO4267 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 18 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin ageing due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

Sequence 184 AA;

every match 18.9%; Score 188; DB 22; Length 184;

Very Match	18.9%;	Score 100; BD 22;	
Best Local Similarity	26.6%;	pred. NO. 2.8e-11;	
Matches	51;	Conservative	41; Mismatches 78;
			Indels 22; Gaps 4;

1 MKFTIVFAGLLGVFLAPALANYNIDVNDNNAGSGOOSVSVNNEHNVANVDNNNGWDSW 60

1 mkilvaf|vyl|t|f|a|a|s|h|a|v|e|v|f|n|i|s|p|s|n|g|a|p|v|a|e|t|v|t|d|n|e|k|n|t|a|i|i|h|a|q|s|c|s|s| 60

Thu Sep 5 11:23:27 2002

GenCore version 4.5
Copyright (C) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:05:07 : Search time 34.18 Seconds
(without alignments)
209.570 Million cell updates/sec

Title: US-09-821-726-13
Perfect score: 994
Sequence: 1 MKFTIVFAGLLGVFLAPALA.....YTTSLVIMVDSIFCGDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	984	99.0	199	1 CLIP_HUMAN	Q9ns71 homo sapien
2	629	63.3	184	1 CLIP_MOUSE	Q9cr36 mus musculu
3	95.5	9.6	719	1 NRPI_YEAST	P32770 saccharomyc
4	91	9.2	623	1 PNT1_DROME	P51022 drosophila
5	91	9.2	718	1 PNT2_DROME	P51023 drosophila
6	84.5	8.5	189	1 YHCN_BACSU	P54598 bacillus su
7	82.5	8.3	858	1 YHCN_DICDI	Q03101 dictyosteli
8	82	8.2	220	1 NUOB_ECOLI	P33598 escherichia
9	81	8.1	666	1 YEAT_YEAST	P40002 saccharomyc
10	81	8.1	828	1 MRKC_KLEPN	P21647 klebsiella
11	80	8.0	695	1 DVLL_MOUSE	P51141 mus musculu
12	80	8.0	695	1 DVLL_RAT	Q9wvb9 rattus norv
13	80	8.0	749	1 MADL_YEAST	P04957 saccharomyc
14	80	8.0	954	1 XYNA_RUMFL	P23126 ruminococcu
15	79	7.9	535	1 ARSB_FELCA	P33727 felis silve
16	77.5	7.8	1178	1 PH81_YEAST	P17442 saccharomyc
17	77.5	7.8	1341	1 YL78_YEAST	Q05854 saccharomyc
18	77	7.7	1675	1 POL_RTBPV	P27502 rice tungro
19	75.5	7.6	191	1 PSCP_MACMU	P55152 macaca mula
20	75.5	7.6	296	1 DPSP_CLOPA	Q46192 clostridium
21	75.5	7.6	731	1 BAF1_YEAST	P14164 saccharomyc
22	75.5	7.6	2021	1 OMPA_RICCN	Q52657 rickettsia
23	75	7.5	1584	1 KYK1_DICDI	P18160 dictyosteli
24	74.5	7.5	457	1 YL62_UREPA	Q9pqy2 ureaplasma
25	74.5	7.5	818	1 PTK2_YEAST	P47116 saccharomyc
26	74.5	7.5	1195	1 YK76_YEAST	P22335 saccharomyc
27	74	7.4	301	1 HSF2_LYCPE	P22335 lycopersico
28	74	7.4	1956	1 ATX1_PLAFA	Q04956 plasmodium
29	73.5	7.4	533	1 ARSB_HUMAN	P15848 homo sapien
30	73.5	7.4	537	1 ARP_PLAFA	P04931 plasmodium
31	73.5	7.4	758	1 YK38_YEAST	Q03825 saccharomyc
32	73.5	7.4	964	1 YIN0_YEAST	P40467 saccharomyc
33	73.5	7.4	2452	1 RPBI_PLAFD	P14248 plasmodium

34	73	7.3	1026	1 STAU_DROME	P25159 drosophila
35	72.5	7.3	398	1 LIPG_HUMAN	P07098 homo sapien
36	72.5	7.3	819	1 SWEL_YEAST	P32944 saccharomyc
37	72.5	7.3	920	1 NIA_CICIN	P43101 cichorium i
38	72.5	7.3	1238	1 YN13_YEAST	P53840 saccharomyc
39	72.5	7.3	1858	1 P3K2_DICDI	P54674 dictyosteli
40	72.5	7.3	2249	1 OMPA_RICRI	P15921 rickettsia
41	72	7.2	334	1 CHM1_HUMAN	O75829 homo sapien
42	72	7.2	335	1 CHM1_BOVIN	P17404 bos taurus
43	72	7.2	721	1 GLGX_MYCTU	Q10767 mycobacteri
44	71.5	7.2	340	1 BYRL_SCHPO	P10506 schizosacch
45	71.5	7.2	661	1 WHI3_YEAST	P34761 saccharomyc

ALIGNMENTS

RESULT	1
CLIP_HUMAN	
ID	CLIP_HUMAN
STANDARD:	PRT; 199 AA.
AC	Q9NS71;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	CAII protein.
GN	CAII.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
NP	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Stomach;
RX	MEDLINE=20296773; PubMed=10835488;
RA	Yoshikawa Y., Mukai H., Hino F., Asada K., Kato I.;
RT	"Isolation of two novel genes, down-regulated in gastric cancer.";
RL	Jpn. J. Cancer Res. 91:459-463(2000).
CC	-!- TISSUE SPECIFICITY: Expressed in stomach. No expression is
CC	detected in cancer tissue or gastric cancer cell lines.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL: AB039886; BAA92433.1; -.
DR	TM: 606402; -.
SQ	SEQUENCE 199 AA; 21999 MW; C095B8B9A1338D7A CRC64;

Query Match	99.0%; Score 984; DB 1; Length 199;
Best Local Similarity	98.9%; Pred. No. 4e-84;
Matches	183; Conservative
1; Mismatches	1; Indels
0; Gaps	0;
Qy	1 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSGQSVSVNNEHNVANVDNNGWDSW 60
Db	15 MKFTIVFAGLLGVFLAPALANYINDVNDNNAGSGQSVSVNNEHNVANVDNNGWDSW 74
Qy	61 NSIWDYNGNGFAATLRFQKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPPKGLM 120
Db	75 NSIWDYNGNGFAATLRFQKTCIVHKMKKEVMPSTQSLDALVKEKKLOGKPGGPPPKGLM 134
Qy	121 YSVNPNKVDLDSKFGKNTANCMRGIPTYMAPEMOEASLFFYSYTCYTTSVLWIVDVSFCG 180
Db	135 YSVNPNKVDLDSKFGKNTANCMRGIPTYMAPEMOEASLFFYSYTCYTTSVLWIVDVSFCG 194
Qy	181 DTVEN 185
Db	195 DTVEN 199

QY	120	MYSVNPVKVDLSKEGKNIANMCRGPIPTVMAEEMQASLFFYSCTYTSVLTWIDISFC	179
Db	118	MYSVNPTRVEDINTFGPKIAGMCRGPIPTVAAEIPGPNQPLYSKKCYTADILWILRMSFC	177
QY	180	GDVTE 184	
Db	178	GTSVE 182	
RESULT	3		
NRPI_YEAST		STANDARD;	PRT; 719 AA.
AC	P32770	012228;	
DT	01-OCT-1993	(Rel. 27, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DE	Asparagine-rich protein (ARP protein).		
GN	NRPI OR ARPI OR ARP OR YDL167C.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
OX	NCBI_TaxID=4932;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AH22;		
RX	MEDLINE=93247548; PubMed=8483449;		
RA	Wheener E.P., Rao E., Brendel M.;		
RT	Molecular structure and genetic regulation of SFA, a gene		
RT	responsible for resistance to formaldehyde in Saccharomyces		
RT	cerevisiae, and characterization of its protein product.;		
RL	Mol. Gen. Genet. 237:351-358(1993).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=S288C;		
RA	Pohl T.M.;		
RL	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: CONTAINS 2 RANBP2-TYPE ZINC FINGERS.		
CC	-!- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	-----		
DR	EMBL; X68020; CAA48159.1; -		
DR	EMBL; Z67750; CAA91579.1; -		
DR	EMBL; Z74215; CAA98741.1; -		
DR	PIR; S31139; S31139.		
DR	HSSP; F04170; 6RXN.		
DR	SGD; S0002326; NRPI.		
DR	InterPro; IPR000504; RRM.		
DR	InterPro; IPR001876; Znf-RanBP.		
DR	Pfam; PF00076; rrm.1		
DR	Pfam; PF00641; zf-RanBP; 2.		
DR	SMART; SM00360; RRM; 1.		
DR	SMART; SM00347; ZnfRBZ; 2.		
DR	PROSITE; PS50102; RRM; 1.		
DR	PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.		
DR	PROSITE; PS01358; ZF_RANBP2_1; 2.		
DR	PROSITE; PS50199; ZF_RANBP2_2; 2.		
KW	Nuclear protein; Zinc-finger; RNA-binding; Repeat.		
FT	DOMAIN 226 322		
FT	RNA-BINDING (RRM).		
FT	ZN_FING 355 384		
FT	ZN_FING 581 610		
FT	DOMAIN 490 564		
FT	ASN-RICH.		
FT	CONFLICT 493 493		
FT	I -> N (IN REF. 1).		
SEQUENCE	719 AA; 79299 MW; ADA9BC09FD582669 CRC64;		
Query Match	9.6%; Score 95.5; DB 1; Length 719;		

```

Best Local Similarity 25.5%; Pred.No.0.32;
Matches 40; Conservative 18; Mismatches 62; Indels 37; Gaps 5;

y 22 YNIDVNDNNAGSGOOSVSVNNEHN-----VANVDNNNGWDSWNSTW 64
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b 508 YNNININGNGNGNGNNNNNNHHHNSINSNTNNNNNNNNNNGNSNCNS 567
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y 65 DYNGCGFAATRL-----FQKTCIVHKMKKEVM-----PSIQSLDALYKEKKLOCK--G 110
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b 568 NIGMGCGSNPFPRAGDWKCSTCTTYHFAKNVVCRLCGGPKISGDASETNHYIDSFTFG 627
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y 111 PGPPPPGLMTSVNPN-----KYDDLSPKGKNIANM 141
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b 628 PASRTPSNNNISVTNNGGSNAGRDTGDNNGKRDISLM 664
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RESULT 4
NTL_DROME STANDARD; PRT; 623 AA.
D FNTI_DROME
C C P51022; P19420;
T T 01-NOV-1990 (Rel. 16, Created)
T T 01-OCT-1996 (Rel. 34, Last sequence update)
T T 01-MAR-2002 (Rel. 41, Last annotation update)
E ETS-like protein pointed Pl (D-ETS-2).
E PNT OR ETS58AB OR ETS2 OR CGI7077.
N Drosophila melanogaster (Fruit fly).
S Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
C Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
C Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
C Ephyrdoidea; Drosophilidae; Drosophila.
X NCBI_TaxID=7227;
X [1]
P SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
P MEDLINE=94038653; PubMed=8223245;
A Klammbt C.;
T "The Drosophila gene pointed encodes two ETS-like proteins which are
T involved in the development of the midline glial cells.";
T Development 117:163-176(1993).
T [2]
X SEQUENCE OF 456-613 FROM N.A.
X MEDLINE=92249640; PubMed=15717186;
X Chen T., Bunting M., Karim F.D., Thummel C.S.:
X "Isolation and characterization of five Drosophila genes that encode
X an ets-related DNA binding domain.";
X Dev. Biol. 151:176-191(1992).
X [3]
P SEQUENCE OF 445-603 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL
P STAGE.
X MEDLINE=88196618; PubMed=2834248;
X Pribyl L.J., Watson D.K., McWilliams M.J., Ascione R., Papas T.S.;
X "The Drosophila ets-2 gene: molecular structure, chromosomal
X localization, and developmental expression.";
X Dev. Biol. 127:45-53(1988).
X -1- FUNCTION: REQUIRED FOR GLIAL-NEURONAL CELL INTERACTIONS AT THE
X VENTRAL MIDLINE WHICH ARE NECESSARY FOR THE PROPER ELABORATION OF
X COMMISSURES IN THE EMBRYONIC CNS.
X -1- SUBCELLULAR LOCATION: Nuclear (Potential).
X -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; P1 (SHOWN HERE) AND P2 (AC
X P51023); ARE PRODUCED BY ALTERNATIVE SPLICING.
X -1- TISSUE SPECIFICITY: EXPRESSED IN A COMPLEX DYNAMIC PATTERN IN
X EARLY EMBRYOS, INCLUDING THE MIDLINE AND MIDLINE GLIAL CELLS.
X -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER
X LEVELS DURING LARVAL DEVELOPMENT.
X -1- SIMILARITY: BELONGS TO THE ETS FAMILY.
X -----
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X -----
X PMID: X69166; CAA48916.1; -.
X DR

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CC SYNDROME; ALSO KNOWN AS MUCOPOLYSACCHARIDOSIS TYPE VI (MPS-VI).
CC MPS-VI HAS BEEN DESCRIBED IN SIAMESE CATS.
CC -!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
CC -----
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DR EMBL; S48472; AAB23941.1; -.
DR PIR; A44475; A44475.
DR HSP; P15848; IFSU.
DR InterPro: IPR000917; Sulfatase.
DR Pfam: PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE_1; 1.
DR PROSITE; PS00149; SULFATASE_2; 1.
KW Hydrolase; Signal; Glycoprotein; Lysosome; Mucopolysaccharidosis.
FT SIGNAL 1 41 POTENTIAL.
FT CHAIN 42 535 ARYL SULFATASE B.
FT ACT_SITE 149 149 POTENTIAL.
FT MOD_RES 93 93 2-AMINO-3-OXOPROPIONIC ACID
FT (BY SIMILARITY).
FT DISULFID 119 523 BY SIMILARITY.
FT DISULFID 123 157 BY SIMILARITY.
FT DISULFID 183 194 BY SIMILARITY.
FT DISULFID 407 449 BY SIMILARITY.
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 428 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 535 AA; 59753 MW; 43A527886A9983C4 CRC64;

Query Match 7.9%; Score 79; DB 1; Length 535;
Best Local Similarity 27.0%; Pred. No. 7.7;
Matches 34; Conservative 18; Mismatches 40; Indels 34; Gaps 7;
Qy 43 NNEHNVANVDN-----NNGWD-----SWNSIWD---YGNQFAATRLFPQKTCIVHKMK 88
Db 293 NNTVFIFSTDNGGQTLAGGNWPLRGKW-SLWEGGIRGVGFVAPLLKOKGV----KNR 347
Qy 89 EVMPISQSLDALVREKKLQKGG-----PGGPPP-KGLMYSVNPKNVDDLSK 133
Db 348 ELIHSDWPLTVLKLARGSTKGTPLDGFVWKTISEGSPSPRKELLHNIDPNFVDISPC 407
Qy 134 FGKNIA 139
Db 408 PGKSLA 413

Search completed: September 4, 2002, 17:05:09
Job time: 1135 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:45:04 ; Search time 158.52 Seconds
(without alignments)
129.628 Million cell updates/sec

Title: US-09-821-726-13
Perfect score: 994
Sequence: 1 MKFTIVFAGILGVFLAPALA.....YTTSLWIVDISFCGDTVEN 185

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues 747574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	984	99.0	185	20	AAW99667 Human secreted pro
2	984	99.0	185	21	AAW99667 Human secreted pro
3	984	99.0	185	21	AAW99667 Human signal pepi
4	984	99.0	185	21	AAW99667 Membrane-bound pro
5	984	99.0	185	22	AAW99667 Human secreted pro
6	984	99.0	185	22	AAW99667 Human secreted pro
7	984	99.0	185	19	AAW99667 Human secreted pro
8	984	99.0	185	19	AAW99667 Cancer associated
9	984	99.0	185	20	AAW99667 Human ovarian tumo
10	189	19.0	184	21	AAW99667 Membrane-bound pro
11	189	19.0	184	22	AAW99667 Human PRO813 (UNO4

12	188	18.9	184	22	AAW23556 Human EST encoded
13	188	18.9	184	22	AAE04211 Human gene 14 enco
14	188	18.9	184	22	AAE04233 Human gene 14 enco
15	178	17.9	176	22	AAU29238 Human PRO polypept
16	154.5	15.5	147	22	AAE04294 Human gene 14 enco
17	95.5	9.6	719	22	AAW07000 S cerevisiae apopt
18	93	9.4	764	21	AAW18282 plasmodium falcipa
19	93	9.4	1176	21	AAW18280 plasmodium falcipa
20	91	9.2	718	22	ABW66061 Drosophila melanog
21	90	9.1	1245	21	AAW18244 plasmodium falcipa
22	88	8.9	286	22	AAW2761 Dictyostelium disc
23	84.5	8.5	2188	22	ABW60733 Drosophila melanog
24	84	8.5	1817	21	AAW18301 plasmodium falcipa
25	83.5	8.4	1979	21	AAW18171 plasmodium falcipa
26	81.5	8.2	537	7	AAW60452 Sequence of the As
27	80.5	8.1	447	17	AAW01622 Oyster pearl prote
28	80.5	8.1	652	18	AAW18010 plasmodium falcipa
29	80	8.0	280	21	AAW63197 Gene 21 human secr
30	80	8.0	695	22	AAW97560 Mouse Dishevelled-
31	80	8.0	954	21	AAW48550 Ruminococcus flave
32	79.5	8.0	943	22	ABW62085 Drosophila melanog
33	78	7.8	540	21	AAW18269 plasmodium falcipa
34	78	7.8	2539	21	AAW18198 plasmodium falcipa
35	77.5	7.8	1714	21	AAW18275 plasmodium falcipa
36	77	7.7	1316	21	AAW30505 A calcium-dependen
37	77	7.7	1337	21	AAW30504 A calcium-dependen
38	77	7.7	2010	21	AAW18218 plasmodium falcipa
39	76.5	7.7	642	22	ABW58549 Drosophila melanog
40	76.5	7.7	794	22	AAW00426 P. falciiparum telo
41	76	7.6	429	20	AAW04382 Potato isoamylase
42	76	7.6	477	22	AAW30815 Amino acid sequenc
43	75	7.5	289	17	AAW88025 Mature Pseudomonas
44	75	7.5	289	17	AAW88024 Mature Pseudomonas
45	75	7.5	289	17	AAW88023 Mature Pseudomonas

ALIGNMENTS

RESULT 1
AAW99667
ID AAW99667 standard; Protein; 185 AA.

AC AAW99667;

XX AAW99667;

XX AAW99667;

DT 07-JUN-1999 (first entry)

XX Human secreted protein clone ej90_5 protein.

DE Human; secreted protein; nutritional; cytokine; cell proliferation;
XX differentiation; immune stimulating; vaccine; haematopoiesis regulation;
KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
KW anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibition; gene therapy.

XX Homo sapiens.

XX W09907840-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16318.

XX 04-AUG-1998; 98US-0130189.

XX 06-AUG-1997; 97US-0906708.

XX (GEM) GENETICS INST INC.

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

PI Werberg D, Racie LA, Steininger RJ, Treacy M;

XX WPI; 1999-167419/14.

DR N-PSDB; AAW19493.

SEARCHING
Human genes

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 4, 2002, 16:45:05 ; Search time 158.52 Seconds
(without alignments)
128.927 Million cell updates/sec

Title: US-09-821-726-16
Perfect score: 993
Sequence: 1 MKLTFMFVGLGLAAPGFA.....TADILWLRLMSFCGTSVETY 184

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	64.5	185	20 AAW99667	Human secreted pro
2	640	64.5	185	21 AAB24067	Human PRO1005 prot
3	640	64.5	185	21 AAY87272	Human signal pepti
4	640	64.5	185	21 AAY66686	Membrane-bound pro
5	640	64.5	185	22 AAB65209	Human PRO1005 (UNQ
6	640	64.5	185	22 AAB50957	Human PRO1005 prot
7	640	64.5	186	21 AAB38329	Human secreted pro
8	640	64.5	194	19 AAW69974	Cancer associated
9	640	64.5	194	20 AAY76591	Human ovarian tumo
10	161	16.2	184	22 AAM23556	Human EST encoded
11	161	16.2	184	22 AAE04211	Human gene 14 enco

12	161	16.2	184	22 AAE04233	Human gene 14 enco
13	160	16.1	184	21 AAY66690	Membrane-bound pro
14	160	16.1	184	22 AAB52213	Human PRO813 (UNQ4
15	155	15.6	176	22 AAU29238	Human PRO polypt
16	138.5	13.9	147	22 AAE04294	Human gene 14 enco
17	93	9.4	618	22 ABB63927	Drosophila melanog
18	91	9.2	553	20 AAY55721	Human forkhead tra
19	91	9.2	553	20 AAY43260	Human FKHL7 protel
20	87	8.8	553	20 AAY41277	Human FREAC3 prote
21	85.5	8.6	335	22 AAB99941	Bovine chondromodu
22	85.5	8.6	346	15 AAB55059	Elk tyrosine kinas
23	85.5	8.6	346	17 AAR91930	Human cytokine elk
24	85.5	8.6	346	18 AAW36055	Human elk-L protel
25	85.5	8.6	346	18 AAW19249	Human elk ligand p
26	85.5	8.6	346	18 AAW44323	Human elk-L. Homo
27	84.5	8.5	539	22 AAU38216	Salmonella typhi c
28	83.5	8.4	782	11 AAR06991	Polypeptide anti
29	81.5	8.2	346	16 AAR82606	Eph transmembrane
30	80.5	8.1	2295	21 AAB18180	Plasmodium falcipa
31	80	8.1	95	22 ABB00897	Novel human diagno
32	80	8.1	2009	22 ABB64069	Drosophila melanog
33	79.5	8.0	82	21 AAY71436	Human ephrin B1 C-
34	79.5	8.0	106	21 AAB54187	Human pancreatic c
35	79.5	8.0	136	22 AAM37534	Peptide #11571 enc
36	79.5	8.0	1215	21 AAY55791	Superheat-resistan
37	79.5	8.0	1215	22 AAB84784	Pyrococcus heat re
38	79	8.0	334	17 AAW00287	Mouse Eph receptor
39	79	8.0	336	17 AAR92742	Murine hepatoma tr
40	77.5	7.8	334	22 AAB99943	Rat chondromodulin
41	77	7.8	619	22 ABB68682	Drosophila melanog
42	76	7.7	479	22 ABB01591	Novel human diagno
43	76	7.7	775	21 AAB36867	Human ECE-3 protel
44	76	7.7	775	21 AAB08132	A human neutral en
45	76	7.7	775	21 AAY15108	Endothelin convert

ALIGNMENTS

RESULT 1

AAW99667

ID AAW99667 standard; Protein; 185 AA.

XX AC AAW99667;

XX DT 07-JUN-1999 (first entry)

XX DE Human secreted protein clone ej90_5 protein.

XX KW Human; secreted protein; nutritional; cytokine; cell proliferation;

XX KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;

XX KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;

XX KW anti-inflammatory; cadherin; tumour invasion suppressor;

XX KW tumour inhibition; gene therapy.

XX OS Homo sapiens.

XX PN WO9907840-A1.

XX XX 18-FEB-1999.

XX PF 06-AUG-1998; 98WO-US16318.

XX PR 04-AUG-1998; 98US-0130189.

XX PR 06-AUG-1997; 97US-0906708.

XX PA (GEM) GENETICS INST INC.

XX PI Agostino MJ, Evans CA, Jacobs K, Lavallie ER, McCoy JM;

XX PI Merberg D, Racie LA, Steininger RJ, Treacy M;

XX DR WPI: 1999-167419/14.

XX DR N-PSDB; AAX19493.

Handwritten notes: "seq ID 18" and "seq ID 18" with arrows pointing to sequence entries.

134 roAsnLysValAspLeuSerLysPheGlyLysAsnIleAlaAsnMet 150
 463 TCGAAGGGATTCCACATACATGGCTGAAGAGATTCAAGGAGCAACCT 512
 151 CysArgGlyIleProThrTyrMetAlaGluGluMetGlnGluAlaSerLe 167
 513 GATTTCGTACTCAGAAAGTCATCAGTCGCAATATATCTCTGGATTCTTA 562
 167 uPhePheTyrSerGlyThrCysTyrThrThrSerValLeuTriPileValA 184
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seq_documentation_block:
 ID AAW99667 standard; Protein; 185 AA.

XX AC AAW99667;

XX DT 07-JUN-1999 (first entry)

XX DE Human secreted protein clone ej90_5 protein.

XX KW Human; secreted protein; nutritional; cytokine; cell proliferation;
 KW differentiation; immune stimulating; vaccine; haematopoiesis regulation;
 KW tissue growth; chemotactic; chemokinetic; haemostatic; thrombolytic;
 KW anti-inflammatory; cadherin; tumour invasion suppressor;
 KW tumour inhibition; gene therapy.

XX OS Homo sapiens.

XX PN W09907840-A1.

XX PD 18-FEB-1999.

XX PF 06-AUG-1998; 98WO-US16318.

XX PR 04-AUG-1998; 98US-0130189.

XX PT 06-AUG-1997; 97US-0906708.

XX PA (GEM) GENETICS INST INC.

XX PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, McCoy JM;

XX PI Merberg D, Racie LA, Steininger RJ, Treacy M;

XX PT WPI; 1999-167419/14.

XX DR N-PSDB; AAX19493.

XX PT New polynucleotides encoding secreted human proteins - derived from
 PT fetal kidney, adult testes, adult brain, adult heart, adult placenta
 PT or adult retina cDNA libraries

XX PS Claim 34; Page 98-99; 107pp; English.

XX CC The present sequence represents a human secreted protein. The secreted
 CC protein can have activities such as; nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The secreted
 CC protein polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. The
 CC polynucleotides are also stated to be useful for gene therapy.

XX SQ Sequence 185 AA;

alignment_scores:

77 Encodes SEQ ID 18

Quality: 775.00 Length: 185
 Ratio: 4.429 Gaps: 0
 Percent Similarity: 94.595 Percent Identity: 75.135
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 us-09-821-726-17 x AAW99667 ..

Align seg 1/1 to: AAW99667 from: 1 to: 185

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 1 MetCysPheThrIleValPheAlaGlyLeuLeuGlyValPheLeuAlaPr 17
 90 TGCCTTGTCTGACTATATAGTATCAGTGTCAACGACGACGCGCAACAGTGGT 139
 17 oAlaLeuAlaAsnTyrAsnIleAsnValAsnAspAsnAsnAlaG 34
 140 GAAGTGGGAGCAGTCAGTCAGTCGTCACAAATGACACACACACGTCGCCAAC 189
 34 lYserGlyGlnGlnSerValSerValAsnAsnGluHisAsnValAlaAsn 50
 190 GTTGACAATAACAATGGATGGAATCTCTGGAATGCTCTGGACTATAG 239
 51 ValAspAsnAsnAsnGlyTrpAspSerTrpAsnSerIleTrpAspTyrGl 67
 240 AACTGCTTTGCTGTACACGAGCTTTCGAGAGAGAGTGCATTCGCTGCTC 289
 67 YAsnGlyPheAlaAlaThrArgLeuPheGlnLysLysThrCysIleValH 84
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 84 lYsMetAsnLysGluValMetProSerIleGlnSerLeuAspAlaLeu 100
 340 GTCAAGAAAAGAGCTTCAGGCTAAGGCGCCAGGGGAGCCACTCCCAA 389
 101 ValLysGlnLysLysLeuGlnGlyLysGlyProGlyGlyProProPro 117
 390 GAGCCTCAGTACTACTAGTCAACCCCAACAGAGTCGACAACTGGACAA 439
 117 sGlyLeuMetTyrSerValAsnProAsnLysValAspAspLeuSerLysP 134
 440 TTGGAATTCATTCGTCGTCATGTCGAGGGGATTCACACATACATGCT 489
 134 heGlyLysAsnIleAlaAsnMetCysArgGlyIleProThrTyrMetAla 150
 490 GAAGAGATTCAGGAGCAACCTGATTTCGTAAGTCTCAGAAAAGTGCATCAG 539
 151 GluGluMetGlnGluAlaSerLeuPhePheTyrSerGlyThrCysTyrTh 167
 540 TGCCAATATATCTGGATTCCTTAACATTTCTCTGTGGAGGAATAGCGG 589
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seq_documentation_block:
 ID AAB24067 standard; Protein; 185 AA.

XX AC AAB24067;

XX DT 29-JAN-2001 (first entry)

XX DE Human PRO1005 protein sequence SEQ ID NO:34.

XX KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;

